

(2) INFORMATION ON SEQ ID NO. 83:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1890 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

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(2) INFORMATION ON SEQ ID NO. 84:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1829 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

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(2) INFORMATION ON SEQ ID NO. 85:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2358 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

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2358

(2) INFORMATION ON SEQ ID NO. 86:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1646 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

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1646

(2) INFORMATION ON SEQ ID NO. 87:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 3096 base pairs
 (B) TYPE: Nucleic acid.
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual
 ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

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3096

(2) INFORMATION ON SEQ ID NO. 88:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1906 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

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acagtataaa catattatcc acatgtaatc accaatagta aatgaagatg tttatgaact 960
ggcattagaa gctttctaaa ctgcgctgtg tgatgtgttc tatctagcct aggggaggac 1020
attgcctaga gggggaggga ctgtctgggt tcaggggcat ggccctgagg gctgggtggc 1080
agcactgtca ggcctcaggt tccctgctgt ttgctttctg ttgtgttat taagacttgt 1140
gtattttctt tctttgcttc ctgtcaccoc aggggctcct gagtataggg ttttcagttc 1200
ctgggcagtg tccctgagtt gttttttgac actcttacct gggcttctct gtgtgcattt 1260
gcgtctggcc tggagtaagc aggtccgacc cctcctcttt tacagcttag tgttattctg 1320
gcatttgggt aagctggctt aatctgttta atgttatcag tacattttta ataggggcat 1380

tgaaatttac tcccaccccc agggcttttt tgggggatgc ctgggccttt aaaaactag 1440
ccaaactcta attaattctc aaatcactgc caggagtctt tgctcctggc tgcaggccca 1500
ggccccaagg tctcctcttt ggggtcacaa acagcagtaa ggaaggagaa tatatagca 1560
ctcagggcct gggaaatttg gggcaatccg ttcttaggga ctggatactt ctggctgctg 1620
gagtatagta ctagctgcct ccccaccagg ttccagtagt tctctgagac tctgctctgc 1680
agggcctagg gttagcctcg gagtgtagaa gtggcctcct tctaactgtt ttcactaaac 1740
agctttttct aaggggagag caagggggag agactatag ttgggtgagg ggaaggaggt 1800
gtcaggggag caagtgtgtt gtgttactgt tccaataaac tgatttaag ttgtaaaaaa 1860
aaaaaaggag ggggggggtg agggggaggga gggggaaaaa aaaaaa 1906

```

(2) INFORMATION ON SEQ ID NO. 90:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

```

gctaagagga caagatgagg cccggcctct catttctcct agcccttctg ttcttccttg 60
gccaaagctgc aggggatttg ggggatgtgg gacctccaat tcccagcccc gggttcagct120
ctttccagg tgttgactcc agctccagct tcagctccag ctccaggctg gggtccagct180
ccagccgcag cttagggcag ggaggttctg tgtcccagtt gttttccaat ttcaccggct240
ccgtggatga ccgtggggacc tgccagtgtc ctgtttccct gccagacaac aactttcccg300
tggacagagt ggaacgtttg aattcacagc tcatagttaa ttctcagag 349

```

(2) INFORMATION ON SEQ ID NO. 91:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2142 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cdNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

```

cagaccaccaga aagtagtgac cagccctcct cggattacc ctcattggct cctcccttgc 60
gcgcgccacc ctccagattt gcataaaaaa ggccaagaaa actctggctg tgccccagca 120
acggctcatt ctgctcccc cgggtcggagc ccccccggagc tgccgcggcg cttgcagcgc 180
ctgcgcccg cgtgctctcc ggtgtcccg tctcccgcg cccagccgcg ggtctgccgc 240
ttttcggggc cccagagtcg acccagcgaa gagagcgggc cccgggacaa ctcgaaactcc 300
ggccgcctcg ccttcccccg gctccgctcc ctctgcccc tcggggctcg gcgcccacga 360
tgctgcaggg ccttggtctg ctgctgtctg tcttctctcg ctgcactctg tgcctgggct 420
cggcgccggg gctcttctct tttggccagc ccgacttctc ctacaaagcg agaattgcaa 480
gcccatcccg gccaacctcg agctgtgcca cggcatcgaa taccagaaca tgcgggtcgcc 540
caacctgctg gccccagaga ccatgaagga ggtgctggag caggccggcg cttggatccc 600
gctggctcat aagcagtgcc acccgggacac caagaagttc ctgtgctcgc tcttcgcccc 660
cgtctgcctc gatgacctag acgagaccat ccagccatgc cactcgctct cgtgtcaggt 720
gaaggaccgc tgcgcccccg tcatgtccgc ctctggcttc ccttgcccg acatgcttga 780
gtgcgacagt ttcccccagg acaacgacct ttgcatcccc ctgcgtagca gcgaccacct 840
cctgccagcc accgaggaag ctccaaaggt atgtgaagcc tgcaaaaata aaaatgatga 900
tgacaacgac ataatggaaa cgctttgtaa aaatgatttt gcactgaaaa taaaagttaa 960
ggagataacc tacatcaacc gagataccaa aatcatcctg gagaccaaga gcaagaccat1020
ttacaagctg aacggtgtgt ccgaaaggga cctgaagaaa tccgtgctgt ggctcaaa1080
cagcttgtag tgcacctgtg aggagatgaa cgcacatcac gcgcctctat tggctcatgg1140
acagaaacag ggtggggagc tgggtatcac ctccgtgaa cgggtgcaga aggggcagag1200
agagtccaag cgcacatccc gcagcatccg caagctgcag tgcagtccc ggcactctga1260
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ccgttcccc agcacactcc tagctgtctc agtctcagcc tgggcagctt cccctgcctc1380
tttgacgtt ttgcaccccc gcatttctgt agttataagg ccacaggagt ggatagctgt1440
tttcaacctaa aggaaaagcc caccggaatc ttgtagaat attcaaaata ataaaatcat1500
gaatatTTTT atgaagttta aaaaatagctc actttaaagc tagttttgaa taggtgcaac1560
tgtgacttgg gtcgtgttgg ttgtgttgg ttgttttgag tcagctgatt ttcacttccc1620
actgaggttg tcataacatg caaattgctt caattttctc tgtggcccaa acttgtgggt1680
cacaaacctt gttgagataa agctggctgt tatctcaaca tcttcatcag ctccagactg1740
agactcagtg tctaaagtctt acaacaattc atcattttat accttcaatg ggaacttaaa1800
ctgttacatg tatcacattc cagctacaat acttccattt attagaagca cattaacctat1860
ttctatagca tgattttctc aagtaaaagg caaaagatat aaattttata attgacttga1920
gtactttaag ccttgtttaa aacattttctt acttaacttt tgcaaattaa acccattgta1980
gcttacctgt aatatacata gtagtttacc tttaaaagtt gtaaaaatat tgccttaaac2040
aacaactgaa atatttcaga taaacattat attctgtgat ataaacttta catcctgttt2100
tacctataaa aaaaaaaaaa aaaaaaaaaa aaaaaaaggg aa 2142

```

(2) INFORMATION ON SEQ ID NO. 92:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1111 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

```

cgtgggcgaa catgggagct gttcctcgcg ggccgcggg tgctgggtcac cggggcgagc 60
aaaggtatag ggcgcgggcac ggtccaggcg ctgcacgcga cgggcgcgcg ggtggtggct 120
gtgagccgga ctcaggcgga tcttgacagc cttgtccgcg agtgcccggg gatagaaccc 180
gtgtgcgtgg acctgggtga ctgggaggcc accgagcggg cgctggggcag cgtgggcccc 240
gtggacctgc gcggagactg cgccgacatg gagctgttcc tcgcggggcgg ccgggtgctg 300
gtcacccggg caggcaaaag tataggcgcg ggcacgggcc aggcgctgca cgcgacgggc 360
gcgcgggtgg tggctgtgag ccggactcag gcggatcttg acagccttgt ccgcgagtgc 420
ccggggatag aacccggtg cggtggacctg ggtgactggg aggccaccga gcgggcgctg 480
ggcagcgtgg gccccgtgga cctgctggtg aacaacgcgc ctgtcgccct gctgcagccc 540
ttcctggagg tcaccaagga ggcctttgac agatcctttg aggtgaacct cgtgctggtc 600
atccaggtgt cgcagattgt ggccaggggc ttaatagcgc ggggagtcgc aggggccatc 660
gtgaatgtct ccagccagtg ctcccagcgg gcagtaacta accatagcgt ctactgctcc 720
accaagggtg ccttgacat gctgaccaag gtgatggccc tagagctcgg gccccacaag 780
atccgagtgat atgcagtaaa ccccacagtg gtgatgacgt ccatggggca ggccaacctg 840
agtgaccccc acaaggccaa gactatgctg aaccgaatcc cacttggcaa gtttgctgag 900
gtagagcacg tgggtaacgc catcctcttt ctgctgagtg accgaagtgg catgaccacg 960
ggttcacatt tgccggtgga agggggcttc tggggcctgct gagctccctc cacacacctc 1020
aagcccatg ccgtgctcat cctaccccca atccctccaa taaacctgat tctgctgccc 1080
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa g
1111

```

(2) INFORMATION ON SEQ ID NO. 93:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 657 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

```

atttaaagcc tggattgtaa ccagattttc ttttttcccc cttctcagct gtagatatga 60
tatctccttt cagggccccc gcttaagggc aaagtgtggt aatgtgtaga caaaggcga120
ggacaagaga gaggtaacat ctgacagctg gaaaaagcca tgggtgtgtg tttctggga180
ccaccaacac ttgcaggttt agctttttcc caggggtgac tacaagaaag aaaaccatgt240
ttttgcaaga ttaaaatgtg gttgagtgtg cctaaattaa ccatcccat ttttatcata300
tttccaccat cacttcaggg ttttaagagt cagtgtccac ctggggcgac tggtagtaca360
ttttgtctct tagaaagcta agtcctgggt tccgtctgat tttaggttcc aggaacttcc420
tgagaacacc cgatcgaga gggtaatttt ctggagtttg ttttgcaggg atagctggga480
gtatggccac cctgtccac gatgcggtaa tgaatccagc agaagtgtg aagcagcgct540
tgcagatgta caactcgag caccggtcag caatcagctg catccggacg gtgtggagga600
ccgaggggtt gggggccttc taccggagct acaccacgcc gagccctatc tcgtgcc 657

```

(2) INFORMATION ON SEQ ID NO. 94:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 863 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

```

ggcggtcggtg  gtgcggcgct  gtttaaagat  ggcggcggag  gaacctcagc  agcagaagca  60
ggagccgctg  ggcagcgact  ccgaaggtgt  taactgtctg  gccctatgatg  aagccatcat  120
ggctcagcag  gaccgaattc  agcaagagat  tgctgtgcag  aacctctctgg  tgtcagagcg  180
gctggagctc  tcggtcctat  acaaggagta  tgctgaagat  gacaacatct  atcaacagaa  240
gatcaaggac  ctccacaaaa  agtactcgta  catccgcaag  accaggcctg  acggcaactg  300
tttctatcgg  gctttcggat  tctccactt  ggaggcactg  ctggatgaca  gcaaggagtt  360
gcagcggttc  aaggctgtgt  ctgccaaag  caagggaagac  ctggtgtccc  agggcttcac  420
tgaattcaca  attgaggatt  tccacaacac  gttcatggac  ctgattgagc  aggtggagaa  480
gcagacctct  gtgcgcgacc  tgctggcctc  cttcaatgac  cagagcacct  ccgactacot  540
tgtgtgtcac  ctgcggtgc  tcacctcggg  ctacctgcag  cgcgagagca  agttcttcga  600
gcacttcac  gaggggtggc  ggactgtcaa  ggagttctgc  cagcaggagg  tggagcccat  660
tgccaaggag  agcgaccaca  tcacatcat  tgcgtggcc  caggccctca  gcgtgtccat  720
ccaggtggag  tacatggacc  gcggcgagg  cggcaccacc  aatccgcaca  tcttccctga  780
gggcttcga  gcccaaggtc  ttaccttgt  ttaaccggt  tggggcaatt  taggtattgc  840
tttttcaaaa  taggggtttg  gtt

```

863

(2) INFORMATION ON SEQ ID NO. 95:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1015 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

```

aattcggaac gaggcgccct gcaagccatg atgacccacc tgcattgtgaa gtctacagaa 60
cccaaaagctg cccctcagcc cctgaatctg gtatcaagtg tcacccctctc caagtccgca 120
tcgggaggctt ctccacagag cttacctcat actccaacga ccccaaccgc cccctcgact 180
cccgctaccc aaggccccc tgtcatcaca accccaagca tgcacacggt gggacccatc 240
cgcaggcgggt actcagacaa atacaacgtg cccattttctg cagcagatat tgcgcagaac 300
caagaatttt ataagaacgc agaagttaga ccaccattta catatgcata ttttaattagg 360
caggccattc tcgaatctcc agaaaagcag ctaacactaa atgagatcta taactgggtc 420
acacgaatgt ttgcttactt ccgacgcaac gcggccacgt ggaagaatgc agtgcgtcat 480
aatcttagtc ttcacaagtg ttttgtgcga gtataaaaacg ttaaaggggc agtatggaca 540
gtggtatgaag tagaattcca aaaaacgaag ccacaaaaga tcagtggtaa ccttccctt 600
attaaaaaca tgcagagcag ccacgcctac tgcacacctc tcaatgcagc tttacaggct 660
tcaatggctg agaatagtat acctctatac actaccgctt ccatgggaaa tcccactctg 720
ggcaacttag ccagcgcgaat acgggaagag ctgaacgggg caatggagca taccaacagc 780
aacgagagtg ccacagctcc aggcagatct cctatgcaag ccgtgcattc tgtacacgtc 840
aaagaagagc ccttcgatcc agaggaagct gaagggcccc tgtccttagt gacaacagcc 900
aaccacagtc cagattttga ccatgcaga gattacgaag atgaaccagt aaacgaggac 960
atggagtgac tatcggggag ggccaacccc gagaatgaag attggaaaaa aaaaa 1015

```

(2) INFORMATION ON SEQ ID NO. 96:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2532 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

```

gctcgatgtg caagtgaagg atgattccag ggccttgact ttagaggcac tgacgtgcc 60
tctggccccc ctgctgactg ccccgaaact catcctggac cagtgggtcc agctcagcag 120
ctctgggtcca aactccagac actgctcatg aggatcctgt acttggattc 180
atcagaaaaa tgcctcccca cggtgctctg ttgtcctcgt gcttggggagc tggacagtga 240
gaatcccccag agaggcagca gtgtggatgc cccacttcga cgcctcctga 300
tagccagttt gggactgagc atgtgcttcg gatccatgta ttagaggccc aggaacctgat 360
tgccaaagac cgtttcttgg ggggactggg gaaggccaag tcagaccctc atgtcaaac 420
aaagtgtggca ggcagaaagt tccggagcca tgttgttcgg gaagatctca atccccgctg 480
gaatgaggtt tttgaggtga tctgcacatc agtccaggc caagagctag aggttgaagt 540
ctttgacaag gactttggaca aggatgattt tctgggcagg tctcaccac 600
agtcttaaac agtggcttcc ttgatgagtg gctgacctg gaggatgtcc catctggccg 660
cctgcacttg cgcctggagc gtctcaccoc ccgtccact gctgctgagt tagaggaggt 720
gctgcagggt aatagtttga tccagactca gaagatgctg gagctggctg cggccctgct 780
atccatctat atggagcggg cagaggacct cccgctcgca aaagggccca agcacctcag 840
cccttatgct actctcactg tgggagatag ttctcataaa accaagacta tttcgcaaac 900
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tcaggggcagc gtgtcactga gagcacagct agggatctct gtgtcccaagc actcgggagt 1140
ggaaagctcat agccacagct acagccacag ctctctcatc ctgagtgaag aaccagagct 1200
ctcggggggga ccccttcaca tcacctctc agccccagag ctccggcgagc gctaacaca 1260
tgtttgacagt ccccttgagg ctccagccgg gccctctggg cagggtgaac tgactctgtg 1320
gtactacagt gaagaacgaa agctggtcag cattgttcat gggtgccgtt ccttcgaca 1380
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gtttgagttg gaaactcccc tggatgaggg ccagagacga aagctggatg tctctgcaal 1560
gtctaatctc tcttctatgt caagagagcg tgactgctgg ggaaggtgca gctggacctal 1620
gctgagacag acctttccca ggggttagcc cgggtgtatg acctgatgga caacaaggac 1680
aagggcagct cctaggagct ggcgagctcc agcctgactg ctctgtcttc ctgccttcgt 1740
ctcgctccat caccgcctca atgtgatgag cctaagacta ggggtccaagg gcagagcctg 1800
tgcccttcag ccccttcacc taacaggccc atattcgggc ctttgctcta ccaagaagaa 1860
gaaccgtatg ttccctttac tgcacggcct ttatccttct gggccctctg ggcggggacc 1920
tgagctggct gtttctcgtt ttgcctgcac attgttctcc ctctctccca actcctcagg 1980
gccttctgtg tctgtcgtct gccagtggca gcactagcag tggattatga tttatgcaaa 2040
tacagctttg gaaggaattt ttttcttta actagatggt caccttcttc cctaccaca 2100
atgggtggga aggtggacag gctaacctct ccagctgtga cctctttaga ctactgcatt 2160
tagcaaatgt tcagcagctc agggccccc atgtcagttct gtccccactg tctcacaacc 2220
tgctcctgaaa attctactgc ttgatggct ggggccagtc tcttgtcact tgggaaacct 2280
aggaacgcgtg gttctacttc aagcctccaa gtatggcat gatcctcttg gagctcctag 2340
ctggtgatac ggagagggct ttggaggact tgggacagca gggccaattt ttttgcccaa 2400
gtgcataagg tctaactca ctgactagaa cttaattctg tactttacac ttttgacca 2460
acctctccaa gccactggat cttacattaa acatcatact caaaaaaaaa aaaaaataaa 2520
ataaaaaaaaa aa

```

2532

(2) INFORMATION ON SEQ ID NO. 98:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 776 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```

tttttttttt tttttttttt tttttttttt ttttgagaca aagtctcact gtgtcaccca 60
gactggaatg cagtgacaca atctcggttc actgaaacct ctgacctcca gggtcaagct120
attctcatcg ctccagcctct caagtagctg ggactacaga tgtggggccc catgtctggc180
taattttttt ttttttttgt agagacaggg ttctcgccatg ttgacgagac tggctctgaa240
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gagccactga gctcgccctt gaagcggttt tctcaaaagg cctcagtgag ataaattaga360
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ctcacacccc ctgatgtttg aagagttcca agttgaaggg aaacaaagaa gtgtttgatg600
gtgccagaga ggggctgctc tccagaaagc taaaatttaa tttctttttt cctctgagtt660
ctgtacttca accagcctac aagctggcac ttgctaacaa atcagaaata tgacaattaa720
tgattaaaga ctgtgattgc caccaaaaaa aaaaaaaaca gccagggaaa aaaggg 776

```

(2) INFORMATION ON SEQ ID NO. 99:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 629 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

```

cggtctgact tccgttactt gctgctggagg accgtgggca gccaggggtcg gtgaaggatc 60
ccaaaatggc tgggcgaaaaa cttgctcttaa aaaccattga ctgggtagct tttgcagagal20
tcatacccca gaacccaaaag gccattgcta gttccctgaa atcctggaat gagaccctcal180
cctccagggt ggctgcttta cctgagaatc caccagctat cgactgggct tactacaagg240
ccaatgtggc caaggctggc ttggtggatg actttgagaa gaagttaaatt gcgctgaagg300
ttcccgctgc agaggataaa tatactgcc ccagggtgatgc cgaagaaaaa gaagatgtga360
aatcttgtgc tgagtggtgtg tctctctcaa aggccaggat tgtagaatat gagaaagaga420
tggagaagat gaagaacctta attccatttg atcagatgac cattgaggac ttgaatgaag480
ctttcccgaga aaccaaatta gacaagaaaa agtatcccta ttggcctcac caaccaattg540
agaatttata aaatttgatc caggagggaag ctctggccct tgtattacac attctggaca600
ttaaaaaataa taattatata aaaaaaaaaa

```

629

(2) INFORMATION ON SEQ ID NO. 100:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 757 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

```

ggcgggggagc aggggggacac caggggtgaat caggaagacc cgaggggttg ccccccacct 60
ttctccaccc acgcggcagg ttccagggtgc cctggctgga gtcagtccct atcgtagtca120
gcaacaacat tgacgaggag gcgctggccc gactggccca ggagggcagt gaggtgaatg180
tcattggcat tggcaccagt gtggtcacct gcccccaca gcccttcctg ggtggcgtct240
ataagctggt ggcggtgggg ggcagccac gaatgaagct gaccgaggac cccgagaagc300
agacgttgcc tgggagcaag gctgctttcc ggtcctctgg ctctgacggg tctccactca360
tgacatgct gcagttagca gaagagccag tgccacaggc tgggcaggag ctgagggtgt420
ggcctccagg ggcccaggag ccctgcaccg tgaggccagg ccagggtggag ccactactgc480
ggctctgctt ccagcaggga cagctgtgtg agccgctccc atccctggca gagtctagag540
ccttgggcca gctgtccctg agccgactca gccctgagca caggcggctg cggagccctg600
cacagtacca ggtggtgctg tccgagaggg tgcaggccct ggtgaacagt ctgtgtgagg660
ggcagtcctc ctgagactcg gaggggggt gactggaaac aacacgaatc actcactttt720
ccccacagga agaggaggtg agggaagagg ggggggcg

```

(2) INFORMATION ON SEQ ID NO. 101:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1262 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

```

aatttgttga agagtgtattc tccctcatcc tctgcaaaaca ttccataggc gataggaaga 60
actatgcttc tgccaagctt tctgagttgc tgccagaaga agttgaagca gaagtgaag 120
cagctgcaga gatatacaatg ggaacagagg ttccagaaga agatattttgc aatatctctgc 180
atcttttgcac ccaggtgtatt gaaatctctg aatatcgaac ccagctctat gaatatctac 240
aaaatcgaat gatggccatt gcacccaatg ttacagtcatt gggtggggaa ttagtggag 300
cacggcttat tgctcatgca ggttctcttt taaatttggc caagcatgca gcttctaccg 360
ttcagatttct tggagctgaa aaggcacttt tcagagccct caaatctaga cgggataccc 420
ctaagtatgg tctcatttat catgcttcac tcgtgggcca gacaagtccc aaacacaaa 480
gaaagatttc tcgaatgctg gcagccaaaa ccgcttttggc tatccgttat gatgcttttg 540
gtgaggattc aagttctgca atgggagttg agaacagagc caaattagag gccaggttga 600
gaacttttga agacagaggg ataagaaaaa taagtggaa aggaaaagca ttagcaaaaa 660
cagaaaaata tgaacacaaa agtgaagtga agacttacga tctctctggt gactccacac 720
ttccaaacctg ttctaaaaaa cgcaaaatag aacaggtaga taaagaggat gaaattactg 780
aaaagaaagc caaaaaagcc aagattaaag ttaaagttag agaagaggaa gaagaaaaag 840
tggcagaaga agaagaaaca tctgtgaaga agaagaagaa aaggggtaaa aagaaacaca 900
ttaaggaaga accactttct gaggaagaac catgtaccag cacagcaatt gctagtccag 960
agaaaaagaa gaaaaagaaa aaaaagagag agaacgagga ttaacagaaa ggaattacga 1020
ttatatcacc cggacacaca tcatgcttaa gattcaactg ggagcatacc agggatgtct 1080
tctaacgtta tcaagggagg gttcagtaag acaaagtgat ttatcatcta taacttcaaa 1140
cctatttttg tcgacatcaa ctctgttaac cttatgtcat ctttcttag agtctttgag 1200
atacaataaa aattttcttt gtatttttaa acaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1260
aa

```

(2) INFORMATION ON SEQ ID NO. 102:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1281 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

```

ggcggaagta gccgcaggca tggcgccggc tatgccgctg ttgctctgct cgtcctgttg 60
ctcctggggc ccggcgggctg gtgccttgca gaacccccac gcgacagcct gcggggaggaa 120
cttgctcatca ccccgctgcc ttccggggac gtatgcccca cattccagtt ccgcacgcgc 180
tgggattcgg agcttcacgg ggaaggagtg tcccattaca ggctctttcc caaagccctg 240
gggcagctga tctccaagta ttctctacgg gagctgcacc tgtcattcac acaaggcttt 300
tggaggaccc gatactgggg gccacccttc ctgcaggccc catcaggtgc agagctgtgg 360
gtctggttcc aagacactgt cactgatgtg gataaatctt ggaaggagct cagtaatgtc 420
ctctcaggga tctctgcgc ctctctcaac ttcatcgact ccaccaacac agtcactccc 480
actgcctcct tcaaacccct gggtctggcc aatgacactg accactactt tctgcgctat 540
gctgtgctgc cgcggggagg gtctgcacc gaaaacctca cccctggaa gaagctcttg 600
ccctgtagtt ccaaggcagg cctctctgtg ctgctgaagg cagatcgctt gtccacacc 660
agctaccact cccaggcagt gcataccgc cctgtttgca gaaatgcacg ctgtactagc 720
atctcctggg agctgaggca gacctgtca gttgtatttg atgccttcac cacggggcag 780
ggaagaaag actggctcct ctcccgatg ttctccgaa cctcacgga gccctgcccc 840
ctggcttcag agagccgagt ctatgtggac atcacacct acaaccagga caacgagaca 900
ttagagggtc accaccccc gaccactaca tatcaggacg tcactcctagg cactcggaag 960
acctatgcca tctatgactt gcttgacacc gccatgatca acaactctcg aaacctcaac1020
atccagctca agtggaagag accccagag aatgaggccc cccagtgcc ctctctgcat1080
gcccagcggg actgtgagtg ctatgggctg cagaaggggg agctgagcac actgctgtac1140
aacacccacc cagtaccggg ctcccggtg ctgctgctgg acacgtacc ctggatatctg1200
cggctgttac atccactacc agcctgcccc ggacgggctg caacccacc tctctggagat1260
gctgattcac ctgccggcca a

```

(2) INFORMATION ON SEQ ID NO. 103:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 716 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

```

gggccccaga aagagaccaa tgtgtgtgtgc gacgggtggg tggcagtgcc agtggcagat 60
ggtaccaggg gccccagaaac cttaaggggg ctcaagtagt ttaaaacccc ggagggtgcc120
tgaacttgggg ccaaggggttt ctatgctcag gcttgacccc tcatggatta gtttctgctg180
gaaaaacttt ttctgccttc ggccaggctct ctatctcctt ctgccttaac atattttgga240
aggttgggttc ccagcagaga cggggccatg ggctcacact ctgacctctc ccacggcatt300
agccctgtct cagcctctgg gctgttacgc aagttaattc ctgcacaaga ctcaacaacag360
ggctgtggag gaagcaaaagg agcccttttt atgcctctgt agtaggaact agagagggccc420
tctggccagg gtgagcctgc tggttcttcc cggactgtac caggccttga ggccgggtat480
ggaaacgccc cactctgggg Cctggcttgg ggaaggggag gcggcagggg ttctttgggc540
ttctcgaggg tataatctga gctctctggg gaacgtgtgt ccattttagt gcagtagtcc600
gacacgtcgg gggactcaac tttaactcgt gacaatctgt gtgtggtctg tttttagaa660
attcatccac acaagagagt ggaggcatga acaggggtgg ccttctctcg atctca 716

```

(2) INFORMATION ON SEQ ID NO. 104:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1160 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

```

tttgttgttg gagaaaggag agaaaggaaa gcgcgagggg ccgcccggcc caccagcgca 60
gagtctctga gctgtgagga gattcggggc gtcaccctgc ctcccctcgg tcccggcacc 120
ggccgcttct gtctctggac ccattccaac aatctcgtaa aacatggtgg attactatga 180
agtcttagcg gtgcagagac atgcctcacc cgaggatatt aaaaaggcat atcggaact 240
ggcactgaag ttgcatccag ataaaaatcc tgagaataaa gaagaagcag agagaaaaatt 300
caagcaagta gcggaggcat atgaaagtgc tgcggatgct aagaaaacggg acatctatga 360
caaatattgg aaagaaggat taaattggtg aggaggaggt ggaagtcaatt ttgacagctc 420
atttgaattt ggcttccatc tccgtaaccc agatgatgct ttcagggaaat tttttggtgg 480
aagggaccoca ttttcatatt acttctttga agaccctttt gaggactctc ttgggaatcg 540
aaggggtccc cgaggaagca gaagccgagg gacggggtcg tttttctctc cgttcagtg 600
atttccgtct ttggaagtg gattttcttc ttttgataca ggatttactt catttgggtc 660
actaggtcac gggggcccca ctctcattct tccaacgtca tttggtggtg ttggcagtg 720
caacttcaaa tcgatataca ctccaactaa aatggttaat ggcagaaaaa tcactacaaa 780
gagaattgtc gagaacggtc aagaaaggat agaattgaa gaagatggcc agttaaagt 840
cttaacaata aatggtgtgg ccgacgacga tgccctcgct gaggagcgca tgcggagagg 900
ccagaaagccc ctccagcccc agcctgcggg cctccgcccc ccgaagccgc cccggctcgc 960
ctcgtctgct agacacggcg ctcaactgtc ctctgaggag gaggggcagc aggaaccgacc1020
tggggcaccc gggccctcgg accccctcgg cgtccgcagc aggattgaaa gaaggtggca1080
agaggaagaa gcagaagcag agagaggagt ttgaaggagg aaggaagtgt gaccaaaggc1140
attgattaga ccggaatttt

```

(2) INFORMATION ON SEQ ID NO. 105:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

```

agcatccgct tccggttccc agactgaatt gtcagtgcgc ggagtctgag gtcgctgtgg 60
actgcccact gggccttgcc cgagatggac agccggattc cttatgatga ctaccogggtg 120
gttttcttgc ctgacctatga gaatcctcca gcatggattc ctctcatgag gagggtacac 180
cacccggaact acaacaatga gttgacccag tttctgcccc gaacctcac actgaagaag 240
cctcctggag ctacagttggg atttaacatc cgaggaggaa aggcctccca cttaggcac 300
ttcatctcca aggtgatctc tgactctgat gcacatagag caggactgca ggaaggggac 360
caagtcttag ctgtgaatga tgtggatttc caagatatgg agcacagcaa ggtgtgtgag 420
atcctgaaga cagctcgtga aatcagcatg cgtgtgcgct tctttcccta caattatcat 480
cgccaaaaag agaggactgt gcatagaaa gttgcagccc acagcccttc atgtggactc 540
tgtcatgaca tgctaactag acttcagggg agccacttct gtttcagccc cctccctgga 600
atagtgaagt gggaggatgg ggagacagct aaccaactgc attaccacaa ccatattgca 660
cttttagttc cctagttttc taggtgagct tcattccctg aaaggaggat gatgatct 720
aggcataacc tagcctgtga ggaacctagt taggaaagac aactgacatt tattgaatat 780
catgcactag tcccttacct atgtcatatt ttaattatag aaatcagtag caaaaagaat 840
cttggggatt ttccatctga ctccctgggc catcttatcc catccttgca ctaccagaag 900
attcatacac ttttgagact ccagtgagac gctgttttca ccccttcttc ctccctgacct 960
ctctcccaaa aagtaaaaca caatgctgaa gaaaaaaa aaaaaaaa aaaaaggggg 1020
gggccggccg gtgggtggcc

```

1040

(2) INFORMATION ON SEQ ID NO. 106:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1336 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

```

cgagggacag aacctggtgc aggaggagtt ggcggcccgcc gggaccacgc ccccggtccat 60
ccgcaacggc ctggacaacag ccgcgaggtc cgcttcgagc gagctgagca ggcctcgccg 120
cggttcagcc agggcccccac acccgctgcc gctgtcccg agggcacggc agccgagggc 180
gctcccaggc agggaaaactg tggtgcccag cagggtccccg caggccgggc actgacacc 240
ctcccagcag ccccgctgccc acctgcgggc cctgacgga tgaggacgtg gtcagggtgc 300
ggcctgtga gaagaagcgg ctggacatcc gtggcaaat ttacctggcc cccctcacca 360
cgtgtgggaa cctgcccttc cgacggatct gcaagcgctt cggggcgcat gtgacatgtg 420
gagagatggc cgtctgcacc aacctgctgc agggccagat gtccgagtg gccctactca 480
aacgccacca gtgtgaggac atctttggcg tcacgctgga gggcgccctc ccgacacca 540
tgaccaagtg tgccgagctg ctgagccgca ccgtggaggt ggactttgtg gacatcaacg 600
tcggctgccc catcgacctc gtgtacaaga aggggtggggg ctgtgccctc atgaatcgct 660
ccaccaagt tccagcagatc gtcctgggca tgaaccaggt gctggatgtg ccgctgactg 720
cacaggcgtc cacaggcgtg caggagcgtg tgaacctggc gcaccgctg ctgcccgagc 780
tgccggactg gggcggtgca ctgctcaccg aaatggggac atcttgatct ttgaggatgc 840
caaccgcgcc atgcagactg gtgtcaccgg gatcatgatt gcccggtggc cctgtgctaa 900
gccgtggtct ttcaaggaga tcaaggagca gcggcaactg gacatctcgt cgtccgagcg 960
cctggacatc ctgcgggact tcaccaacta cggcctggag cactggggct cggacacgca 1020
ggcgctggag aagaccggcg gctttctgct cgagtggctg tcttctctgt gccggtacga 1080
tccggtgggg ctgctggagc ggctccaca gaggatcaac gagcgccgcg cctactacct 1140
ggcccgagac tacctggaga cgctgatggc cagccagaag gcagccgact ggatccgcat 1200
cagcagatg ctctctgggc cagtgcctcc caccctcgct tcttgccgaa gcacaaggcc 1260
aacgcgtaca agtagcctca ggctttccca gggggcaccct ggggcgagga gagtacaata 1320
aattttatct ttttaa
1336

```

(2) INFORMATION ON SEQ ID NO. 107:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 812 base pairs
 (B) TYPE: Nucleic acid

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

```
ggcagcccaa tgtctcctgc acgtgcaatg caaacgctct ttgttcaga gcatggagat 60
cacggagctg gagtttgttc agatcatcat catcgtgggtg gtcaogtgcc tgcagagccal20
ctacaagctg tctgcacggt ccttcacacg cgggacacgc caggggaggga ggagagaaga180
tgccctgtcc tcagaaggat gcctgtggcc tcggagacac agtgtcaggc aacggaatcc240
cagagccgca gtcttacgcc ccgctcgggc ccaccgaccg cctggccgtg cgcccttcgc300
ccagcggagc gttttccacc gttgccagcc caatgtctcc tgcacgtgca actgcaaacg360
ctctttgttc cagagcatgg agatcacgga gctggagttt gttcagatca tcatcatcgt420
ggtggtcagc tgcctgctga gccactacaa gctgtctgca cggctcctca tcagccggca480
cagccagggg cggaggagag aagatgccct gtccctcaga ggatgcctgt ggcctcggca540
gagcacagtg tcagggaacg gaatcccaga gccgcaggtc tacgccccgc ctccggccac600
cgaccgctg gccgtgccc ccttcgccca ggggagcgc ttcacccgct tcacgcccac660
ctatccgtac ctgcagcagc agatcgacct gccgccacc atctcgtgtg cagacgggga720
ggagcccca ccctaccagg gccctgggac cttcaaggtt cgggacccc aggaggagtt780
ggaattgaa cggggattgg gtgcggagac cc
```

812

(2) INFORMATION ON SEQ ID NO. 108:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 2681 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

gatgcttggt	atcatcatca	tgatgacgct	gtgtgaccag	gtggatattt	atgagtgcct	60
ccatccaag	cgcaagactg	acgtgtgcta	ctactaccag	aagttctctg	atagtgcctg	120
cacgatgggt	gcctaccacc	cgctgctcta	tgagaagaat	ttggtagaagc	atctcaacca	180
gggcacagat	gaggacatct	acctgcttgg	aaaagccaca	ctgcttggt	tccggaccat	240
tactctgtaa	gcacaggctc	ctcactcttc	tccatcaggc	attaaatgaa	tggctctctg	300
gccaccccag	cctgggaaga	acattttcct	gaacaattcc	agcctgctcc	ttttactcta	360
ggggcctctg	tcagcaagac	catggggact	tcaagagcct	gtggccaagg	aatcagggtc	420
agccttccct	gtagccagac	agtttatgag	cccagagcct	ctgcccacac	acatgcacac	480
atatctagca	ttctttccag	acagcatcct	ccccgccttc	caacctggta	gatgcaaggt	540
ctatctctcc	catcagggtc	gccaaagctg	ggctttgttt	ttcccagcag	aatgatgcca	600
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aggtgttaca	ggggatttga	aacatgctcc	gcgcctccag	agaaaagtgt	ctcccagggt	780
ccatgcccc	ggaacgtgtt	cctcatcctc	tggctgggtg	ggctggtctc	tagactgggt	840
gcttatgatt	aaagggtctt	ggttagccca	ctttccctct	ccatgtggag	atggaaggt	900
gagaaggata	cagtgtctat	cctcaagtgt	ctacggttca	gtgagagagg	cagacatctg	960
aacaggcagg	taggatctag	tgtgctcagt	gcactgggga	tttgagaga	gatgggcttg	1020
ctctctctgt	gcacccagg	gggccacgca	cttaaaactg	tgtttgtgga	tcagagaagg	1080
ctttatagca	cagggggcat	tcagatgagt	cttagaggaa	gagaagaaac	atggcaagca	1140
gattacatct	gagccgtttg	aattgtgttt	ttctttcttc	ccatgtttat	tttctaagat	1200
ctacctgaac	ttagagactc	aagatatttt	tttaggaaac	ctcctaccca	tgtctgaggt	1260
agcaagtgc	gcctcacgac	agataccagg	caatccagag	ccacaaaacg	tgattcctcc	1320
aggctctgcc	tggcctgacc	ctgtcctgtc	agctgggttt	acataccagt	ccattctctc	1380
cttttcaata	aataccccca	aatctttctc	taaccaccat	taaagcattt	tttgtcttaa	1440
aagcatcctg	acccccattt	ctttgagctc	acgggccttt	tgtggaaggt	ctctcagggt	1500
gtagtgggtg	ggctctctgg	acttaacgtc	actctcagag	gtcagaacct	tggagatcag	1560
aactgattct	caccagggtg	gagaggtgtg	gtagcagatt	gcaatgctct	gcacctcttc	1620
cttgcgaagt	agcaacttca	ggctctctgg	gcagaggctg	gcccactgta	gtttgcagac	1680
atgctctcca	gatggtttta	ctaaagtcct	tctcctgat	agggaaatcct	gctgggaccag	1740
cgacgctctg	gtgtggagag	gttaaaaagc	ttgcacagga	tcaccaagtc	atgctgtaga	1800
gccagggattc	ctagaccagag	ggctctgcac	tctcaaggct	ggccccatgt	gctcaagggg	1860
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ccctcagctt	atgtagctag	aaagggccct	ggagtggaga	agcctggatt	ttcaaatgga	1980
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caoctgtcct	ggctctgtac	ctggcacgta	gtagggtgct	agttctcctg	ggttctcttc	2160
ctgctctttg	tagggacctg	ctctgtgctc	acacctcgcc	tgcatgcacc	ctgctgtgac	2220
ggagacttag	gtgggaagag	tctgtctctc	agggaaattaa	ctgtcttatt	gggagacaac	2280
aactgtctctc	cttgggaacac	ccaagaaaacc	atgcaaaagca	gttgacaaca	cagaaacgcg	2340
ctctctctctc	gctcgtcgca	gctccaatct	gattctgctt	gggaatgggc	gggacacgtg	2400
ggctcgttaa	ctgctgtata	ggacaagccc	cttaccctct	tctgggccca	tgaattcctg	2460
gcttctgttta	tgttctgatt	tgacacactg	atttttaact	ctgaatcatg	acactgagtg	2520
cacagaggagt	ggcattccga	cagcaggaca	tacatgttgg	tgtgaagact	gggacagcac	2580
tgggtagaat	ctagttttta	attattatta	atataaagga	tcaaaattat	ttaaaatgag	2640
atccgaagtc	cacagaactt	taagtgtctg	gcggccatgt	t		2681

(2) INFORMATION ON SEQ ID NO. 109:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1407 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

```

cttgggacgg aagcctagct ggggtggggg cccggggctg gagccttcgc aggggagcgg 60
gtccagtcac caccctgcgc cccagagtga ctccagcccc acgtcccccac ccattccccgg 120
ggagccaggg ccgcagaggg aggtagataa gtgggggtgc agcctgggtc ggccagagag 180
ttcaggccac cccggccggg cgcctgccac ttgctgtcac tgtgccgctg tcatggcagc 240
ctccgggagt gccacggcac ctgccggggc tccgggagcc cctccacgga gccccaccca 300
gaggctggta caggatgtca gtgggcccc gtgggagctg cgccttcggc tctgccacct 360
gcgaaaggga cctcagggct atgggttcaa cctgcatagt gacaagtccc ggccccggca 420
gtacatccgc tctgtggacc cgggctcacc tgccgccccc tctggcctcc gcgccaggga 480
ccggctcatt gaggtgaacg ggcagaatgt ggagggactg cgcctatgct aggtggtggc 540
cagcatcaag gcacgggagg acgaggcccg gctgctgtgc gtggaccccc agacagatga 600
acacttcaag cggcttcggg tcacacccac cgaggagcac gtggaaggtc ctctgcctgc 660
accctgcacc aatggaacca gccctgccca gctcaatggt ggctctgcgt gctcgtcccc 720
aagtgcacct cctggttccg acaaggacac tgaggatggc agtgccctga agcaagatgc 780
cttcaggaga agcggcctcc acctgagccc caccggcgcc gaggccaaag agaaggctcg 840
agccatgcga gtcaacaacg cgcgcgcaca gatggaactg aacaggaagc gtgaaatctt 900
cagcaacttc tgagccctt cctgcctgtc tcgggacccct cgggacccctc ccgcacggac 960
cttggggctc agcctgcgcc gagctccccc agcctcagtg gactggaggg ttgctctgcc 1020
attgccaga aatcagcccc agccccgggt gtcgccctgc ctgccctgc ccaccaggta 1080
ctgggggctc gtggcagcaa gataggggga gagagaccca gagatgtgag agagagtcag 1140
agacagagac agagagagag acagagagag acagagagag agcgagcgag 1200
cgcggggcag ccgcggggcg agggcctttg ctgctctgcc ggggcctgct gactgaaagg 1260
aatttgtgtt tttgtttttt ttccaaaaag atctccagct ccacacatgt ttccacttaa 1320
taccagagac cccccccgtc aaagcccccc tcccggcccc cttgggacgc gctctaaata 1380
attgcaataa aacaacacct tctctgc

```

1407

(2) INFORMATION ON SEQ ID NO. 110:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1376 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

```

cgaagaagcc ccgccccgtc cgccttagac aatgccccgg agccgcccaga ccgtcgcgcc 60
cctgccccat cgtagtatat gagctcgcc acacaaggac ccccgctaaa agccagagct 120
cccagtcgcc gaggcttgaa gacggggact cctcttcca ccaactctgt cctcgggggg 180
tggggcccca gccagatca cagcgcgaca ggagtggggg tggccgctgg agacaggtga 240
agaaaacaaga aaactaagaa atccgagcgg ttgagggggg agtctgtgtg gatgggatgg 300
ggacgcgggg ggaggggctg gcccgctgct cccatgccct gatccgggga gtcccagaga 360
gcctggcgctc gggggaaggt gccggggctg gccttccgcg tctggatctg gccaaagctc 420
aaagggagca cgggtgctg ggaggtaaac tgaggcaacg actgggggta cagctgctag 480
aactgccacc tgaggagtca ttgcgctgg gaccgctgct tggcgacacg gccgtgarcc 540
aaggggacac ggccctaata acgcggccct ggagcccccg tcgtaggcca gagtgcgatg 600
gagtcgcgaa agccctgcga gacctggggc tccgaattgt ggaaatagga gacgagaacg 660
cgacgctgga tggcactgac gttctcttca ccggcccgga gtttttcgta ggccctctca 720
aatggaccaa tcaccagga gctgagatcg tggcggacac gttccgggac ttcgccgtct 780
ccactgtgcc agtctcggtt cctccaccac tgcgcggtct ctgcgcgatg gggggacctc 840
gcactgttgt ggcagggcagc agcgacgctg cccaaaaggc tgtccgggca atggcagtcg 900
tgacagatca cccatatgcc tccctgaccc tcccagatga cgcagctgct gactgtctct 960
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aagtagaagg ggaaggaggg ttagatagag aatgctgaat aggcagtagt tgggagagag 1260
cctcaatatt gggggagggg agagtgtagg gaaaaggatc cactgggtga atctccctc 1320
tcagaaccaa taaaatagaa ttgacctttt aaaaaaaaa aaaaaaaaa agttct 1376

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(2) INFORMATION ON SEQ ID NO. 111:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 854 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

```

acgtatagtc  gggctcggtcgt  gtggagtagc  tcagagtagg  gggagcgccg  taattgacac  60
atctcttatt  tgagaagtgt  ctgttggcct  cattaggttt  aattacaaaa  ttgtatcacg  120
atcatattgt  agtctctcaa  agtgctctag  aaattgtcag  tggtttacat  gaagtggcca  180
tgggtgtctg  gagcaccctg  aaactgtatc  aaagtgttac  atatttccaa  acatttttaa  240
aatgaaaagg  cactctcgtg  ttctctcac  tctgtgcact  ttgctgttgg  tgtgacaagg  300
catttaaaag  tgtttctggc  attttctttt  tattgttaag  gtggttgtaa  ctatggttat  360
tggctagaaa  tctctgagtt  tcaactgtat  atatctatag  ttgttaaaaa  gaacaaaaac  420
accgagacaa  acccttgatg  ctcttgctc  ggcgttgagg  ctgtggggaa  gatgcctttt  480
gggagaggct  gtagctcagg  gcgtgcactg  tgaggctgga  cctgttgact  ctgcaggggg  540

catccattta  gcttcaggtt  gtcttgtttc  tgtatatagt  gacatagcat  tctgtgcca600
tcttagctgt  ggacaaaagg  gggtcagctg  gcatgagaat  attttttttt  ttaagtgcgg  660
tagtttttaa  actgtttgtt  tttaaacaaa  ctatagaact  ctctattgtc  agcaaaagca  720
agagtcactg  catcaatgaa  agttcaagaa  cctcctgtac  tttaaacaga  ttcgcaact780
tctgttattt  tttttgtatg  tttagaatgc  tgaaatgttt  ttgaagttaa  ataacagta840
ttacattttt  aaaa

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854

(2) INFORMATION ON SEQ ID NO. 112:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1681 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

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ttcagctttt gccgaaatgg gtagtgatca cacacagtca tctgcaagca aaatctcaca 60
agatgtggac aaagaggatg agtttggtta cagctggaaa aatcagagag agcgtttatgg 120
aacccctaaca ggcgagctgc atatgattga actggagaaa ggcatagtg gtttgggcoct 180
aagtctctgct gggaacaaaag accgatccag gatgagtgtc ttcatagtgg ggattgatcc 240
aaatggagct gcaggaaaaag atgggtcgatt gcaaaattgca gatgagcttc tagagatcaa 300
tggtcagatt ttatatggaa gaagtcatca gaatgcctca tcaatcatta aatgtgcccc 360
ttctaaggatg aaaataattt ttatcagaaa taaagatgca gtgaatcaga tggccgtatg 420
tcctggaaat gcagtagaac ctttgccttc taactcagaa aatcttcaaa ataaggagac 480
agagccaact gttactactt ctgatgcagc tgtggacctc agttcattta aaaatgtgca 540
acattctgga gcttcccaag gaggcagggg ggtttgggta ttgctatcag cgaagaagat 600
acactcagtg gagtcacat aaagagctta acagagcatg gggtagcagc cacggatgga 660
cgactcaaa gtcggagatca gatactggct gtagatgatg aaattgttgt tggttaccct 720
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gaaggagcag catgtaaaga tggaaagactc tgggctggag atcagatctt agaggtgaat1140
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cagagagctgc gcctgacact ctacagagat gaggccccat acaaaagagg ggaagtgtgt1260
gacacccctca ctattgagct gcagaagaag ccgggaaaaa gcctaggatt aagtattgttl320
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gcgatggaa gactgatgca gggagaccag atattaatgg tgaatgggga agacgttccgt1440
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cttgggaagt tgggaaggat tcaaagctgg gtcccgtccc gtttcaggag gagggagggt1560

cgtttttcaa aggcagccca gggttgagtt tgaaggggca gcctctttcg tcttttttca1620
cgtttttccc acttttttgg ggatccccct ttacattttg agttccactt ggaggagttal680
9

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1681

(2) INFORMATION ON SEQ ID NO. 113:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 852 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

```

ggcaatttcc gttaggtgct gaaggctgtg gcgcgcggct gtccccattc ccacgtgaag 60
cgctacgcta gcatcgctcg gctggcggct ccacagctcg cgcgagcag tcccggcagc120
agcgggggac cggaagtggc tcgcggaggc tcagaagcta gtcccgagc ccggcgtgtg180
gcgcctcgga gcacggtgac ggcgcctatg ccctaactct ctccatctct aacgaagtgc240
cggagcaccc atgtgtatcc cctgtctcta atcatgttta tgagcggcgg ctcacgcaga300
agtacattgc ggagaatggt accgacccca tcaacaacca gcctctctcc gaggagcagc360
tcacgcacat caaagtgtgt cacccaatcc ggcccaagcc tccctcagcc accagcatcc420
cggccattct gaaagctttg caggatgagt gggatgcagt catgctgcac agcttcactc480
tgcccgagag ctgcagacaa cccgccaa ga gctgtcacac gctctgtacc agcacgatgc540
cgccctgcgt gtcattgccc gtctcaccaa ggaactgtg aaggggatgg gcaggagggc600
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ccctgcacaa ggctcacagc cctctccctt tctgtcgtt caatggacgt ggtggtggt720
gttccacacc cattttgttg cagttcctgt gagacaggag aggcgtgacc aaggggaact780
tgaaggggat ggcaggagg gcttgcgcag ggtttgttaa gcagtgcatt agtttcatta840
aaaaaagaga ac                                     852

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(2) INFORMATION ON SEQ ID NO. 114:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1739 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

```

gaagcccgagg gcttggcgac gcgcacgagg agcgaggagg cagcgacacg gggcgatcgc 60
ttcacggatg cggacgacgt agccatcctt acctacgtga aggaaaatgc ccgctcgccc 120
agctccgctca ccggttaacgc cttgtggaaa gcgatggaga agagctcgct caccgacgac 180
tcgtggcagt ccttgaagga ccgctacctc aagcacctgc ggggccagga gcataagtac 240
ctgtgggggg acgcgccggt gagccctctc tcccagaagc tcaagcggaa ggcggaggag 300
gaaccggagg ccgcgcatag cggggaacca cagaataaga gaactccaga tttgcctgaa 360
gaagagtagt tgaaggaaaga aatccaggag aatgaagaa cagtcacaaa gatgcttgtg 420
catataacta tgtgtgatga tgatccacc acacctgagg aagactcaga ttttgaaata 480
gatgaggagg aagaagaaga agaagaaaaa gtttctcaac cagagtgagg agctgccatt 540
aagatcattc ggcagttaat ggagaagttt aacttggatc tatcaacagt tacacaggcc 600
ttcctaaaaa atagtgggtg gctggaggct acttccgctc tcttagcgtc tggtcagaga 720
gctgatggat atcccatttg gtcccacaaa gatgacatag atttgacaaa agatgatgag 780
gataccagag aggcatttgt caaaaaatgt ggtgctcaga atgtagctcg gaggattgaa 840
tttcgaaaga aataattggc aagataatga gaaaaaaga aagtcattgt aggtgaggtg 900
gttaaaaaaa attgtgacca atgaacttta gagagttctt gcattggaac tggcacttat 960
ttcttgacca tcgctgctgt tgctctgtga gtcctagatt ttgttagcca agcagagttg 1020
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aatgtgttta tgaaaggagg atctaaatca gacaggagtt ggtctacata gtatgaatcc 1140
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aggccatttc aggcagcata agtaattctc tgtcctttgg cagaagctcc tttagattgg 1260
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tttttgagc ccttctcagt caagtctgcc ggatgtcttt cttacctac ccctcagttt 1500
tctctaaac gcgcacacaa ctctagagag tgttaagaat aatgttactt ggttaagtgt 1560
ttattattgt agtatttgtt gtgctaagca ttgtgttaga tttaaaaaat tagtgattgt 1620
actccacttt gttgtgttgt tttcattgtt gaaaaataat ataactttgt attcgaaaaa 1680
aaaaaaaaaa aaaaaaaaaa gaggagaaaa agagggggaaa gggggaagag gaggcaaaa 1739

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(2) INFORMATION ON SEQ ID NO. 115:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 805 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

```

ataggcgac cccaaggta gggteacctc gagcctccag acaactgctt caccttgacg 60
accaactgaa aaaacccgaa gggatggaag cagcggatca tctcgcgata tctggagcggt120
ctgcgcctgc ctctctgacc tgggaactgt ttccagctct cgcgagactt tcagggggtcg180
gagcgcgggg gccgcgcgag aggaaagctg gaggcgcggg tggggaacat gtctgagtcg240
gagctcggca ggaagtggga ccggtgtctg gcggatgcgg tcgtgaagat agaatcctgg300
taattgatgt ccaccgcaga aatccctgca gatgttccag cctctgtcta gtccagatag360
ccacaggaag ggtactggtt ttggattagg aattgttttc tcacttacct tctttaaaag420
aagaatgtgg ccattagcct tcggttctgg catgggatta ggaatggcct attccaactg480
tcagcatgat ttccaggctc catatottct acatggaaaa tatgtcaaaq agcaggagca540
gtgacttcac ctgagaacat ccagcgggga ggacaagaga aatcatgttt attcctcagg600
aatactgaag tgccctggag taagctgcca ttcttctgta acaatgttat cagtaatgct660
ttaaactcca gcacctggtt atgcatttga aaccaagtct gtttctgttt ttgtattttt720
tctctggaag ttgtaaggag gtggtcttaa ataaattaaa caaaaatag agtccaaaa780
aaaaaaaaa aaaaaaaaaa aaaaa

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805

(2) INFORMATION ON SEQ ID NO. 116:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1483 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

```

tgaaaaaac ccaacgcca cactgggtgc cttttgcagc cagcgccca ccatccgtgc 60
ccggaccctt gggaatgcc gcggtccag aggaataaac ccagggaagg ggccctccgt 120
gcgggggggc ggtcgtcttc tgggaacttc gtcgtttccg gcgctggctg gctggctggc 180
tgtaaacac tgaagcccc cggccgcca cccctgaaag cagaacctgg cctccctggc 240
cacagcagc ttaccaccgc ctctacgtgt cccgggcact tcccgagcc ttcccgcccc 300
ttctcatcg gccttgtagt tgtacagtgc tgttggttg aaaaggtgat gtgtggggag 360

tgcggtcat cactgagtag agaggtagaa tttctattha accagacctg tagtagtatt 420
accaatccag ttcaattaa gtgatttttt gtaattatta ttatttttgt gggacaattct 480
ttaattttct aaagatagca ctaacatcag ctcataggcc acctgtgcct gtccccgcct 540
tggcccggtt ggaatgaagc gcttccccgc agggccccca ctcccagtg gctgcttctt 600
ggggacccag ggcaccccg cacttcagg cacgctcctc agctggctac ctcccggctt 660
tgccgttcag atggggctcc tgaggctcag gagtgaagat gccacagag cgggctcccc 720
taggtcgtgt cgggcagtgt tggaaagtgg cctgccagga ccttccacc ttgggctcgt 780
gtcagccgcc ggcctccgc acctggaag cacacggcct ctgggaagga cagccctgac 840
cttcggtttt ccgagcacgc tgtttcccaa gaattctggg ctggcgccct ggtggcagt 900
ctggagatga ccccgagccc ctccccgtgg ggcacccagg agggccctgc cggaatgtgc 960
agcctgtggg tagtcggctg gtgtccctgt cgtggagctg ggtgctgtga tctggtgctc 1020
gtccacgcag gtgtgtgtgt taaacatgta tgtgtgtgac agagagacgc gtgtggagag 1080
agccgcacac cagcgcacc caggaaaggc ggagcgggta ccagtgtttt gtgtttattt 1140
ttaatcaaga cgtttccctt gttttcctat aaatttgctt cgtgtaagca agtacataag 1200
gacctcctt tgggtgaatc cgggttcgaa tgaatatctc aaggcaggag atgcatctat 1260
ttaagatgc tttggagcag acagctttag ccgtttccaa tccttagcaa tgccttagct 1320
gggacgcata gctaatactt tagagaggat gacagatcca taaagagagt aaagataag 1380
gaaaatgtct aaagcatctg gaaaggtaaa aaaaaaaaaa tctatttttg gacaaatgt 1440
attttatccc ccatgggatg cttgggtatg gcggggggga ggc

```

1483

(2) INFORMATION ON SEQ ID NO. 117:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1347 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

```

tgaggctctc catgactgca agtgttatat tggactggat ggtcatgaag tccctttcat 60
agccagagat tttgtgtggc tgctaaaatg cttacatctc tggctatgaa agggacttca 120
tgaccatgca gtccaatata acacttgcag acagagaaac tgaggctctc catgacttgc 180
ctagtctccc agctagtttg aggcaaaact ggattccac tctggtattc tttctccct 240
ttacatcatt ttccctcctt tataatgtcc tgagagacca gaactcacac cagaatcgat 300
tattcctcag gtgaagcata gactctttca tggtagacag atttcacgac tcagagatag 360
aaatctcttg ctatcatcag gtccacgggca gctcctgtgg agtctgtccc aacttatgtg 420
gcttccataa aatggcaaca gtccaggctc cttgcctaata tttagagcat taactcccta 480
attgccagta agcaaggagg tggatctctg caaacctaca ctgtctatga cagctctagt 540
tgtacttggt gtgactaaat acctcaaagg caacctgctt ctgcaggttt tgaagtgtca 600
gcttcataag acactgaggt ttagaattgt ttgattctag accataactg aagggcataa 660
atggaaacag gatatgaagg gaaacaagta gcatcatgga gctgaaaagt ggtgcataac 720
ccaatggcta gcacaaacaa ggatcacact gtccattctc ttgtctgcta aattaagcat 780
ttctctgcct cctttgcttc atcttttcc aacagctgga tagagggatc agaaatgact 840
gtgtcatggt gctcattcac tgcaaaactcc cagttgcaag ctccctggct ccccccggagg 900
gagcaagaat ctcatagttc agagacacag agggcctttt agccctaattg accttttga 960
tgggactgca actcatgact atcctgatat tgggaagaaag gactttgtta atcttctccc1020
ccatagctct gctgcgtagg tctacatctt actcagaatc actacacatt cctttagctt1080
tcttccaaagc tccagagcca ttggtacaaa tgctttattg aaactaaata cataatacac1140
acaatgagat gaagacaata tagaagtccg catagtcac ataatcccg tccctggccg1200
gttgaggcag ctcaaggctc gagcccagtc aagccaaccc gcagcttcac tcacgacttc1260
aagatttgat gctaatctct ttggatttct acagttatta aataagtgtc tgagtggaaal1320
aaaaaaaaa aaaaaaaaaa aaaaaat

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1347

(2) INFORMATION ON SEQ ID NO. 118:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1683 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

```

aattcggcac gatgggggga atctccgacc ccgacaccct acacatctgg aagaccaaca 60
gccttctctc ccggttctgg gtgaacatcc tgaagaacct ccagtttgtc ttgtgacatcg 120
acaagacaga ccacatcgac gcctgccttt cagtcatcgc gcaggccttc atcgacgcct 180
gctccatctc tgacctgcag ctgggcaagg attcgccaac caacaagctc ctctacgcca 240
aggagattcc tgagtaccgg aagatcgtgc agcgctacta caagcagatc caggacatga 300
cgccgctcag cgagccaagag atgaatgccc atctggccga ggagtcgagg aaataccaga 360
atgagttcaa caccaatgtg gccatggcag agatttataa gtacgccaaag aggtatcgccg 420
cgcagatcat ggccgcgctg gaggccaacc ccacggcccg gaggacacaa ctgcagcaca 480
agtttgagca ggtggtggct ttgatggagg acaacatcta cgagtgtctac agtgaggcct 540
gagacacatg gagatttggg caggctgctg ctgggagaaa tggacgcccc ctgggcctca 600
acttgatctt ctaccccgtg cctgtgactc agactgggaa atactgagca gagacggctg 660
gggccccggc agggaggagg gctgctctct gagacagggg cgcctccgcc ttgacccctg 720
ggcaccctca tcccctccca cctgtcccca gatcagctctc tgggatggag gccacagagc 780
tggtcaggct ccccatctg cccagcacgg cctgcactgt gccaccaccac ttgtccca 840
acgtccagtt ggtctctgtg ccaagagccc cgtgcattca ggcgcccaag cacaaactgg 900
gggagaggag gccgccagcc cggaggctgc agcccaaaa ctctaccctca tcccaactgg 960
tgacaggagc cctccttgaa ctgacctttg attggtttct gcttcaacta ccaaaatggt1020
atctccactt cccctcacc cgtagaggat cctggccaca gacagtttca agtagtgtcal080
gatttttgtt gcttgggcgg ctggttgtag agtgggcagt gcccgcccca tggggtgctcl140
tgtgtgcttc tccaggagca gggagggtgg aggggggga tggggggcac aggagctggg1200
agccccgtct ccaggaaaag gagaggggtt aagatgcacc gaggtctgag ctgggctact1260
tgatcttgct gaaagtgttt ctaaagatag caccactttt ttttttaaag cttttatata1320
ttaaaaaacc tatcatgcac caactgtgaa tagctgcgcg ttgcgcagag gaccggggga1380
ggggtcccca gaggtctccc atgcaacact ggaatgact gttccagaga gcgggcagac1440
ctggcagagc gccctggcgg cctgagacta ccaccactc cgttctctgc agaaacgacc1500
ctctgtggcc ctggtggcat gcgggccccc gcagcccaac tcagccagtg ttgggactgg1560
ctcagagccc atgggggctg gaggggggca gctgggactc tggaaatcttc ttataataal1620
aagcccttag gacaaaccta aaaaaaaaaa aacaagacaa gagaggggaaa gggaaagaa1680
ggg

```

1683

(2) INFORMATION ON SEQ ID NO. 119:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1355 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

```

acaagcatgg aagctttact gtttcggctc ttcaaacttc cagcaactac actcgggtgc 60
atcggaacttc gacgcccgcct ggtgacgcac acgctgcgcc ggaagtgtga acacaaagcc 120
tcagggtttt gtcatggcggg ctgctgctgc acgctggaac catgtgtggg tcggcaccga 180
gactggggtc ttgaaagggg taaatcttca gcgaaaacag gcggcgaaact tcacggccgg 240
aggacagccg cggcgcgagg aggcagtgag gcgccctgtgt tggggcaccg gcggcgagac 300
ccagatgctg gtgggctgcg cggacaggac ggtgaagcac ttacgaccg aggatggcat 360
attccagggt cagagacact gcccgggcgg ggaggggcatg ttccgtggcc tcgccaggcg 420
cgacggcacc ctcatcacat gtgtggattc tgggattctc agagtctggc atgacaaggga 480
caaggacaca tctctgacc cactcctgga actgagagtg ggccctgggg tgtgtaggat 540
gcccgaagac ccagcacacc ccatgtggtg tgccacaggt gggaaagaga atgctttgaa 600
gatattggac ctgcagggct ctgaggaacc tgtgttcagg gccaaagacg tcggaatga 660
ctggctggac ttgcgggttc ccatctggga ccagacata cagtttctcc caggatcaca 720
gaagcttgct acctgcacag ggtaccacca ggtccgtggt tatgatccag catcccccca 780
gcgcgggcca gtccctagaga ccacctatgg agagtagcca cactcatggg cagctggcag aaattgacct 900
tcggcgaggc aactcagtgat ttgtgggaaa cactcctggg ggggctggca ggcagtgctg gtgggttgca 960
tgccaccctc tcaaaagcctc tactagcctc ctgtggcttg gacagagtc tgaggatata 1020
caggatccag aatccacggg gtctggagca taaggtttat ctcaagtctc aattgaactg 1080
cctcctcttt tcaggcaggg acaactggga ggaatgagccc caagagcctc aagaacccaal 1140
caaggtgcc ctagaagaca cagagacaga tgaactttgg gcatccttgg aggcagctgc 1200
caagcggaag ctctcgggtt tggagcagcc ccaaggagct ctccaaacga gacggagaaal 1260
gaagaagcgg ctgggtcca ccagcccctg acgccctctg gccaccatttg taaaataact 1320
gctgaacacc caaaaaaaaaa gaaaaaaaaa agggg

```

1355

(2) INFORMATION ON SEQ ID NO. 120:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1816 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

```

ggtcagagag attctgaaaa gtaatccaaa gtgttccgta gctaaacatg gtgcaggctc 60
gttgtaaccac tgcaaccgac tgacgttact gtagtcccta gaatgctgtg agggcggggg 120
gttcagatca acataaagcc taacttgctg gagttgtagt ctcaaggctt totctcttgc 180
ttaactaaaa cctaaggacc actgtttttg gtagcaatta tatggttact atccactgca 240
gtccctcagtt gtgtgggtaa atcccacatg gcagagtaag gcacccaca gaaattaact 300
tggagagcct gagaaattcc cagtggcctt gccatagctg tctagaacac catctctagg 360
aaaaattaat tctgtccctg gccagctatt gtcttccac ttgcttttct gctgtcccaa 420
ggccagatga gtggaatcac catctgaact ttgtcaataa aatgtatctg gcgtgaacag 480
caggtaaac ccagtttccc acataaggat aaccttacct gaaaccttcc tgctgacaac 540
catgcagagg aatttttcca cttaagtcag agccttccct cccatctgga attcacagct 600
gttccctggc agcacacagg agggatttaa ggacctttgt gaggctaggt acactgtcca 660
cacctctttg ggggaagttac gatTTTTTTT ttccatcata attcagttct ttcttattct 720
acagtggtgca ctttatgcct ctgcctcttt gataatagtt gtctcagtga ggaagtcagc 780
tgccagaata ttaagaagggt tctcccttta tgcagtaca actgttaggg cggccttccc 840
atttacttta ggtttcaaga ggattcacgc gaagcacatg ccccggtcta gtcccatttg 900
aaacagttct gctttactga gacctaggc cggctctcct gctgacctta gcgctgctgc 960
ctaggtgccca ttctctttcc tctccagtca aatcacaggct gcacattttg tcacttaagt 1020
ccagtaaat ctgtgttact cctaaggact ttggggattt tgatgagacc tgcgagggag 1080
aagacactga gaagccagtg atctgcaagc atctgctctt gtttccacat cactctgggg 1140
atatttccagc tgtgtgttcc aaatggcaaa tcatcaacta aaagcacttg ttccaagt 1200
tgtctgcac tcccacagct gaagtgttag attgagctga ataacatagg gaagtgaacc 1260
agcaaaagaca ctcgattgga gtcagttaga tattgtacc ctcaagtggag cctctctggt 1320
cttttcttcc actctctgag aatttctctt agcaaatact tctttctctt tggctgctct 1380
caccatgata tttgaataag agatggccag aggataacac ttgtctotta aaaactaagc 1440
taaaaagaac ctagaacctt caattgagca gttgtgaaaa ttgcttaatg tgccaaagggc 1500
aagcaaaagag ttccagaaaa tgactgagaa ggagcgataa ccccagaat gcaaaatcag 1560
gggcatactt atccgggtgt tgaacaagga gctccgctct acaactgtgt ttttaggac 1620
ttgtgaggaa cacagcaacg gaaatccatc cacaaaggat gcagtgcccc aactgtact 1680
gcgcctgaat agtcatgtga taatttactg aagaaatcta gtgtacttta aattttttct 1740
ataaaagttt acattgtatc gtaggttaac attaaatggt ttatagcaaa aacttcaaaa 1800
aaaaaaaaa aaaaaa

```

1816

(2) INFORMATION ON SEQ ID NO. 123:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 740 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```

tttagaatc agcataggtt gaggtcagaa agcaattcag gcatgagcca cagtgcocgg 60
cttcacacccc atttctttaa aaaggatccc gtacgaggca gaaaagcccc ttccatcctg120
ctcctctgat actgtgcccc ctggagata ttccgctcct ccacccacgt gtctgtggct180
ggaaactgccc agcctgtccc tggccccctg gaagcctccc cacagctggt aatctggact240
taaggattgc tgggccaccg cctctctgcc taccaccatt ccatatttaa gtggagcccc300
tacgtagaaa ggcctggggg ctttatttta gtctcctttt cagggatgtc gtggcgggg360
gaggggggttc ttggtgttac agcctctccc ccaccctaa agggacggcg acgctgtttg420
ctgccttcac cacatattag tgcttgaccc tggcagggga ccccatggaa aagatgggga480
agagcaaaat acatggagac gacgcacctt ccaggatgct cgctgggatt cccacgcca540
ccactgtccc ccaccccatg gctgggaggg gcctctgaac ggaacagtgt cccacagag600
cgaataaagc caaggcttct tcccaaaaaa aaaaaaaaaa aaaaaaaaaa aagataggt660
agttaagggc gccgaaggtt tttttccott tagtaagggt tagtttttag tttgggggtg720
gccttcgttt ttaagaacgt

```

740

(2) INFORMATION ON SEQ ID NO. 124:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1493 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

```

aacacctgcc  ctggttcagc  gctttaggga  gggcggtcca  ggcgccccgg  agcaggcaga  60
gtgctgtgag  ctgctgtctg  ccctggggca  gcctgcggag  gagctgtgag  aggagttcct  120
ggcgcacgccc  cgcgggccggc  tggagaagga  gctgagaaac  ctggaggccg  agctggggcc  180
ctcacctccg  gctcccgacg  tgtttagagt  caccgaccat  ggaggcagtg  gcttcgtggg  240
cgccctctgc  caggtggcgg  cgccctacca  ggagctgttt  gcggcccagg  gccagcagg  300
tgccgagaag  ctggcgccct  tcgcccggca  gctgggcagc  cgctattttg  cgctggtgga  360
gcggcggtcg  gcgcaggagc  aggggtggtg  tgacaaactca  ctgctggtgc  gggcgctgga  420
ccgcttccac  cgcgctctgc  gggctcccg  ggcctgtctg  gcgctgccc  ggctgcgaga  480
cgctgccacg  gagatcgtgg  aacgagtggc  ccgcgagcgc  ctggggccac  acctgcaggg  540
tctccggcg  gccttccctg  gctgcctgac  agacgtccgc  caggcgctgg  cagcacctcg  600
cgtggctggg  aaggaggccc  ctggcctggc  cgagttgctg  gccaatgtg  ccagctccat  660
cctgagccac  attaaggcct  ctctggcagc  agtgacacct  ttcaccgcca  aagaggtgtc  720
cttctccaac  aagccctact  tcgggggtga  gttctgcagt  cagggtgtcc  gtgagggcct  780
catcgtgggc  ttgctccact  ctatgtgcca  gacggctcag  agcttctgcg  acagccctgg  840
ggagaagggg  ggtgccacac  cactgcctct  gctcctgctg  ctctcccgcc  tctgcctgga  900
ctacgagacg  gccaccatct  cctacatcct  cactctcact  gatgaacagt  ttctgggtga  960
ggatcagttc  ccagtgcagc  ccgtgagcac  gctgtgtgca  gaggccaggg  aaacggcgcg  1020
gcggctgctg  acccactacg  tgaaggtgca  gggcctggtc  atatcacaga  tgctgcgcaal  1080
gagcgtggag  actcgcgact  ggctcagcac  tctggagccc  cggaatgtgc  gggccgtcat  1140
gaagcgggtg  gtggaggata  ccacggccat  cgacgtgcag  gtggggctcc  tgtacagaal  1200
gggtgttcgc  aaggcccaga  gcagcgactc  cagcaaagg  actttctccg  tgtacagcag  1260
ctctcggcag  caggggccgt  acgccccag  ctatacccc  agtgcgccga  tggacaccaal  1320
ctctctgagc  aatatccaga  agctattctc  tgaacgtatt  gatgtgttca  gccctgtggal  1380
gttcaacaag  gtgtcgtg  tgacggcat  catcaagatc  agcctgaaga  cgcttgcgtg  1440
gagtggtgc  gggctgcgaa  cctttttggc  cctttgcggg  cttcaacaag  ggg  1493

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(2) INFORMATION ON SEQ ID NO. 125:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

```

ccagactgaa ttgtcagtga gccgatctga gggcggtgtg gagtggccag tggggcttgg 60
ccgagatgga caaccggatt ccttatgatg actagccggt ggtttcttgc ctgccctatga120
gaatcctoca gcatggaatc ctctcatga gagggtaaac agccggacta caacgatgag180
ttgacccagt tttggcccga accatcacac tgaagaagcc tcctggagtc attgggatta240
agatcgaggg
250

```

(2) INFORMATION ON SEQ ID NO. 126:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 1202 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

```

tcggggggag cggcgcgagg cgcggggagt tggttctaaa gagtggtgag tcagaagaga 60
cgctcaggcag caagcgactt ggcccatggc ctctgacctt gacttctcac ctccggagggt 120
gcccgagccc actttcctgg agaacctgct acggtacgga ctcttcctgg gagccatctt 180
ccagctcctc tgtgtgctgg ccatcatcgt acccattccc aagtcaccag aggcggaggcg 240
tgaacogtct gagcccagaa gtgctgaggt gacgaggaaag cccaaggctg ctgttcccttc 300
tgtgaacaag aggcccaaga aagagactaa gaagaagcgg tagaagagga ggctcgagga 360
gctggggcgg cagggaagag gtcttgggga cagccctcct gggaatctac attgtgttcc 420
cccgcatctc aggcctcagg tctgaggagg ctgtgacgac ctatgaccgc agagatctag 480
acagtctgaa cagtcccccag gctccagctg ggcaatccac cacttccctt tcttctgct 540
tctgtgacgg tttagagtca agggggctga aacacactgt gagcatagac tgtattaggt 600
ttgttcagaa gccgggtcag ctacacagagt cacattttct tgcttagtca tgtgtccctc 660
cttgagttgc cccctccttg tgggtttaca ctacattttg gagtcattgt ctaatgctga 720
caagcacacc ctctcccat atttgtgcac tacagatctc ctgctgatca gtcacctttg 780
ttgctgtgtg gtacacagag ccaggccctca cctgtttggt taggccaaga tgccatggac 840
atgcatcggt agtgatccca ctagctgtga cagccaggcc cagaaaatgc ctggcgtgag 900
agccagcaga cagccaggcc aggggttaggc agtgctgct tctgctccat cagggtcagg 960
ggatttggtc gaaggcgtgc atatttcctg ggcacaaact tcttgagcct ctgaaatggg1020
aggtcgtgca atttcagacc aacctctttt caaccatca tagcacgttc aagggtgtgcc1080
ttttactctt acctgtacat ccccatcccc ttcaattctt tcattccctg accagtgagall140
gggttctctg gggaagtatg gtgaataaac tgacatgcat gcttcagaaa aaaaaaaaaa1200
aa

```

(2) INFORMATION ON SEQ ID NO. 127:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 1014 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
- (A) ORGANISM: HUMAN
 - (C) ORGAN:

- (vii) OTHER ORIGIN:
- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

```

cccttttttt ttctttttga gatgggggga aagtcttagc aaaaggcagg agttagcatt 60
ttcctttaac aagactttct aatgctaaac aaagaccaac ttctttttaa aggggttggt 120
ttggttggtg gtgaaaaata ctgtactgta atgatctgct tgggttttaa gcaaaagaga 180
tcctgacatg tgaacccaat acacccaaat gccaaagtcca caaatgaaca aaacaagtgc 240
ttaaaaaaaa aattcttctg ctcttatatt tttggaggaa gctgctgatt ttggctgtca 300
gatttcactt agaaaagggtc accttctgag atgctttttc ctcacagaat ctgtagataa 360
actcattaaa agattgtccc atttcaaaat caccoccaa gctagcagca ctgttttttt 420
tttttttaag ttttgtttta aaattacaaa ccaagtaaga agtccaacat cctcttccat 480
gaacagcttt gtgacagagc tcttgagtgt gtgcagcccc cactgtgctc tgaatacagt 540
ctctgcagct ccagtggtgc ctcttttcoag gaaggaaaagc atattcaata cattcactat 600
ctgtaccccc tggaaactgc acatgctgac gagctattat aagccaactc atccccagct 660
ctcttcgggg actggtcacc ccttgtaaaa coattctgta taagtctctt ttgaaatttc 720
tgatcttgag cagcatattc agaaaagtca gattccaccg ccggaggagg aatgtttgga 780
ataaatttag aaaaatagagt tggagccatc tgaaccacct ctggtctgag ggtatacagg 840
cctttcacaa tatttgccat agttgaaggt gtgacctgaa atggtgttga ctgggcttct 900
aaaagtaaa gcattaggcc gtaaatgtgc ttttctgcaa catgttccgt aaacagcttt 960
ataagggcac ctttaagccc gggtaaagctg gtccatggga acctatcgtt ttg 1014

```

(2) INFORMATION ON SEQ ID NO. 128:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1171 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

```

caccaaaatta atcagggttta cagacaggggt cccaccgggta ttcacattct tgttagtgat 60
cagatgggttc agaatttttca agatgagagt tggtttttat tctccacagt aaaagctgaa 120
agtagtgatg gcatccocat aattttgaaa tgatgtctta tatagactga actgtattca 180
gtaccaataa gtcacggtta aaagtgtgtg aagactgaat ccaagaagtc ttgggattgg 240
attttaccat atgaaatgtt tcatattgaa aacacaagat gacctttcta atgagctgta 300
tgagaggtga atctctcac tgtcactgcc atagccaagc atctctatga gagtgagcac 360
atcgggacag catgcatcca gctctggagg ccacggtgca ggcatagctg cctgctgctc 420
tggcacagtc cagtaaatac agttctctaga agcagccttt gctgtctttt tacactgtat 480
gcgggtttgga aatgaatgta gaaacttact gtgggcattt acctttctgt gccagtttgg 540
cttttattgc ctgaacctta tgcgtgacct gagaggagat gggggacagt gctgttggg 600
ggccagcagt gaatctgtat gcggagaggt gtgttgtgct gatgtggccg ttggttgcca 660
ggtaagaggc tcggcacctt ctgtgaagaa atcatgtctg aggggtgacg ttgatatga 720
tcatgccaga ttggagaaga tccaagccag gaagatgggc ttgaagcaaa ctgcattatc 780
aggagtacct ttgtgagagg atcagtgtaa atcctaatag gtacaaagac ttttgtgttt 840
tggctttgtc acagatttat tgaaaaactt tttgtctct gcttccattt ttagcatttt 900
agtttctggt ttctattttt ggagattcct tgccttttaa actcgtggtt ttctctcat 960
tttcttccct cctctccctc atctctgacc acccccacc taacccccca cccccaccat1020
cctattaaac atttttaaag ccttaccoca gacattggga aataggtgga cccaagtagg1080
ggggaggaaa agtattgatt tgtttgata ggcttgtgga ttagggtgtt aaggggttct1140
tggattatgg aacaaggtgg aatttttttt g 1171

```

(2) INFORMATION ON SEQ ID NO. 129:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 353 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

```

ggcgccggagc caggggcaaa cagagccatgg ctgtctacgt cgggatgctg cgccctgggga 60
ggctgtgcgc cgggagctcg ggggtgctgg gggccgggc cgccctctct cggagttggc120
aggaaagccag gttgcagggt gtccgcttcc tcagttccag agaggtggat cgcatggctt180
ccacgccccat cggaggccctc agctacgttc aggggtgca caaaaagcat cttaacagca240
agactgtggg ccagtgcctg gagaccacag cacagagggt ccagagaacga gaggccttgg300
tcgtctccca tgaagacgctc aggttgacct ttgcccaact caaggaggag tgg 353

```

(2) INFORMATION ON SEQ ID NO. 130:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 205 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

```

cggtgtagcg gccccgcagc caacccccga ggagcggcgc gctggcgtgc cgtggcgcc 60
caggagtgg ggatgtccta caaacccatg cgcccctggc tgcccagcag cccccctgg120
tctgccaggg accccctggg gcccggggca ccccggttcc ctgacagggg gccgtgcgcg180
tgccgcgtgc ggggtgcagc tgtcc
                                         205

```

(2) INFORMATION ON SEQ ID NO. 131:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 211 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

```

aaatcacctt acaaccatt tctcagaaca tgtttctatt gttaaacac acacaactat 60
tttatttatg tgttttatt atgcctgac accaatatca ataactgaaa cacagcagtt120
tagtaataat ttaatacaca ccataacctg cctattgaga atggcattat atttgttttc180
attgtagtgg ctccatccaa aataaaatga t

```

211

(2) INFORMATION ON SEQ ID NO. 132:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 867 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```

gtcttcccaa gatggagatg ctaacgaaac tgagaagggg gcgtatgttt gacgaaggtt 60
tgtgcaagtc aggcccttct ggaacacagc agggcctaca acgagggggc tttcgatggl20
gctgtgagga tgggggttgt ggggaagaatt ggccacgtta gagaccocat gccacccacac180
catgggtgagt gctctgtgac tctgtctcac ctgtggtgag tgggcgagct gggcgagctg240
ggcgagctgg gctggggaga gctctgtgag accgagagga gaaatgagaa gaaggaaacaa300
aaatattatt tctatgtaat ttatatTTTA ctatgccaa attatttatg ataatttgc360
attgctatac tgtaccagtg tcaaatgctg cagcctgcc aagctgtgatt ttgtgaggct420
tgtccctatg taggatgcac cgcaggcccc tggccactga aagagtgtgc agtggactgt480
gggtctccca tatgcggtgc cgcccaaagg tggctttgcc tcaagcaacc tacctgatg540
ttttactcat tggaaatgtt ttccccgatt gtggatgact tottttctga tggagagagt600
ccaggaggga tggaaaacgc ctggatttaa gctcagcatc cccccacatgg gcttttcgat660
catcttcagg cctgaagctg cagcagctga agttcgctg catttatcag cctcttttgt720
gctgctcctt gccaccttgg ggttcctgct ggggacctat tgtggttgtg gcatgtgtga780
gcagaaggga ggatgaggaa aaaagagaag gaaacccccg ttagtgacaa gtgttttttt840
gagttgccag gttttgccat cattaata

```

867

(2) INFORMATION ON SEQ ID NO. 133:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

aattcagact cccattctta acttggcatt tttgtagctt acaggaacca gcttgggtga 60
 ccttctctta tgagatgcag ctggaaagcc atttatgcaa gaggtggttt cacttttgc120
 gctcctccat tcattgaccc ttcagccttt aaaaaattag aatgtgaaaa ttagtagcaal80
 agagtgcaga gatattagct taagggataa ataaatgaaa gtacgaagta gctcattatt240
 tatgaagagt aataatt 257

(2) INFORMATION ON SEQ ID NO. 134:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 204 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

```

gactggctca tggcctctgt aaatggctgc tggcgggact gtctgcctag cgggtgccct 60
tggaaacctag cccttgggtgg gttttgagga aatgattcct gaatgaggag tgcattgccg120
tgtgaagggc tgggtggcacg gcacccgcgt gagctacgag tgccctcagt gcgcttctgt180
attgactggc catgggtgct caca
204

```

(2) INFORMATION ON SEQ ID NO. 135:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 245 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

```

ttgcacatg gtaaacgtgg ataatacagt atcatttttg agcagttttt taaatgtaaa 60
tctgtatctt actcagagtg tgggtctgaa gttattaagg acatttcccc acgttactgg120
cccatttccc tttgtaatca gaggaattct gtttcaagat tattgttggg tgtgatctgt180
ggctcttgat cagaatgaag ttaaatggcc acaggaggat taagctatga ggttggcatt240
tttca
245

```

(2) INFORMATION ON SEQ ID NO. 136:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1637 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```

ggggaggggac gagtatggaa ccttgaaggt agcaagtcca ggcactggcc tgaccatccg 60
gctccctggg caccaagtcc caggcaggag cagctgtttt ccattcccttc ccagacaagc 120
tctattttta tcacaatgac cttagagag gtctcccagg ccagctccaag gtgtcccact 180
atccctctgt gagggaaagag cagggaatat tctcccgggg tccctgtcat gctactttct 240
ccatcccagt tcagactgtc caggacatct tatctgcagg cataagagaa ttataaggca 300
gtgatttccc ttaggcccag gacttgggcc tccagctcat ctgttccctt tggggccatt 360
catggcaggt tctgggtcca aagctgaact ggggagagaa gagatacaga gctaccatgt 420
gactttacct gattgcccct agtttggggt tgcttattgg gaaagagaga gacaagaggt 480
tactttgttac gggaaatatg aaaagcatgg ccaggatgca tagaggagat tctagcaggg 540
gacaggattg gctcagatga cccctgaggg ctcttccagt cttgaaatgc attccatgat 600
attaggaagt cggggggtggg tgggtggtggt gggctagtgt ggtttgaatt taggggccga 660
tgagcttggg tacgtgagca ggggtgttaag ttagggtctg cctgtatttc tgggtccctt 720
ggaaatgtcc cctctctcag tgtcagacct cagtcaccgt gtccatatcg tgcccagaaa 780
agtagacatt atcctgcccc atcccttccc cagtgcactc tgacctagct agtgccctgt 840
gcccagtgac ctggggggagc ctggctgcag gccctcactg gttccctaaa ccttggtgtg 900
tgtgattcag gtccccaggg gggactcagg gaggaatatg gctgagttct gtagtttcca 960
gagttggctg gttagacctt ctgagaggttc agaattattg cttcaggatc agctgggggt 1020
atggaattgg ctgaggatca aacgtatgta ggtgaaagga taccaggatg ttgctaaaag 1080
tgaggggacag tttgggtttg ggacttacca ggggtgatgt agatctgtaa ccccaagtgt 1140
aggctggagg gagttaaggt cagtatggaa gatagggttg ggacaggtgt ctttggaaatg 1200
aaagatgac cttagagggc tccttggggc tcaggaaatgc tcctgtctgt gtgaagatga 1260
gaaggtgctc ttactcagtt aatgatgagt gactatattt accaaagccc ctacctgctg 1320
ctgggtccct tgtagcacag gagactgggg ctaaggggccc ctcccaggga agggacacca 1380
tcaggcctct ggctgaggca gtacataga ggatccattt ctacctgcat ttcccagagg 1440
actagcagga ggcagccttg agaaaacggc agttcccaag ccagcgctgt gctgttctct 1500
cattgtcoact gccctctccc caacctcttc tctaaccac tagagattgc ctgtgtctct 1560
cctctgtcct cttgtagatg gcagctctgt ccctcaataa atgcttctct cattcatctg 1620
caaaaaaaaa aattttc

```

1637

(2) INFORMATION ON SEQ ID NO. 137:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

```

aaaagcatag ctcactctgt aataggctat ttctcatgatt tcaagtgggt ttatgaagaa 60
acagaaagca gtgatgatgt tgaagtgtctg actctcaaga aattcaaagg agacctggccl20
tacagacgac aagagtatca ggtagaattc aacatatgggt gcttgaagtg ggctcttgggt180
ttatcagtta tggcatatgt aaataacagt gtaccaagtt agtgtggtgt ttatgaagat240
gagtttaatc ttttgtgatg
260

```

(2) INFORMATION ON SEQ ID NO. 138:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 957 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

```

ggggaatttg tctttggaaa gcttgtgcaa cctctacaac tggcgataca agaattctagg 60
aaacttacct catgtgcagc tcttgccaga gttagtagaca gcaaatctgtg gcttactgtal20
tgactttccag ctcatataatg ttgaagattt tcaaggagtg ggagaatctg aacctaatccl80
ttactttctat cagaattcttg gagaggcaga atagttagta gcacttttta tgtacatgtg240
tttactttggt taccctgctg acaaatcag tattctaaca acatataatg gccaaaagca300
tcttatttcgc gacatcatca atagacgatg tggaaacaat ccattgattg gaagaccaa360
caagggtgaca actgttgata gatttcaagg tcaacagaat gacttatattc ttctttctct420
ggtacgaacc agggcagtg ggcactctgag ggaatgtccgt cgcttggtag tggccatgtc480
tagagccaga cttggacttt atatcttcgc cagagtatcc ctcttccaaa actgtttttg540
actgactcca gctttcagtc agctcacagc tcgccccctt catttgata taattccaac600
agaaacttttc ccaactacta gaaagaatgg agagagacca tctcatgaag tacaataaat660
aaaaaatatg cccagatgg caaacctttgt atacaacatg tacatgcatt tgatacagac720
tacaatcat tatcatcaga ctttattaca actaccacct gctatggtag aagaggggtga780
ggaagtccaa aatcaagaaa cagagttgga aacagaagaa gagggcatga ctgttcaagc840
tgacatcata ccagttccaa cagacaccag ctgccgtcaa gaaactccag ccttttgagcg900
tgagagccgc cccggtgggg aagggggcaat tgcgttgggg gggcttggtt gtttttt 957

```

(2) INFORMATION ON SEQ ID NO. 139:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 760 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

```

gtggaataca atagatatta atttgtgtt ggtttttctg cctgctttaa atgaaatgta 60
ttatgtttct gggttccttt tttagctgta aaaatacttc gtcactaaag catgaaattt120
aatcagcagt tgttcttcaa gttcctgaaa gctataaaag tttctcatga cttgagtgtt180
tttttccctg cccaccagag gagaaagccc ttgtagaatt ctgcagtggt acaagtgttc240
cctacaaaaa ctgaaaccaa cagctcctct ttaacaagtt ggcttttttaa aagcacgtaa300
ttacaattta atgtgtattct gtaaaagtgt gctctaggca taattttaat tctttttaat360
gactatattt cttcaaaact ttgaaagaaa aatgtgttct ttttgctgca tcctttgttaa420
gaagactgcc aacagaggaa aaaggacttt acaaaattaag accatcttgg tttcattttcc480
acaaagatga gaacaaatca tgggtttagg aaaggatcct tagaagaaca caagaatttg540
aaagcccttg gtggttatca ctactatat tcatatttcc acagaagtga cttagccaag600
ctctgcattt tgagcctgct gactttcatt taaaagggaat gaaagggtga aaatccaggc660
tgctgtgtct gtagataaa gtcacaccat gtttgagttc ttcactgttg tgtccacctg720
aataaaactg agtaagtaat gaaaaaaaaa aaaaaaaaaa 760

```

(2) INFORMATION ON SEQ ID NO. 140:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 260 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

```

aggaaccctc cggcctagaa gttcagatgt cttgccaaata tatctgtgct tcacaacttg 60
cctactctct ctgaccoccta acattttcac atacttttcc aattctgctt gtcataaatt120
tgctgcttgc cctaaagtag aatgttgatt cctgtcaaac acacagccta gccctgattc180
ctcctcttct ctcaagcagt gatattgtca acaatgataa acaactacta tgtactgagt240
gtttttttat gtgctgtcca cacttttatac acatgtatag 280

```

(2) INFORMATION ON SEQ ID NO. 142:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 461 base pairs
- (B) TYPE: Nucleic acid

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```

gcgggccgctc gagggaaagca ccgcccgggtt ggccgaagtc cacgaagccg ccctctgcta 60
gggaaaaccc ctggtttctcc atgccacacc tctctccagg tgccctctgc ctcttcaccc120
cacaaagaagc cttatcctac gtccttctct ccatctatcg gaccccagtt tccatcacta180
tctccagaga tgtagctatt atgcgcccgt ctacaggggg tgcccgcaga tgacggtgcc240
ttcgcgagtc aattactctt cgggtcccaa ggtttggett tcaegcgctc cattgccccg300
gcgtggcagg ccattccaag cccttcgggg ctggaactgg tgtcggagga gcctcggggtg360
tategtacgc cctggtggtg gtgttgcttc actcctctga gctcttcttt ctgatcaagc420
cctgcttaaa gttaaataaa atagaatgaa tgataccccc g 461

```

(2) INFORMATION ON SEQ ID NO. 143:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 436 base pairs
(B) TYPE: Nucleic acid
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:
(A) ORGANISM: HUMAN
(C) ORGAN:

(vii) OTHER ORIGIN:
(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```

caaagatgtc atgtggccag aatcatcttt tagtctcacc actccacact gatggtcaca 60
tagaggggtg agttgggaag ttgttaaata caagaggggt tgagcttctg gagaagaggal20
aaatgtaaaa gtattttttc cttaaagaaa gataaaaagg taagcctaaa ccttggcggc180
caccgaagtc agctgttacg catgtgtagt taaatttcac tgtaaatatt tcataaggg240
tcttagaatg gagccaggtt gacatcacag ccccaactgt accaaaaggaa ccatttcatt300
caataaagcc aacattttcca aagaaacacg aatgtctatg gcagagttaa cataaggcca360
gaaaatcctc tggaagaaat tcgggtatca atgtttataa tctctgcatt taggggtttg420
ccagtgtggg caaaaaa

```

436

(2) INFORMATION ON SEQ ID NO. 144:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 287 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

```

ctttaaagta gggctgtgga agggggatat agtagagggg gagagggtg ttttatacac 60
gtataaatgg tataccaccat ttatacacgg tggtcagaga agctctgato aggtgacgtal20
tgtacagaaa gtcactgtgg cctgagttaga gtcaaggaga aggagcagca agagttagcl80
ttagggaggt ggagaagggg tggaatagat caagcaagac cttggccctg gtagggatct240
gggatttaaa gtgagaggac aaccgttggg atgttgtgag cacagaa

```

287

(2) INFORMATION ON SEQ ID NO. 145:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 555 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

```

ggcgacgcct cggtactgac ctctgcagag cgggttgag cccattgacg tccagcgaac 60
gaggagcagc gatggacggt cgggtgcagc tgataaaggc cctcctggcc ttgccgatcc120
ggcctgcgac gcgtcgctgg aggaacccga ttccctttcc cgagacgttt gacggcgata180
ccgaccgact cccggagttc atcgtgcaga cgggtctcta catgttcgtg gacgagaaca240
cgttctccag cgacgcctcg aaggtgacgt tcctcatcac ccgcctcaca gggcccgccc300
tgcagtgggt gatccctac atcaagaagg agagccccc cctcaatgat taccgggggt360
ttctggccga gatgaagcga gtctttggat gggaggagga cgaggacttc taggccggga420
gaccctcggg cctggggcg ggtgctctgg ggggggtccg ctgtgttact gggcccgccc480
agggtcgcca cggggccct ccctccgca gtccctccc ctcgaaaccg ccgcgaagtc540
ccctgcgggt ctgtt                                     555

```

(2) INFORMATION ON SEQ ID NO. 146:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1790 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

```

agtgagaaaag cagggactct tcggcctagg cagccgggac ccagccagcc ctgcgcctcg 60
cgccgctcgcg catcgctcct ggtctttctc tagagttgta tatatagaac atcctggagt 120

ccaccatgaa cggacagttg gatctaagt ggaagctaact catcaaaact caacttgggg 180
aggatatctg gcgaattcct attcataatg aagatattac ttatgatgaa ttagtgtcaa 240
rgatgcaacg agttttcaga ggaaaacttc tgagtaatga tgaagtaaca ataaagtata 300
aagatgaaga tggagatctt ataacaattt ttgatagttc tgacctttcc tttgcaattc 360
agtcgagtag gatactgaaa ctgacattat ttgttaatgg ccagccaaga ccccttgaat 420
caagtcaggt gaaatatctc cgtcgagaac tgatagaact tcgaaataaa gtgaatcggt 480
tattggatag ctctggaaacca cctggagaac caggaccctc caccaatatt cctgaaaatg 540
atactgtgga tggtagggaa gaaaagtctg ctcttgattc ttctggaaaa cagtctactc 600
aggttatggc agcaagtatg tctgcttttg atcctttaaa aaaccaagat gaaatcaata 660
aaaaatgtat gtcagcgctt ggcttaacag atgatcaggt ttcagggcca cccagtgtct 720
ctgcagaaga tcgttcagga acacccgaca gcattgcttc ctctcctca gcagctcacc 780
caccagcggt tcagccacag cagccaccat atacaggagc tcagactcaa gcaggtcaga 840
ttgaaggtca gatgtaccaa cagtaccagc aacaggccgg ctatggtgca cagcagccgc 900
aggtcccacc tcagcagcct caacagtatg gtattcagta ttcagcaagc tatagtccgc 960
agactggacc tcaacaacct cagcagttcc agggatatgg ccagcaacca acttcccagg 1020
caccagctcc tgccttttct ggtcagcttc aacaactgcc tgctcagccg ccacagcagt 1080
accaggcgag caattatcct gcacaaaact acactgcca aacttctcag cctactaatt 1140
atactgtggc tctgcctct caacctggaa tggctccaag ccaacctggg gctatcaacl 1200
caagaccagg ttttacttca ctctctggaa gtaccatgac cctctctcca agtgggctal 1260
atccttatgc gcgtaacctg cctccctttg gtcagggtca taccacaact ggacctgttt 1320
atcgataagg aggcctcctc acaccaatta atgtagctgc tagctattgg cctcccaaaa 1380
gactccagta ctattttaat ttgtattgaa gaagttcaga aattttaaag cagagcattt 1440
tttatgatat cattgttggt gtttaattgaa agtataattt gctggaacac aaagaccaal 1500
atgaaagtgt tttcctcctc gcttaaaaaa gtatgcagctt cttagtactc ttggaacact 1560
actcttacat gtataaagtg attgacttga cttctagct tccttgtcc ggaggtattt 1620
aaaatgcttg ggtgaggttt agccatctta cttggctttt tactattaac atgatgtact 1680
aaagtagagc cctttgagaa tacaagatat tatgtataaa atgtaacct gatgataggt 1740
taataaagat gattgtaattc aaaaaaaaaa aaaaaaaaaa aaaaaaaaca 1790

```

(2) INFORMATION ON SEQ ID NO. 147:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2357 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

```

ctcgagcgga atcggtctga gcgcagacct gcagcgggca aagagctccc gaggaagcac 60
agcctggggtc aggtctcttc cttctttaat gttagagaca gctaccggaa ggaggggaaac 120
aaggagttct cttccgcagc cctttccccc acgcccaccc cagctctcca ggggaccttg 180
cctgcctctc aggcctggaag ccatggctccc gaagtgtagg gcaagggtgc ctcaggacct 240

tttggctctc agcctccctc agccccagg atctgggtta ggtggccgct cctccctgct 300
cctcatggga agatgtctca gagccttcca tgacctcccc tccccagccc aattgccaaagt 360
gactctggag ctgcacaaaag tcagcaggga ccaactaaat tccaaagacct ggtgtgcgga 420
ggcagggaqca tgtatgtctg caggtgtctg acacgcaagt gtgtgagtgt gagtgtgaga 480
gatggggcgg ggggtgtgct etagggtgct etgggcctgt gtgtgggtgg ggttatgtga 540
gggtatgaag agctgtcttc cctgagagt ttccctcagaa cccacagtga gaggggaggg 600
ctcctggggc agagaagttc cttaggtttt ctttggaatg aaattctctc ttccccocat 660
ctctgagtag aggaagccca ccaatctgcc ctttgcaagt tgcagggtgg aaggtaaag 720
gttggtgtgg agttggggct gccatagggt ctgcagcctg ctggggctaa gcggtggagg 780
aaggtctctg cactccaggc atatgtttcc ccatctctgt ctggggctac agaatagggt 840
ggcagaagtg tcacctctgt ggtgtctccc tcgggggctc ttccctcaga cctccccctc 900
acctacataa agctcccttg aagcaaagaa gagggctcca gggctgcaaa actggaagca 960
cagcctcggg gatggggagg gaaagacggt gctatatcca gttcctgctc tctgctcatg 1020
ggtggtctgt ataacctctg cctcacttga ttcatctctg gttttcttgc caccctctgg 1080
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tcagctatca tgggtgtttt tgtcaactgc ttgttaattg atttggggat ttttgcccgc 1260
aatgagaggt tgaggaaaaag actgtgggtg gggaggccct gcoctgaccca tcccttttcc 1320
ttttgcggcc cagcctagggt ggaggcgaagt ggaatatctt atattggggc atttgggggc 1380
tcggggaggc agagaatctc ttgggagttc tgggtggcgc tgggtgcattc tgtttcctct 1440
tgatctcaaa gcacaatgtg gatttgggga ccaaaggtca gggacacatc cctctagagg 1500
acctgagttt gggagagttg tgagtggaa gggagagcag caagaagcag cctgttttca 1560
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tcctcttaact cttctgtcc taaaaatagg ggccgttttc ttacacacc cagagagagg 1680
gagggaactgt cacactgggt ctgagtgacc gggggctgct gggcgctgtg tctttacca 1740
aaccatccat ccttagaaga gcacagagcc ctgaggggct gggctgggct gggctgagcc 1800
cctggtcttc tctacagttc acagaggtct ttacgctcat taaatccca gaaagaggca 1860
tcaaagctag aatgtgaata taacttttgt ggaccaatcc taagaataac aagaagccca 1920
gtggtgagga aagtgcgttc tccacgacct gcoctcctgt ttctccctct catgtccctc 1980
caggggaaaa gactttattg cttaatttct gcctttcccc cctcacacat gcacttttgg 2040
gccttttttt atagctggaa aaaaacaaat accacccctac aaacctgtat taaaagaaga 2100
acagaaatga ccacgtgaaa ttgcctctg tccaaacatt tcatccgtgt gtagtgtgat 2160
gtgtgtgagt gtgtgaagcc gccagttcat ctttttatat ggggttgttg tctcattttg 2220
gtctgttttg gtccccctcc tcgtgggctt gtgctcgcca ccaagagaga aaacctttg 2280
ggggcttgta atttatcctg aaaaaattaa ctttagcgca aaggggggag tgtttaccg 2340
tgggggggta aaataaa

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2357

(2) INFORMATION ON SEQ ID NO. 148:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 907 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

```

gttcattgtc tggcaccaag ctccctgggg tgaattttct tccaaaagag tccggggagt 60
ccagggtcctt ctctcctggtt actcataaacg cgccccccatt tctcactccc attgggcgtc120
gggtttcttag agaagccaat cagtgtcgcc gcagttccca gggttctaaag tcccacgcac180
cccgcgggac tcataatttt ccagacgcgc gaggttgggg tcattggcgcc ccgaagcctc240
ctcctgctgc tctcaggggc cctgcacctg accgatactt gggcggttga gtgcgggggtc300
cagagagaaaa cggcctctgt ggggaggagt gaggggcccg cccggtgggg ggcgaggact360
caggggagccg cgcccgagg aggtctctggc ggggtctcagc cctcctcctgc cccagggctc420
ccactccttg aggtatttca gcaccgctgt gtgcggggccc ggcgcgggg agccccgcta480
catcgccgtg gagtacgtag acgacacgca attcctgcgg ttcgacagcg acgcgcgcat540
tccgaggatg gagccgcggg agccgtgggt ggagcaagag gggccgcagt attgggagt600
gaccacaggg tacgccaaag ccaacgcaca gactgaccga gtggccctga ggaacctgct660
cgcgcgttac aaccagagcg aggtcgttga gtgaaccccg ccgggggcgc aggtcacgag720
cacccccctat ccggcacggg accgcccggg tccttcagag ttccgggtgc gaaatgtacc780
ccgagggagg ggaggcgttg gattcttga gtggatactg ggggggtttt acgcaggttc840
attttcagtt taggccaaaa tccccgcggg ttgggggggg atgggggggg gttaggtggg900
cgggggtt

```

907

(2) INFORMATION ON SEQ ID NO. 149:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1987 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```

aggaggcgtg gggggggggg cggggggagtc aggggaagagc accatcgtca agcagatgaa 60
gatcatccac gaggatggct actccgagga ggaatgcggc cagtaaccggg cgggtgtgcta 120
cagcaaacacc atccagtgcca tcatggccat tgtcaaaaggc atgggcaacc tgcagatcga 180
ctttgcgcag cccctccagag cggacgacgc caggcagcta tttgactgt cctgcaccgc 240
cgaggagcaa ggcgtgctcc ctgatgacct gtccggcgctc atccggaggc tctgggctga 300
ccatggtctg caggcctgct ttggccgctc aagggaaatac cagctcaacg actcagctgc 360
ctactacctg aacgacctgg agcgtattgc acagagtgc tacatcccca cacagcaaga 420
tgtgctacgg acccccgcta agaccacggg gatcgtggag acacacttca ccttcaagga 480
cctacacttc aagatgtttg atgtgggttg tccgctgtct gagcgggaaga agtggatcca 540
ctgcttttag ggcgtcacag ccatcatctt ctgctgtagt tgagcgccta tgactgtgtg 600
ctagctgagg acgaggagat gaaccgcgat catgagagca tgaagctatt cgatagcatt 660
tgcaacaaa agtggttcac agacacgtcc atcatcctct tccccaacaa gaaggacctg 720
tttgaggaga agatcacaca cagtccccctg accatctgct tccctgagta cacaggggcc 780

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aacaatatg atgaggcagc cagctacatc cagagtaagt ttgaggacct gaataagcgc 840
aaagacacca aggagatcta cagcaacttc acgtgcgcga ccgacaccaa gaacgtgcag 900
ttcgtgtttg acgcggtcac cgtatgtatc atcaagaaca acctgaagga ctgcggccctc 960
ttctgagggg cagcggggcc tggcgggatg ggccaccgcc gactttgtac ccccccaacc1020
ctgaggaaga tggggggcag aagatcacgc tcccgcctgt ttcccccgcc cctttttctc1080
tctttctctc ctttgttttc agctccccct gtccccctag ctccagacgt aggggagggg1140
ttgccacagg cctccctgtt tgaagcctgc ccttgtctga gatgctggta atggccaagg1200
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ggggggcaca tgcgtagctc cccaaggctg cgtctggagg ggccccctgt gtccagcct1320
ggacccccag ctttgcccaa caccagcccc tgccccagcc caagtccaaa tgtttacagg1380
gagcctctct cccagttccc caacccccag cgtccggagg cccccaaaga aaaaagcaca1440
gaagcgtgag acgccaccat tccctgaaac cacagttcac ctgctcattc tctgtagctt1500
ttaaaaaaat gaaagttaaag gaaaaaaaaa aaactgcmaa tctagaaaaa tttttagaga1560
aaaactattt aaaaactgtca gatcctgacc agcaagcgcc cccccagccc ccttccaaag1620
tgactccgtg ccttgagtgt gtctgcgtgt ttacaccogt cctcttgctg gcccccgcgc1680
tgcgagcgcc acccctgcc tgcctccac agaattgggt tccaaagggt ctccagcaga1740
actgcacaag tcaactgagg ccttccccca cgggccccgt cccagagctc tatcaacct1800
aaatgtagct ccttagcgct aaactaggaa ccgcgcgtgc ccttcgtggg gccaagcccc1860
tcatgcctt gtcccagccc cggggccttc agcgttgaa acctccttgc ttttttca1920
tgttttatgg aattgttcac ctggtttgaa ataataaaat gtgaaaagga aaaaaaaaaa1980
aaaaaaa

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(2) INFORMATION ON SEQ ID NO. 151:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2906 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

gtccagaagc	aaaaattaag	ttcccgaagt	tttccatgcc	caagatcgcc	atcccagggtg	60
tgaaaatggg	gggtggggga	gccagaggtcc	atgccacagct	accctctctt	gaaggagagct	120
tgagaggacc	agatgttaag	ctcgaagggc	cogatgtttc	tctaaagggg	ccaggagtag	180
acttgccctc	agtgaacctc	tctatgccaa	aagtctctgg	gctcgacctt	gatctgaact	240
tgaaggagcc	aaagtttgaag	ggagacctgg	atgcactctg	tcccagcatg	aagtgcatg	300
ctccagggtg	caacctcagt	ggtgtcgggtg	gcaaaatgca	ggtggggagg	gacggtgtga	360
aagtgccagg	gatcgatgcc	acaaacaaagc	ttaactgttg	ggcaccagat	gtgacactga	420
ggggaccagg	cctcgaggga	gatctggctg	tctctgggtg	catcaaatgc	cctaaagtag	480
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tgaagctgcc	ccaatttggc	atctctactc	cgggggtccga	cttgcacgtc	aatgccaaag	600
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gggcccactg	tgagatcaaa	ggccccactg	tcggaggagg	tcttccaggc	attggtgttc	780
aaggccatga	aggaaacctc	cagatgcctg	gaattaaagt	ctctggatgt	gatgtgaacc	840
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ggcatttgag	tgttaaaagt	tcgggggggtg	agtgtgaagg	accccaagtc	tcctctgtct	1140
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aaggtcactt	gaaaagtgtg	tctggaaaag	taacattccc	taaaatgaag	atccccaaat	1320
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gtgatttcgg	gtcaaaagcg	aaaggtcatt	atgaggtgac	tggggagcat	gatgagacag	1860
gcaagttaaa	ggggagtggt	gtgtccctgg	cctctaagaa	gtcccgaact	tcctctcttt	1920
ctagcaatga	cagtggaagt	aaaggttgga	tccagcttcc	cgaggtggag	ctgtcagttt	1980
ccacaaagaa	agagtagcag	gcctttgtag	aacaaaacat	cagccttggt	tgtgtgtgtg	2040
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tggcccggtg	gcaagcgcgt	aaaaaccgac	cgctgtgag	ctctgggaac	tatacagata	2160
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ttagaatctg	tttgcaaat	gtccaaacca	ccccctcaac	atgagggcct	tcctatttct	2640
gtgttttgtg	agggaactgt	ttccttcagt	cgcctatgtt	ctgatattta	gttctgattt	2700
cttttttaaca	aatgttatca	tgtattaagaa	aatttccagc	actttaatgg	ccaattaaact	2760
gagaatgtaa	gaaaattgat	gctgtacaag	gcaaaataag	ctgtttatta	accttgaaaa	2820
aaaaaaaaaa	aaggggggga	ggggggggag	ggggggagg	gggggggggt	aggggggggg	2880
agggaggggaa	agggggggcg	ggggagg				2906

(2) INFORMATION ON SEQ ID NO. 153:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2367 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```

gctcccgcc  cgccgcctct  gtctccctct  ctccacaac  tgcccaggag  tgagttagctg  60
ctttcggtcc  gccggacaca  ccggacagat  agacgtgcgg  accgcccacc  acccccagcc  120
gccaactagt  ccgctcgccg  ctggcgctct  cctctccag  gtccatccgc  catgtggccc  180
ctgtggcgcc  tegtgtctct  gctggccctg  agccaggccc  tgccctttga  gcagagagcc  240
ttctgggact  tcaccttgga  cgatgggcca  ttcatgatga  acgatgagga  agcttcgggc  300
gctgacacct  cggggctcct  ggaccgggac  tctgtcacac  ccacctacag  cgccatgtgt  360
cctttcgctt  gccacttgca  cctgcgggtg  gttcagtgct  ccgacctggg  tctgaagtct  420
gtgcccaaat  agatctcccc  tgacaccacg  ctgtgtgacc  tgcagaacaa  cgacatctcc  480
gagctccgca  aggatgacct  caagggtctc  cagcacctct  acgacctcgt  cctggtgaac  540
aacaagatct  ccaagatcca  tgagaaggcc  ttcagccacc  tgcggaagct  gcagaagctc  600
tacatctcca  agaaccacct  ggtggagatc  ccgcccaccc  tacccagctc  cctggtggag  660
ctccgcatcc  acgacaaacc  catccgcaag  gtgcccaagg  gagtgttcag  tgggctccgg  720
aacatgaact  gcatcgagat  ggccgggaac  ccactggaga  acagtggctt  tgaacctgga  780
gccttcgatg  gcctgaagct  caactacctg  cgcactctag  agggccaagct  gactggcctc  840
cccaagagcc  tccctgagac  cctgaatgaa  ctccacctag  accacaacaa  aatccaggcc  900
atcgaaactg  aggaacctgt  tctgtactcc  aagctgtaca  ggctgggctt  agggccaac  960
cagatcagga  tgatcgagaa  cgggagctct  agcttctcgt  ccacctctcg  ggaagctcc  1020
ttggacaaca  acaagtgtgc  cagggtgccc  tcagggtctc  cagactccaa  cctgtccctg  1080
gtggtctatc  tgcaactcaa  caacatcacc  aaagtgggtg  tcaacgactt  ctgtccctat  1140
ggcttcgggg  tgaagccggc  ctaactacaac  ggcatacgcc  tcttcaacaa  ccctgtcccl  1200
tactgggagg  tgcagccggc  cactttccgc  tgcgtcactg  accgcctggc  catccagttt  1260
ggcaactaca  aaaagttaga  gcagctgcag  ccacgcgggg  cctcgaagtg  ggctctctgg  1320
ggaaacacag  cagacatctt  gatggggagg  cagagccagg  aagctaagcc  agggccagcc  1380
tggttcacac  ccagccccc  acctcgggtc  cctgacccca  gctcgatgcc  ccatcaccgc  1440
ctctccctgt  ctcccaaggg  tgcaggtggg  cgcaaggccc  ggcccaccat  acatgtttcc  1500
ttggctctag  agctgcctct  gctctccacc  cacagccacc  cagaggcacc  ccatgaagct  1560
ttttctcgtt  tcaactccaa  acccaagttg  ccaaggctct  agtctctagg  gaacagtcct  1620
tgggtcagca  gccagggagg  ggtccataag  aatggggaca  gtgggctctg  ccagggctgc  1680
cgcaactgtc  cagacacaca  tgttctgttc  ctctctctca  tgcatttcca  gcctttcaac  1740
cctcccagca  tctggcgctc  cctcagcccc  ccttgaagt  tcatggctgt  tctctccaag  1800
acctctgtc  cactggcctt  tcgaccagtc  ctccctctgt  ttctctcttt  cccctccttt  1860
cctctctctc  tctgtgtgtg  tgcgtgtgtg  gtgtgtgtgt  gtgtgtgtgt  gtcttgtgtg  1920
tctctcagcc  ttctctgctt  ctgagcttgg  tggcctgttc  cctccatctc  tccgaacctg  1980
gcttcgctgt  tccctttcac  tccacacct  ctggccttct  gccttgagct  gggactgctt  2040
tctgtctgtc  cggctctgac  ccagccccct  cccacaaaac  cccagggaca  cgggtctccc  2100
cagctctgct  tgcctaggcc  ttgcccccaa  acctgtactg  tcccgaggga  ggttgggagg  2160
tggagggcca  gcatcccgcg  cagatgacac  catcaaccgc  cagagtccca  gatcccggtt  2220
tctctagaaa  cccctcaccc  ccaactggcc  actggtggct  aggtctcccc  ttatccctct  2280
ggtccagcgc  aaggaggggc  tgcttctgag  gtcggtggct  gtcttcccat  taaagaaaca  2340
ccgtgcaacg  tgaaaaaaaa  aaaaaaa

```

2367

(2) INFORMATION ON SEQ ID NO. 154:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1314 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```

cacacacctg cacatactca tgcatgcaca tgtacacacg cagtcacaca tgcactcacg 60
cagtttgaca cacacgcgat ctoactccca cactgtgtgc actcaggtag ctgtgttgga 120
cagttggggc cagggtctcc ctgctgtcct gtggggccgg catctgctct cttctcttct 180
ccccaggtac ttctactccc gaaggattga catcaccctg tcgtcagtca agtgcttcca 240
caagctggcc tctgcctatg gggccaggca gctgcagggc tactgcgcaa gccctettgc 300
catcctcctc ccccaggacc cctcgtttcca gatgccctg gacctgtatg cctatgcagt 360
ggccacaggg gacgcccctg tggagaagct ctgcctacag ttctggcct ggaacttcga 420
ggccttgacg caggccgagg cctggcccag tgtcccaca gacctgctcc aactgctgct 480
gcccaggagc gacctggcgg tgcccacgga gctggcccta ctgaaggcgg tggacacctg 540
gagctggggg gagcgtgcct cccatgagga ggtggagggc ttggtggaga agatccgctt 600
ccccatgatg ctcccaggag agctctttga gctgcagttc aacctgtccc tgtactggag 660
ccacgagggc ctgttccaga agaagactct gcaggccctg gaattccaca ctgtgccctt 720
ccagttgctg gcccggtaca aaggcctgaa cctcaccgag gataccctaca agccccgat 780
ttacacctcg cccacctgga gtgcctttgt gacagacagt tctggagtg caccgaagtc 840
acaactggtc tatcagtcga gacggggggc ttgtgtcaaa tattcttctg attacttcca 900
agccccctct gactacagat actacccta ccagtccctc cagactccac aacacccagc 960
cttctctctc caggacaaga ggggtgctctg gtcctgtgct tacctcccca ccattccagag 1020
ctgctggaaac taagcgtctt cctgctcctc ggacgagctc cctgtctctg gcctcaccaa 1080
gtctctggcg tcagatcgca ccattgccta cgaaaaaaaa gccctgatgc tctgcgaagg 1140
gctcttctgt gcagacgtca ccgatttcga gggctggaa gctgcgattc ccagtgcctt 1200
ggacaccaac agctcgaa gaacctcctc cttccctctc ccgggcagag cttttcaaac 1260
gggctttccg caacgggtca atccgcgcct ttctaacttg acaaaacttt tcag 1314

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(2) INFORMATION ON SEQ ID NO. 155:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 965 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```

cctcccaaaag gaactcccca atactagaac tcatcccaaa ccccttgcac ttcaacaaat 60
taacgaaccc attccccaac ccacaatacc ccacccctcca acaacctaata acaacgactt120
catgctcccg tgcccaaaaac gcacagacct tcaacctgga cggctccctg arctatgaaa180
gaactcccatc gtcttgacagt cgggtctcac cagcgtgcgg cagaaaaatcg agaaggagga240
tgacagtcaa ggcgaggaga gtgaggagga ggaagagggc gaggaggaag gctccgaatc300
cgaatctcgg tccgtcaaaag tgaagatcaa gcttgcccgg aaggagaagg cacaggaccg360
gctgaagggc ggcgggcggc ggcggagccg agggctcccg gccaaagccgg tcgtgagtga420
cgatgacagt gaggaggaac aagaggagga ccgctcagga agtgggcagcg aagaagactg480
cttagcagta acgggtagca gcagatgtag ttccagactt ggagtaaaac tgtataaaca600
aaagaatctt ccatatctat acagcagaga agctgtagga ctgtttgtga ctggccctgt660
cctggcatca gtagcatctg taacagcatt aactgtctta aagagagaga gagagaattc720
cgaattggggg aacacaacgat acctgttttt cttttccggt gctggcagta ctgttgcgc780
gcagtttgga gtcactgtag ttaagtgtgg atgcatgtgc gtcaccgtcc actcctccta840
ctgtatttta ttggacaggt cagactcgcc gggggcccg cagagggtatg tcagtgtcac900
tggatgtcaa acagtaataa attaaaccaa caacaaaaac caaaaaaaaa aaaccaagg960
cgaga                                     965

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(2) INFORMATION ON SEQ ID NO. 156:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 3101 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```

ctcgcgccgg acacaggagg cagcggagcac gcgtttcccg caaccggata ccatgggaca 60
ggattttctcc gcctcagccc aacggggagg gctagtgtgca catagtgtatt tagatgaaaag 120
agctatttgaa gctttaaaag aattcaatga agacggtgca ttggcagttc ttcaacagtt 180
taaagacagt gatctctctc atgttcagaa caaaagtgcc tttttatgtg gagtcatgaa 240
gacttacagg cagagagaaa aacaaggggac caaagttagca gattcttagta aaggaccaga 300
tgaggcaaaa attaaggcac tcttggaagg aacagggtac acacttgatg tgaccaactgg 360
acagagggaag tatggaggac cactccaga ttccggttat tcaggtcagc agcctttctgt 420
tggcactgag atatttgtgg gaaagatccc aagagatcta tttgaggatg aacttggttc 480
attatttgag aaagctggac ctatatggga tcttcgtcta atgatggatc cactcactgg 540
tctcaataga ggttatgcgt ttgtcacttt ttgtacaaaa gaagcagctc aggaggctgt 600
taaactgtat aataatcatg aaattcgttc tggaaaaaat attggtgtct gcatctcagt 660
tgccaacaat aggccttttg tgggctctat tcctaagagt aaaaccaagg aacagattct 720

```

3101

(2) INFORMATION ON SEQ ID NO. 157:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 983 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

```

ggggcgggag cggcggtcca gactggggag ggacgcgcac cggccaggag gcttcaagag 60
gggggcacta gggccctgcg agcggcgctct taaccggcgg cgctaggact cgcggggaaa120
cggcgggggg ggacgggagg caccaggacc cagggggaacc gcgacgggcg ggcggcgagc180
aggcccgggg ggcggggagt gcgggcgggc ggcgtggacc cgacggggcg agagagggccc240
cgagatgccg agcaagaaga agaagtacaa cgcgcgggtc ccgccgggcg ggatcaagaa300
gatcatgcag acggaacgaag agattgggaa ggtggcgggc gcggtgcctg tcatcatctc360
cggggcgctc gagctcttcc tagagtgcgt gttgaagaag gcctgccagg tgaccagctc420
gcggaacgga aagaccatga ccacatccca cctgaagcag tgcatcgagc tggagcagca480
gtttgacttc ttgaaggacc tgggtggcat tgttcccgac atgcaggggg acggggaaga540
caaccacatg gatggggaca agggcgcccg caggcccgga agccaggcag cggcgggccg600
aagaacggtg ggatgggaac gaaaagcaag gacaagaagc tgtccgggag agactcggag660
caggaggatg aatctgagga cacagatact gatggggaag aggagacatc acaaccccca720
ccccaggcca gccacccttc tgcccacttt cagagccccc cgacaccctt cctgcccttc780
gcctctactc tgcctttgcc cccagcgccc ccggggccct cagcacctga tgaagaggac840
gaagaagatt acgactccta gcgccttctg ccccccagac catagccctt tttagtgtgt900
tttagttgct ctggggggag gagagaaggt agagctgttc ttaaaattat taaaaaaa960
aataaaaggg aaaaaaaaaa aaa

```

983

(2) INFORMATION ON SEQ ID NO. 158:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 293 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

FIDSYRCFQP KQEGAFTCWS AVTGARHLNY GSRLDYTLGD RTLVIDTFQA SFLLEVMGS 60
DHCPVGAVLS VSSVPAKQCP PLCTRFLPEF AGTQLKILRF LVPLEQSPVL EQSTLQHNNQ120
TRVQTCQNK QVRSTRPQPS QVGSSRGQKN LKSYFQSPS CPQASPOIEL PSLPLMSALM180
TPKTPEEKAV AKVVKQAQT SEAKDEKELR TSFWSVLG FLRTPLCGGH REPCVMRTVK240
KPGPNLGRRF YMCARPRGPF TDPSSRCNSS SGAGFAEFME AWGHLAWSPL HMI 297

(2) INFORMATION ON SEQ ID NO. 159:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 131 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

ETLREKQEEA QGRGAGLRSC AGVTMPDVPR PPLVQLGLLQ RKNCTGRRGQ WEDPGAWHTC 60
RSGGPSWVLA SSQYASHMAP CGPHRGVCAR APPAQTSRMR SVTPSHLWLL KSWPAPSPLW120
PLPSLLESSG S 131

(2) INFORMATION ON SEQ ID NO. 160:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 94 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

KRRPKLGGPF FTVRITHGSL WPPQRGVRKG PASTDFQNEV RNSFSSLASE VLACPFTTLA60
TAFSSGVFGV MRALISGRLG SSMSGEAWGQ LGEG 94

(2) INFORMATION ON SEQ ID NO. 161:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 136 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

LHQLAAQRLY LRPVRVGAWA LSLPGERRAE ISNQWSALVT WIEPEGREGST VSSAADCCSK 60
NVSTSFESP SHGNPSTPTR DPTPAVSRIS STCTSRDPND SCTNEHYGSC SNCLSTHCYV120
GWKAFGRKKK SSRLKG 136

(2) INFORMATION ON SEQ ID NO. 162:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 281 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

PGSQKVAKAV FFPQRTAAV RMSFPPHLNR PPMGIPALPP GIPPPQFFGF PFPVPPGTPM 60
IPVPMISAP APTVLVPTVS MVGKHLGARK DHPGLKAKEN DENCGETTV FVGNISEKAS120
DMLIRQLLAK CGLVLSWKRQ QGASGKLQAF GFCEYKEPES TLRALRLLD LQIGKKLLV180
KVDAKTKAQL DEWKAKKAS NGNARPETVT NDDEEALDEE TKRRDQMIK AIEVLIREYS240
SELNAPSQES DSHPQEEEG KEGGHFPQIS SGPTDPLSTH H 281

(2) INFORMATION ON SEQ ID NO. 163:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 103 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

CSLVQESLGS LEVQVEEILE TAGVGSVLGV LGFPWEGDSN EVKTFLLQQ SAAEETVLPS 60
 RPSGIQVTS A LHWFEISARR SPGRLSAQAP TRTRKYSRC AAS 103

(2) INFORMATION ON SEQ ID NO. 164:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 127 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

NISLLDHPGL QSCLYFLFWI LFTNRERYIS AWKWPDVWKL DIWHFGLSH GYYSHNKDGS 60
 GNSFLDLDP SRYLGIYYIL FCIFLVLWRD SLAIFGLPEY VFCVYSA PVK WFCLVCHNPH120
 GCYMSIS 127

(2) INFORMATION ON SEQ ID NO. 165:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 382 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

```

HEVLCCRMALP LQKAKVIRLI KISPEKPTIL AVGDGANDVS MIQEAHVIGIG IMGKEGRQAA 60
RNSDYAIARF KFLSKLLFVH GHFYIIRIAT LVQYFFYKRV CFITPQFLYQ FYCLFSQQTLL120
YDSVYLTLYN ICFTSLPILI YSLLEQHVDP HVLQNKPTLY RDISKNRLLS IKTFLYWTIL180
GFSHAFIFFF GSYLLIGKDT SLLGNGQMFG NWTFGTLVET VMVITVTIKM ALETHFWTWI240
NHLVTWGSII FYFVFSLFYG GILWFLGSQ NMYFVFIQLL SSGSAWFALI LMVVTCLEFLD300
IIKKVFDRLH HPTSTEAQAM YSNTVALSDE FIALQPLSRA RNQLSKLSLL KQMNVSSAWT360
PCAVSRKEKQ RVHLLLECWN EL
382

```

(2) INFORMATION ON SEQ ID NO. 166:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 85 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

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QELNKKHIHI LGAQKWPNP SIKQGKYKIK YNRSPGNEMV DPSPKMSFQS HLYCDCNNHD60
CEDQSAKCEV SKHLAISQKR CIFY
85

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(2) INFORMATION ON SEQ ID NO. 167:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 496 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

RLEKGPLPFQ MPGMRLPETQ VLPGEIDETP LSKPGHDLAS MEDKTEKWSS QPEGPLKLKA 60
 SSTDMPSQIS VVNVQQLWED SVLTVKFPKL MVRPFSFPAP SSEDDVFIPT VREVQCPEAN120
 IDTALCKESP GLWGASILKA GAGVPGEPQV DLNLPLEAPP ISKVVRVHIQ AQVESQEVTI180
 HSIVTPEFVD LSVPTFTSTQ IVRESEIPTS EIQTPSYGFSS LLKVKIPEPH TQARVYTTMT240
 QHSRTQEGTE EAPIQATPGV DSISGDLQPD TGEFFEMISS SVNVLGQQTLL TFEVPSGGHL300
 ADSCSDEEPA EILEFPDDDS QEATTPLADE GRAPKDKPES KKSGLLWFWL PNIGFSSSSVD360
 ETGVDSKNDV QRSAPIQTQP EARPEAELPK KQEKAGWFRF PKLGFSSSPT KSKSTEDGA420
 ELEEQKLQEE TITFFDARES FSPKEKEEGE LIGPVGTGLD SRVMVTSAR TELILPEQDR480
 KADDESKGSG LGPNEG 496

(2) INFORMATION ON SEQ ID NO. 168:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 125 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

SLFASMYWDS KSHSLKFLLA TSLQTAVQMR SQQKFLSFPPL MIAKRQPHHW QMKAGLQKTN 60
 QKVKNLVCSG FGFQTLGFPL LLMRQVLIPK MTSRDLLPFK HSLRHDQRQN CLKNRRRQAG120
 SDFPN 125

(2) INFORMATION ON SEQ ID NO. 169:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 130 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

MGADLWTSFL ESTPVSSTEE ENPMFGSQNQ SRPDFLLSGL SFGALPSSAS GVVASWLSSG 60
 GNSRISAGSS SEQLSASWWP EGTSNVSVCC PSTLTLEEII SNGSPVSGWR SPEMESTPGV120
 ACMGASSVPS 130

(2) INFORMATION ON SEQ ID NO. 170:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 123 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

VVYRGVKCFI DKKKKTALEP TYSSSSSSSS SSSSSSSSSS SSSSSSSSSS SFFFLLFSA 60
 LTTFFFAAGS FPLARYAAS FSYFSFTSQP SFHKAACHLQ QCYSTSLPVS SQHHQWTGQD120
 VLL 123

(2) INFORMATION ON SEQ ID NO. 171:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 157 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

KKLYLLRSIQ NVNKTAAIFF LQLQSGIQLT EQQLSSYKHL QRQLKMKKIK PKKKTKRKKK 60
 KKQKTKLPSP YITNLCCAPT RTCEKFFCQF TTPILYQARL VAIENTTTRTG LSKDTFGSVL120
 TIQKKTLYSL KTNLTQPYIS IFFFKRSELC TGGNLAL 157

(2) INFORMATION ON SEQ ID NO. 172:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 152 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

```

LNMGKGDPKK PRGMSSYAF FVQTCREEHK KKHDPASVNF SEFSKKCSER WKTMSAKEKG 60
KFEDMAKADK ARYEREMKTY IPPKGETKKK FKDPNAPKRP PSAFFLFCSE YRPKIKGEHP120
GLSIGDVAKK LGEMWNNTAA DDKQPYEKKA AK                                     152

```

(2) INFORMATION ON SEQ ID NO. 173:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 281 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```

SGSAGGPRG PRATESGKRM DCPALPPGWK KEEVIRKSGL SAGKSDVYFF SPSGKKFRSK 60
PQLARYLGNT VDLSSFDFTI GKMMPSKLOK NKQRLRNDPL NQNKGKPDNL TTLPIRQTAS120
IFKQPVTKVT NHPSNKVKSD PQRMNEQPRQ LFWEKRLQGL SASDVTEQII KTMELPKGLQ180
GVGPGSNDST LLSAVASALH TSSAPITGVV SAAVEKNPAV WLNTSQPLCK AFIVDEDIDR240
KQEERVQQVR KKLEALMAD ILSRAADTEE MDIEMDSGDE A                               281

```

(2) INFORMATION ON SEQ ID NO. 174:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 102 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

IIDIIYIKNTS KKALVSAIKK LYVLGYIFFL TGKSQWKHFC SISRNELLGK VGRKLDPDHL 60
RLHLHCPFQY PSLLYQQLAT RCLPSVLLPI SCVLAVLALP VS 102

(2) INFORMATION ON SEQ ID NO. 175:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 147 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

IYTSKIHLLKR HWLVLLKSSM CSGTFFFLQA KASGNIFVQF LGIFSWGKSV ESYLIIFLGF 60

ISTVHENIHL FCISSSRQDV CHOCFFQFLA YLLYSFLFP DVFICDNKSF AEGLRCVKPN120
SRVLFHSSGD LPCDWRRACV QSTGNSR 147

(2) INFORMATION ON SEQ ID NO. 176:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 85 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

ECPLGARGFW EPRHPFPLGR GARSRHPCTH GLAPPQSFP HSQQPFHSHC PSRSPQPSLR60
PHPHPLRAQG CNFSLSTTHR WYSWG 85

(2) INFORMATION ON SEQ ID NO. 177:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

NALWGPGAPG SPATLSHLAG VPAAATPARM AGWHPPRALP TASSLSTVTA LPAVPSLPYG 60
LIRTPSEFRA ATPHYPPRTD GTAGAEQPHV EPERVPGARG QDAGGRMTAC PCLTSWGTLL120
DRGIGQDP 128

(2) INFORMATION ON SEQ ID NO. 178:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

MPFGGQGPLG APPFPFTWPG CPQPPPLHAW QAGTFPEPSP QPAAFPQSLP FRQSPAFPTA 60
SPAPFQSPGL QPLIIHHAQM VQLGLNNHMM NQRGSQAPED KTQEAE 106

(2) INFORMATION ON SEQ ID NO. 179:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GNPELPWRKF QCQHSCSLWP SPTLWPEIPQ SNLEPKRTQR TLDPNCPRPS PEVGVTNSSG60
 LRHMKKLYIN PRQATNF 77

(2) INFORMATION ON SEQ ID NO. 180:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

PPTHTRQVGE EIQSCHGENS SVSILAPCGP LLHSGQRYHS QTWSQKGHKG LSTQTAPDPL60
 QRLG 64

(2) INFORMATION ON SEQ ID NO. 181:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 206 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

RLSCAGTLSG SGPHPSRRLT QGRWVRKSRV AMEKIPVSFA LLLVALSYTL ARDTTVKPGA 60
KKDTKDSRPF LPQTLSRGWG DQLINTQTYE EALYKSKTSN KPLMIHHLD ECPHSQALKK120
VFAENKEIQK LAEQFVLLNL VYETTDKHLs PDGQYVPRIM FVDPSLTVRA DITGRYSNRL180
YAYEPADTAL LLDNMKKALK LLKTEL 206

(2) INFORMATION ON SEQ ID NO. 182:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 206 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

RVFQEEELVR RQRNGASGPR PGLRRLRGGR RAVRRKERLL HRQLPAVHKR GARVKLSSPE 60
RDVERDVFLY RAYLAQRKFG VVLDEIKPSS APELQAVRMF ADYLAHESRR DSIVAELORE120
MSRSVDVTNT TFLLMASIIY LHDQNPDAAL RALHQGDSLE CTAMTVQILL KLDRLDLARK180
ELKRMQDLDE DATLTQKVL VSLQRV 206

(2) INFORMATION ON SEQ ID NO. 183:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 111 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

LPRPRESEGQ HRGRAGPRDE QERGRDQHHL PAHGRHLHLSF RPEPGCRPAC AAPGGQPGVH 60
SHDSADPAEA GPPGPRPEGA EENAGPGRGC HPHFAQGLGK LATGVKAQGS F 111

(2) INFORMATION ON SEQ ID NO. 184:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 165 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

GTILPIPEIR RILELLHPLQ AYQDLELGEG GILVQVLHSL QLLPGEVQAV QLQQDLHCHG 60
CALQAVPLVQ RTQGGIRVLV VEIDGGGHEQ EGGVGHVHAF AHLVSVQLGHD AVPPTLVGEVI20
VSKHAHGLEL RGRGGLDLIQ DHTELPLRQV RSIQEDVPLH VSLWA 165

(2) INFORMATION ON SEQ ID NO. 185:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 75 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

LLSMRMILKP QSMILMMLR SSNRVTWKLL LIGLDYIRYQ MENQKTSLLL MENSKTRLLL60
LKLLNPLINV GKXCL 75

(2) INFORMATION ON SEQ ID NO. 186:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 340 amino acids
- (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```
RTVIDAMSAL LRLRLTGAPA AACRLRGTSA GTGSRRAMAL YHTEERGQPC SQNYRLFFKN 60
VTGHIYISPFH DIPLKVNSKE ENGIPMKRAR NDEYENLFNM IVEIPRWTNA KMEIATKEPM120
NPIKQYVKDG KLRVYANIFP YKGIWNYGT LPQTWEOPHE KDKSTNCFGD NDPIDVCEIG180
SKILSCGEVI HVKILGILAL IDEGETOWKL IAINANDPEA SKFHDIDDDVK KFKPGYLEAT240
LNWFRLYKVP DGKPENQFAF NGEFKNKAFA LEVIKSTHQC WKALLMKKCN GGAINCTNVQ300
ISDSPFRCTQ EEARSLVESV SSSPNKESNE EEQVWHFLGK 340
```

(2) INFORMATION ON SEQ ID NO. 187:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 131 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```
LSILYILFNG IHWLLGGNLH FSICPPRYFY NHIKQILIFI ISCFLHRNAI FLFRVHLQRN 60
IMKGGNVVTS YILKEEAVIL RAGLAALLSV VQGHSTARPG PCTGPQPQAR SGWGTRAQQP120
QQRAGHVNDG P 131
```

(2) INFORMATION ON SEQ ID NO. 188:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 436 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```
GRGMGRVQLF EISLSHGRVV YSPGEPLAGT VVRVLGAPLP FRAIRVTCIG SCGVSNNKAND 60
TAWVVEEGYF NSSLSLADKG SLPAGEHSFP FQFLLPATAP TSPEGPFPGKI VHQVRAAIHT120
PRFSKDRKCS LVFYILSPLN LNSIPDIEQP NVASATKKFS YKLVKTGSVV LTASTDLRGY180
VVGQALQLHA DVENQSGKDT SPVVASLLQK VSYKAKRWIH DVRTIAEVEG AGVKAWRRRQ240
WHEQILVPAL POSALPGCSL IHIDYYLQVS LKAPEATVTL PVFIGNIAVN HAPVSPRGL300
GLPPGAPPLV VPSAPPQEEA EAEAAAGGPH FLDEPVFLSTK SHSQRQPLLA TLSSVPGAPE360
PCPDGSPAS HPLHPPLCIS TGATVPYFAE GSGGPFVFTTS TLILPPEYSS WGYPYEAPPS420
YEQSCGGVEP SLTPES 436
```

(2) INFORMATION ON SEQ ID NO. 189:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 127 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

```
SVLFTGVVSP GFSLLPPPPFQ PQGEEGCGRC AGRGWAGPEW ARLQCERRHE ALGAPVPGQR 60
PGLPGEGSTG SALRGQAGFH AAAALLIRRW GLIGVAPRTV LWRKNQGAGS GHWPFGALCK120
VGDSGTC 127
```

(2) INFORMATION ON SEQ ID NO. 190:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 213 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

LVLNVGMQLQ CLPHHIAAEI SAGCEDHAAR LHQLVGELLG GRGHVGLLNW WDAVQVQGAQ 60
DIEHEAALVI LGKFWRVDDG PHLVHDLPER TLKGRGCSGR KQELEGEAVL SSGQAPLVQC120
RQGTVEVTLH HYPRCVISLV GDPAGTVAGH PDGSEQRCP QAHAHGSPQR LPGAVDDAAV180
AQADLEELHS PHAAASPASR AATPPPAARE SRL 213

(2) INFORMATION ON SEQ ID NO. 191:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 635 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

GGVSPWRACV QORMEESEPE RKRARTDEVF AGGSRSEAE EDDDEDYVPVY PLRQRRQLLL 60
QKLLQRRRKG AAEEEQQDSG SEPRGDEDDI FLGPQSNVSL LDQHQHLKEK AEARKESAKEL20
KQLKEEEKIL ESVAEGRALM SVKEMAKGIT YDDPIKTSWT PPRYVLSMSE ERHERVVRKKY180
HILVEGDGIP PPIKSFKEMK FPAAILRGLK KKGIIHPTPI QIQGIPTILS GRDMIGIAFT240
GSGKTLVFTL PVIMFCLEQE KRLPFSKREG PYGLIICPSR ELARQTHGIL EYYCRLLQED300
SSPLLRCALC IGGMSVKEQM ETIRHGVHMM VATPGRLMDL LQKKMVSLOI CRYLALDEAD360
RMIDMGFEGD IRTIFS YFKG QRQTLFSAT MPKKIQNFAK SALVKPVTIN VGRAGAASLD420
VIQVEVYVKE EAKMVYLLEC LQKT PPPVLI FAEKKADVDA IHEYLLKGV EAVAIHGGKD480
QEERTKAIEA FREGKKDVLV ATDVASKGLD FPAIQHVINY DMPEETENVV HRIGRTGRSG540
NTGIATTFFIN KACDESVLMD LKALLLEAKQ KVPVVLQVLH CGDESMLDIG GERGCAFCGG600
LGHRITDCPK LEAMQTKQVS NIGRKDYLAH SSMDF 635

(2) INFORMATION ON SEQ ID NO. 192:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 147 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

KPSRRRCRPEC RCIAGMSEC WTLEESAAPV SAGAWVIGSL TAPNSRLCRP SRSATSVART 60
 TWPTAPWTSE PTVFPSLQEA SVPKTATSLH IQQPPGQNH FSSAGLEWAR LVLARCSLCS120
 SELLFLFPET PAAIKAQTS PPKKKKKK 147

(2) INFORMATION ON SEQ ID NO. 193:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 150 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

DILLALPECL DGLSPFLLVF APMDGYGLNP LEQQVLVDGV HVCLLLCKDE YRRGCLLQAL 60
 EQVHHLGLLL HIFYLLDDIQ AGSPSAPHID GHRLYKGTLS KVLNLLRHGG TEEQGLSLAL120
 EVGEDGTDVT LEAHVDRAVS LVQQQVATDV 150

(2) INFORMATION ON SEQ ID NO. 194:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 310 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
 (iii) HYPOTHETICAL: yes
 (vi) ORIGIN
 (A) ORGANISM: HUMAN
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

EAPAAARTQS PAAAAQRGDN VYVVTEVLQT QKEVEVTRTH KREGSGRFSL PGATCLQGEG 60
 QGHLSQKKTV TIPSGSTLAF RVAQLVIDSD LDVLLFPDKK QRTFQPPATG HKRSTSEGAW120
 PQLPSGLSMM RCLHNFLTGD VPAEGAFTED FQGLRAEVET ISKELELLDR ELCQLLLEGL180
 EGVLRDQLAL RALEEALEQC QSLGPVEPLD GPAGAVLECL VLSSGMLVPE LAIPVVYLLG240
 ALTMLSETQH KLLAEALESQ TLLGPLLELVG SLLEQSAFWQ ERRPCPCPPG SWGTAGAKEH300
 RPGSCWTSVA 310

(2) INFORMATION ON SEQ ID NO. 195:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 244 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

TTGIASSGTS IPEDNTRHSR TAPAGPSRGS TGPRLWPCSS ASSKARRASW SRSTPSRPSS 60
 SSWHSSLKSS SSSLEMVSTS ARRPWKSSVN APSAGTPSVR KLWRHLIMER PEGSCGQAPS120
 LVERLWFPVAG GWKVLCLFLSG KRRTSKSESI TSWATRNARV LPEGMVTVEF WLRWFPSPC180
 KHVAPGRENR PEP SRLWVRV TTSFVCVST SVTTYTLSPR CAAAAGLCVL AAGASHGAE240
 SARC 244

(2) INFORMATION ON SEQ ID NO. 196:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 229 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
(A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

TGHMATGLLA FLGLAAGGQT LCPAGELPGH ARAQASGAPG SVLIAVPGRR RVHTCGPGPA 60
 APSTRGECPP PALGHTRPAP PRPVLLRPSC SPGARGAGTW SALLPRGTLT QEAHQLERP120
 QQGLRLQLRL QQLVLRFTQH GQCPQVDNR DSEFRHQHSG GQHQALQDST CWTVQGLHRP180
 KALALLQRL QGSQGLVLPQ HPLQALQQQL AQLSVQKLQF LGDGLHLCF 229

(2) INFORMATION ON SEQ ID NO. 197:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 95 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
(A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TEILPVFVRL AGVPICSTGN ASAMLQPKP GLSLQQQAEF CLWSGAVHSS VCLVLGLELD60
 RGGVSSPSLN SEQTLCLAPV CPGNSPGPHW EPLVF 95

(2) INFORMATION ON SEQ ID NO. 198:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 101 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
(A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

AVPRGSLRED GKVRMSNLL MAGSPCLPLS LALVIAELCA QCCGLAVARL FLWGARAGCG 60
 NQSSQTDVSG AEDSFLAEVS PHLQVSGWGG ARRGRHTPCL T 101

(2) INFORMATION ON SEQ ID NO. 199:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

```

VRHTSHLAVL TQGAPGHCS AAWALLLRTP RAPNEGLGNC LGTLGPGTGS VLNSGKVKRP 60
HLYPAQAQEQ GRQSCGQHPT TDTVLPAGV RGLVSEAAAW HWHCLCYRWG LLRVSIQGEI20
FQFTQPKGPV CRAALTRAQ HSTELGKGRG ERVKD                               155

```

(2) INFORMATION ON SEQ ID NO. 200:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

```

RMKCSQPPRC HFQSDFKCA PCPRAQTHWL EPPGRVQTIS SMRNAQKGFA DSIRLWRLPA 60
SGVGWVVSPP IQTQEVAPQG MYLVGSSSGT LGGCRALTQV FLSSLGCV CACACACLCF120
SLWAHQDAPR RACARVPT                               138

```

(2) INFORMATION ON SEQ ID NO. 201:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

VHGREARLGT LAGTAALKPA LLSCYQTFKG QDVLRRVPVA ARRPAAGACPR VTAWRCWGSG 60
HLPCLCQEG EAFEEASVLA ARSLSQPLPG SCTGQGLIPC HAGPLEQVGW GWIVLSPQFW120
QPCPLGKVIS DL 132

(2) INFORMATION ON SEQ ID NO. 202:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 131 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

RLFICGSLQN KQRWDWGESL GPCTFLSRAY NHVHRPGRGP ALCPTKSSLH QSSWSPLLRD 60
PAQLPRSWG I GTRVPWRVQE MRRIPCTLR TTPPELWSRG HCERRQRERH VEDTLTDPVG120
SGRAEDRHTK P 131

(2) INFORMATION ON SEQ ID NO. 203:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 76 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

LAAIKDQLEG VQQALSAAP IPEEDTDTEE GDDFELLQDS ELDQIESELG LTQDQEAQAQ60
QNKKSSGFLS NLGGH 76

(2) INFORMATION ON SEQ ID NO. 204:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 102 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

RVCSKHFLRL PPSQKRTQTL KKVMTLNYLT SQSWIKLRVN WDLHKTRKQK HSKIRSLQVS 60
FQICWEAINL GISLQQSTKN TKKISNKKKK KKRKRKKLNC KL 102

(2) INFORMATION ON SEQ ID NO. 205:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 80 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

ICLHHNHCLC DTQLLAFYGL IPPTARLEMA VNGACFFTNK PKSTTAEITW KRFSLSRVLK60
YTFKFFPKKL ILIVFPKSFN 80

(2) INFORMATION ON SEQ ID NO. 206:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 76 amino acids

(B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

GKPAALEAHQ GSRLQGRSRE QAAIPPLLSS RTQCLGLGFL FAGLAPCRTL VLELEGPILP60
 RGDSQGCGRI GWRRLV 76

(2) INFORMATION ON SEQ ID NO. 207:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 72 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

NLRVSQLEPWK PTRAPDCREE AGSRQPYLHS CPQGLSCVAL DFFLRDLRPA GHWCNWSRWL60
 SCPGVTPRVA GG 72

(2) INFORMATION ON SEQ ID NO. 208:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 73 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

PGMSSLQDRH GRTIWFQVGP YCSHRQRPQE ADGWKRGVTI TGVVMLRVCL DPPRTTFLRLR60
VTPLPSHASQ GCS 73

(2) INFORMATION ON SEQ ID NO. 209:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 182 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

QRWLWTSSTS PCWIRAFLLP AGQVWPCLSG RAPAPLTTLQ LTMQLMPKLW CPVCSSPGSH 60
CHLQRGSLLR PTLHLAPPW LLAWFNLAFC AMLELELLLF FRGGNRVESG KGLAPKCCCC120
GFFAFSKDAL PGPKLQTAVL SKQVRSLSFG AHLLSGSISI LLLATSGQRP PPHIARCWQ180
KG 182

(2) INFORMATION ON SEQ ID NO. 210:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 130 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

VGPQKQFWWG QVQCGSQQG TPLKVAVAPR AAAHWTPQLW HQLHGELQSG QRGWGPAPRA 60
RPDLPSEGRQE GPDPAARRSRG SPQPPELLIA TGTSGORLCS WESRSPGFVG LPAGDRHVSH120
RERPGSRPQL 130

(2) INFORMATION ON SEQ ID NO. 211:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 111 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

VTGKGRDPGL SCSSSWKRWs RTVTIHADTE QQYETEQLRA VSSSAEAANA ATPPFNCNHPM 60
 MSPPHLTsrw GwMAEQMKPA LWRGSLTEMH TFMGEVDGHL TSLMFHTVDC T 111

(2) INFORMATION ON SEQ ID NO. 212:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 243 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

DVQVAGPEPD CRVHSHVLPG QAHR LAPGY SVGESLQPRE GCEDCDRQKA NLRIRFKPSL 60
 FQHVGTSSSL AGKIQKLKDK DFGKQALRKE HVNPPAEVST SLKTYQHFTL EKAYLREDDFF120
 WAFTPAAGDF IRFRFFQPLR LERFFFRSGN IEHPEDKLFN TSVEVLPPDN PQSDKEALQEL180
 GRTATLRYPR SPDGYLQIGS FYKGVAEGEV DPAFGPLEAL RLSIQTDSFV WVILSEIFLK240
 KAD 243

(2) INFORMATION ON SEQ ID NO. 213:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 244 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

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GRIGVSVVMG IPSVRREVHS YLTDTLHS LI SELSPQEKED SVIVVLI AET DSQYTS AVTE 60
NIKALFPTEI HSGLLLEVIS PPHFYDPFSR LRESFGDPKE RVRWRKQNL DYCFLLMYAQ120
SKGIYYVQLE DDIVAKPNYL STMKNFALQQ PSEDWMILEF SQLGFIGKMF KSLDLSLIVE180
FILMFYRDKP IDWLLDHILW VKVCNPEKDA KTVTGRKPTC GSASNRPS SS TWALTRWLA240
RSRN
244

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(2) INFORMATION ON SEQ ID NO. 214:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 210 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

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PAESQPADPL QTVPLPARGH SLLAGWQDPE TEGQRLWKAG AAE GACEPAS RGEHEPEDIP 60
ALHPGESLPA RGLLLGLHPC RGGLHPLPLL PTSKTGAVLL PQWEHRAPGG QALQHVCGGA120
ALRQPSVRQG GPAGGPHRHP FVPSEPRRLP PDRLLQGS G RGRGGPSLRP SGSTAPLDPD180
GLPCVGDSE RDLPEKGRLSC GLLRVPCGQP
210

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(2) INFORMATION ON SEQ ID NO. 215:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 128 amino acids
(B) TYPE: Protein
(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

GGAGLVHGS A DWPCLAPWRV SSCFLPGTEL RGLGAPGAKS RLWCRGGGLS LNRHPEVLLR 60
CWVHPewHGE QLWPVLLFRP VLGKLSGGPS LQRFRMGWVN GTNGEWFEEL RVKRAPVCWL120
QRPGAPLS 128

(2) INFORMATION ON SEQ ID NO. 216:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 124 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

FPQDWPRKEH RPQLLEVPFLR VDPASQEHLR VSVKRQASTP APEPALSSRC PQTPQLCARQ 60
EAARHTPGRQ ARPVRGPMDB PSPASGKTGP FFTGHAPELW QIAGAIVWGE FNKSPFENEK120
KKKK 124

(2) INFORMATION ON SEQ ID NO. 217:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 142 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

VPHTHPILGL CKEGPELSFP RTGLGRSTGH SCSPCHSGWT QHLRSTSGCR LRDRPPPLHQ 60
 SLLAPGAPR PRSSVPGKKQ LDRQGAHKG QSADFWTSPA PPQKGQGLSL QDTPQSCGRLL120
 QEPSCGENLI KALLMKMKKK KK 142

(2) INFORMATION ON SEQ ID NO. 218:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 379 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

RRLEGFGNG WTEPMGILWM EPTQPPDFAL AYRPSFPEDR EPQIPYPEPT WPPPLSAPRV 60
 PYHSSVLSVT RPVVVSATHP TLPSAQPPV IPATHPALSR DHQIPVIRAN YPDLPASAYQP120
 GILSVHSAQ PPAHQPPMIS TKYPELFFAH QSPMFPDTRV AGTQTTTHLP GIPPNHAPLV180
 TTLGAQRPPQ APDALVLRQ ATQLPIIPTA QPSLTTSRS EVSPAHTISV PAATQPAALP240
 TLLPSQSPFN QTSPISTPH HSKAPQIPRE DGSPKALW LPSAPATAAP TALGEAGLAE300
 HSQRDDRWLL VALLVPTCVF LVLVLLALGIV YCTRCGPAP NKRITDCYRW VIHAGSKSPT360
 EPMPPRGLT GVQTCRTSV 379

(2) INFORMATION ON SEQ ID NO. 219:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 157 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

VDTDECQIAG VCQQMCVNYV GGFECYCSG HELEADGISC SPAGAMGAQG SSQLGDELLD 60
 DGEDEEDEDE AWKASTVAGR RCLGSCGWSL RSRLTLFWPI DRASQRTESE RYPTRSPPGH120
 PRSVPPGSFT TPQCSFSPGL WWSLPRIPIHC LLPTSLL 157

(2) INFORMATION ON SEQ ID NO. 220:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 211 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

PPPPGPLCLL PIKSLCLLPP SPQSPPPSCP LRAPLTRPHP SALHIPIPKP PKSQGKMAV 60
 PSWPCGCCHQ LPQQPQQPFWG RLVLPSTARG MTGGCWWHSW QQRVSFWWSC LHWASCTAPA120
 VAFMHPTSAS LTAIAGSSML GARAQONPCP PGAASQGRCP AEPACDGVQT PLMEYGALDT180
 WPGHLQGPMG AAQLDRWLPA PQAQPGSSLN H 211

(2) INFORMATION ON SEQ ID NO. 221:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 117 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

LGEPQISGAQ PGRVWGQLCQ STSQAHPLPG MPWDHGQGR L WGSETPLLT PSQNTLRVSG 60
 LWREWGGRKN WHLPREGDER FALILREASE KCFKCVCMRQ AVSGSGLSSP LPPSFPK 117

(2) INFORMATION ON SEQ ID NO. 222:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 198 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

NKELSSLSKSS DVMTHTESC ITVASRATHL FGLSDGHSFT TQQQTPHTGT RMSASTWEAV 60
 AEPGRWPGPD HGLSGAGHQG VRVPMLPQGV GMTGRSLVTR QWTSLGEGWR ERAGQAPAAH120
 RLAHANTLKA LLGGFSENQG EALVSFPRKV PILPPAPLSP EPRDPQGVLA GGAKQRCLRP180
 PEPSLPMIPR HARQGVGL 198

(2) INFORMATION ON SEQ ID NO. 223:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

SHGMPGRGWA CEVDWHSCPH TLPGWAPETW GSFSQHGVLG ACPGPFTRTE APHPLSHFSR60
 WKTQRRKRPW GGVPSCLQLA PWVFLCGGSP DSISASASE 98

(2) INFORMATION ON SEQ ID NO. 224:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 298 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

ATRRRAAEAG MAAVLQQRVER LSNRVVRVLG CNPGPMTLQG TNTYLVGTGP RRILIDTGEP 60
 AIPEYISCLK QALTEFNTAI QEIVVTHWHR DHSGGIGDIC KSNINDTTYC IKKLPRNPQR120
 EEIIGNGEQQ YVYLKDGDOI KTEGATLRLV YTPGHTDDHM ALLLEENAI FSGDCILGEG180
 TTVFEDLYDY MNSLKELLKI KADIIYPGHG PVIHNAEAKI QQYISHRNIR EQQILTLFRE240
 NFEKSFTVME LVKIIYKNTF ENLHEMAKHN LLLHLKKLEK EGKIFSNTDP DKKWKHAHL 298

(2) INFORMATION ON SEQ ID NO. 225:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 58 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GFSGWGRSPLG RCWCLGGSWD PGYSPTHARL DWTAARRAAV QQPFPPQPPA GVSPWIWL 58

(2) INFORMATION ON SEQ ID NO. 226:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 73 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

SGSLSLNHIS IFQINILLIS ISYNFFSLRI PWEFFNAIGS VIIDAFTNIS YASRMISVPV60
SHYNFLDCCV KFS 73

(2) INFORMATION ON SEQ ID NO. 227:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 141 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

AFLLRPSVTA STRLLPVCAS PRSSPGPSPA QQQQAWQQAW SSARAPSRCR ARPSSSERPC 60
PAVGRLASLY CCCMVAFSPP RRGRTWVHCT GWPRLATGLW PLTCQVWGTP RKQQLPLLLG120
SWPLAASWRL WMPWSWAPR L 141

(2) INFORMATION ON SEQ ID NO. 228:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 244 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

VPPPALGHRQ HAPASRLRES TQLPRPFTST AAAGMAASVE QREGTIQVQG QALFFREALP 60
GSGQARFSVL LLHGIRFSSE TWQNLGTLHR LAQAGYRAVA IDLPGLGHSK EAAAPAFIGE120
LAPGSFLAAV VDALELGGPV VISPSLSGMY SLPFLTAPGS QLPGFVPVAP ICTOKINAANI80
YASVKTALI VYGQDPMGQ TSFEHLKQLP NHRVLMKGA GHPCYLDKPE EWHTGLLDLF240
QQLQ 244

(2) INFORMATION ON SEQ ID NO. 229:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

WTDHNRGAQL QGIHHSROEA ARGQLPNRGR GCCFLGVPTQ WQVNGHSPVA SLGQPVQCTQ 60
 VLPGLGGEAN TMOQQYREAS LPTAGQGLSE EEGLALHLDG ALALLHACCH ACCCCAGEGP120
 GELRGLAQTG SRRVLAVTEG RRRN 144

(2) INFORMATION ON SEQ ID NO. 230:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 135 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

LEFFIPCLGS VNEACLFPGV SFHGLYFSSS SGSFAGSSLW KLHERWLGLG FAGVYSRVKA 60
 EWDLRPRLGT TQAEKGRFHH SQCPHSTTS ARAPPSLLPH PAIVRGATVG RRVPRRGLFL120
 LPVPEKAFPL LKFKH 135

(2) INFORMATION ON SEQ ID NO. 231:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GGPVCNEPQV TPFSSYSVPG ASCPPLQILG KENVYVAGYC MVTSEGRPLG THLPTAAQAR60
AQAHLLVLRP QIKPSPHHMA SDRFLPSRKF CGCAVL 96

(2) INFORMATION ON SEQ ID NO. 232:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 83 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

CCGETVNDG NVPSOPGSCS TWVSNTPLPS PWSTLQSRG PANAREVSTE KSLQNSHWKR60
RNKGHGKKPQ GRDRPRSQT GRE 83

(2) INFORMATION ON SEQ ID NO. 233:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 52 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

ASPASLAQAT SRQPAPSRA RSHLATSTSW TSSARSDAGC GECRRDPGAP PR 52

(2) INFORMATION ON SEQ ID NO. 234:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

LGSAAWQLRR PEASETLRLV GTHRPQRAL PRQRVASPPP RRGLGLTSPP VRLGQVVEGL60
 MPGVVSAAGT QVRRLEDEVA SLRLQHHLQL REGL 94

(2) INFORMATION ON SEQ ID NO. 235:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 95 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

ARFSRSWRWC CSRSDAGTSS RRRTWVPAAL TTPGIRPGTT CRRRTGGEVR PSPRRGGGLA60
 TRCLGKARWR GLCVPTSRV SDASGRASCC QAEPR 95

(2) INFORMATION ON SEQ ID NO. 236:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 174 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

APTNTRSSSK FATSGSPGYF IASSGASPEV RQRRTTFFRF RPGESLGGDM KLLTHNLLSS 60
HVRGVGSRGF PLRLQATEVR ICPVEFNPNF VARMIPKVEW SAFLEAADNL RLIQVPGKPV120
EGYEENEEFL RTMHLLLEV EVIEGTLQCP ESGRMFPISR GIPNMILLSEE ETES 174

(2) INFORMATION ON SEQ ID NO. 237:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 225 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

YRAQKHCVCW HWVKGWGYTR QNSETGYRST KIHSHNKKNW RLAQSTLSFL FTQQHVGDPA 60
ADGHTSRFR ALQGALYHFH LQQQVVHGFP KLLILLISLN RPFRLDQQTQ VIGRLQERRP120
LHFRYHTRHE VGVEFHRA DT DLGGLAQGE ATGPHPPHMR AQQIVGKQFH VAAQTLARPEL180
PEKGRPPLPH FRGCSTRCYW IARTGSGEL AGTSRVCGSS FLYAN 225

(2) INFORMATION ON SEQ ID NO. 238:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 209 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

TFNEKKIYNT ELKNTVEGVI GSRVGDTHGR IRKQIGDQQK YTVITRKTGA WHNQLSVSSS 60
LSSMLGIPRL MGNIRPDGSH CRVPSITSTS SSRWCMLVRN SSFSSYPSTG PFGTWIRRL120
SAASRNADHS TLGIIRATKL GLNSTGQIRT SVAWRRRAGKP RDPPTPTCEL SRLWVSSFSMS180
PHKLSPGGRN KKVVLRLCLS GDAPDLAIG 209

(2) INFORMATION ON SEQ ID NO. 239:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```

INAFSHRNAK ININPPDAVA AALRPKSQRP RLTIKVFSE SVGVSVNGCA LGGTVERCAK 60
SELQTIGQGH GVATRRRLSA GAPRTHSQQ SSHWEELANK HLQGRGKRPR SRRSRARASAL20
ARGAPTGSQR GGSFKRARSQ RSRVLA                                     146
  
```

(2) INFORMATION ON SEQ ID NO. 240:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 134 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```

SRTFSFLSFL HCANILTLFV SFOEPHRHIQ VKRSLNKCLQ PSQCKNKYQS SRRSSSRAAP 60
KVPTATPNNY KSVQRECNRE CEWVCAGGHG GAVCKIGVAN HRTRAWSGYF PPTQRGRASP120
HTLTAEFALG RVKK                                             134
  
```

(2) INFORMATION ON SEQ ID NO. 241:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 147 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

PARTRRPRL ARFGLEPRCE PVGAPLAALA LARERRERGR FPRPKCLFF NSSQCELCCE 60
 CVRGGAPALS RRRVATPCPC PMVCNSDEAH RSTVPPSAHP FTLTPTLSLN TFIIVRRGRW120
 DFGRSARATA SGGILIFIAL RMLKAFI 147

(2) INFORMATION ON SEQ ID NO. 242:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

PVLCRGNSGS LSRKFPPKFP KPADKDHPT CVYLENRSPG KSDLSATPGR SGLESGYQNL60
 LRQHQPGRGC PTWPGSRWKV PRRFPGYG 88

(2) INFORMATION ON SEQ ID NO. 243:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

QDGCPSDGGDF AALQSLLKAS SKDVVRQLCQ ESFSSSALGL KKLLDVTCS LSVTQEEAEE 60
 LLQALHRLTR LVAFRLDSSA EAILALFFEN FHQNLKNLLT KIILEHVSTW RTEAQANQIS120
 LPRLVOLDWR VDIKTSSDSI SRMAVAPPGL VPDGRFQGGG QAMG 164

(2) INFORMATION ON SEQ ID NO. 244:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 87 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

FAWASVLQVD TCSRMI FVSR FLRFWWKFSG KRARIASAE DRSRNATSLVR RCRAWSSSSA60
 SSWVTDKLEH VTSKSF FFKPR AELEKLS 87

(2) INFORMATION ON SEQ ID NO. 245:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 129 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

DGPGGPTAHP HRCAPFPVC FGQAPAHLLL CAAAPGHFGQ GQQAAGGLV GDADRGDLE 60
 CSPRIFLHP RLHPPRLHGS CHLDRCGCGA GWSCCLALRE TGWVILGPAE DSASAGSFLH120
 SHRCPTLE 129

(2) INFORMATION ON SEQ ID NO. 246:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 268 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```

ASPNSQPTS PASAPALPPP ARSRGAQTV SLTMGTADSD EMAPEAPQHT HIDVHIQES 60
ALAKLLLTCC SALAPRATQA RGSSRLLVAS WVMQIVLGIL SAVLGGFFYI RDTLLVTSGL20
AAIWTGAVAV LAGAAAFIYE KRGGTYWALL RILLALAAFS TAIAPALKWN EDFRYGYSYY180
NSACRISSSS DWNTPAPTQS PEEVRRRLHC TSPMDMLKAL FRTLQAMLLG VWILLLLASL240
APLNLYCWRM FPTKGKRDQK EMLEVSIGI                                268

```

(2) INFORMATION ON SEQ ID NO. 247:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 103 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

```

DCTQDPQHDL HHPRGHQQPA AAPGLGGFGP QRRAGEQEL GQGRLLVDVH IDVGLWGLR 60
GHLITVGCSS CQGHSLRSSG PASGRREGWG AGWRSGLRVG GGG                                103

```

(2) INFORMATION ON SEQ ID NO. 248:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 86 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

GSRRRDGGGA GAAPVAPRAL GRRARAGRCS EDEGGGGAQR VWGEQPVLAS GQSPPGQEGS60
 FTRVWTRASL PTLGQVLQPG GVHVQV 86

(2) INFORMATION ON SEQ ID NO. 249:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 154 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

ARGGAMAAGL ARLLLLLGLS AGGPAPAGAA KMKVVEEPNA FGVNNPFLPQ ASRLQAKRDP 60
 SPVSGPVHLF RLSGKCFSLV ESTYKYEFCEP FHNVTQHEQT FRWNAYSGIL GIWHEWEIAN120
 NTFTGMMWRD GDDCRSRSRQ SKVELACASP SNCV 154

(2) INFORMATION ON SEQ ID NO. 250:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 95 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

PLDAVARART RQLHLALPAP GTAVVTVPHE HAREGVVGD LPLVPDAEDPT VGVPAEGLLV60
 LGHVVERAEL ILVRGLHAQE ALARESEEMH GSRHG 95

(2) INFORMATION ON SEQ ID NO. 251:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 240 amino acids
- (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

KVTDGHTRTF RSGVPRQHEA GSPGLTASHA MSIHLAGSLT AMDSICASER SQGVWRAPTP 60
GCQGLSPGPR EGELPGGSSP EERLGRLAVA GPPRGAQNV S QAGFEAEAPP LRFHAWGAQ120
TPRLGAPGW TPLETLPSHI PFWSTPAQ RKEGTEEGQ GRANPQGGDE DISGPCSRL190
LWEEPCVCK LLGLAARPTA GPSLDPCTWP SSCPLAAPGL GTGIEPRGLG WLGGQGRDREG240

(2) INFORMATION ON SEQ ID NO. 252:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 216 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

GLVMPGELRR PGLGFQAHGL PSPLCPPIFF LFGPRHQHKE RRGSRQKARA EPGPREGMRT 60
FPVQVAAGCS GRKSHASVNC WGWPRAPLQG PALTPARGHP AALWLPLALA QASSLEGWAG120
WARAGTGRGS TSDPDVGWLC PPRREAQQT S YTKAKSTIGE PRSHEMGRRP RFQGPQSKAR180
GRFIPEDSPF GAAPAWGGVS RPLGCLSVCG TPWSTP 216

(2) INFORMATION ON SEQ ID NO. 253:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 218 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

VLRRLYIYIL YITNMKWFST QPLWLNTKQR SHRRGPGPPP APLSGVLGSR GLPHHPSQGW 60
 GRAGPRAGAN VAWNSNCIVR WVGQWARGC SQPGFTTNL AMTCGGPWGS GCLLGSTLSE120
 VSPWAPPSCP QGHFVLPTRL WANGLDPLC RVRVGAGHGS RHQPDAPGV ARSWDGVVRN180
 TAPKTQNKNT TNGRRSPFPT EVGFPELLIF FVSFLQPW 218

(2) INFORMATION ON SEQ ID NO. 254:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

RDGGGAGAAP VAPRALGRRR RAGRCSEDEG GGAQRVWVS SLAGWRLERG TARARSPLTL60
 PLPVGGTTRS CLREVASRP 79

(2) INFORMATION ON SEQ ID NO. 255:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

LGLEATGLRQ ERVVPTGSG KVSGERARAV PRSSRQPRL LTQTRWAPPP PSSSLHLPAR60
ARRPRARGAT GAAPAPPPS 79

(2) INFORMATION ON SEQ ID NO. 256:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 79 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

WPGGDWPEAR TGCSTYGKRQ GQRGTGPRP PLEPPAREAA HPNALGSSTT FFAAPAGAG60
PPAESPRSNR SRASPAAL 79

(2) INFORMATION ON SEQ ID NO. 257:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 51 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

GHLGGPTGSV CSRILLASSP FYMNCCINKH RVPETTEVII LPTECWFGQA W 51

(2) INFORMATION ON SEQ ID NO. 258:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 49 amino acids
- (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

GGGFLGQIDK SKDNISLTV IQLHSYTVAL EGLSHEEVLV TNYFVGCF

49

(2) INFORMATION ON SEQ ID NO. 259:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 48 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

AFTRNTTNKV SDMLANQARL RSLRRPNWLC LLKDSGLVLS ILHELLHK

48

(2) INFORMATION ON SEQ ID NO. 260:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 179 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

PGISVSDVKM ESSPFNARQW TSLSLRVTA ELVLNKNKS SAIVEIFSKY QKAAEETNME 60
KKRSNTENLS QHFRKGTLLV LKKWENPGL GAESHTDSL R NSSTEIRHRA DHPPAEVTSH120
AASGAKADQE EQIHPRSLRL SPPEALVQGR YPHIKDGEDL KDHSTESKMM ENCLGESRH 179

(2) INFORMATION ON SEQ ID NO. 261:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 56 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

QATLLLEPKL TKKNKSTPDL DSGHLLKPSF RVDIPTSRV RILKTTQQKV KWKIV 56

(2) INFORMATION ON SEQ ID NO. 262:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

DSAPSPGFSH FFFNTVRVPF LKQWERFSVL LLFFSMFVSS AAFWYLENIS TIADOLFLLT60
RESSLAVTLN DSEVHCRLLN GDSILSTDT EIPG 94

(2) INFORMATION ON SEQ ID NO. 263:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

VMSSDPADKAA RADSSARAARG KRKKNVEENM AYSALMEVAG YCLIERMLWN PMLKIKSVWL60
 CSYAVMVIPR QLAKV 75

(2) INFORMATION ON SEQ ID NO. 264:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

AMFSSTFFFL LPRAARAESA RAALSAGSLI TYAFYKRLPK KLLTRNVOK PLKANKQQTV60
 VFAFSYSWQA EVRA 74

(2) INFORMATION ON SEQ ID NO. 265:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

DSKAFSLSS NQPLPSKLSR PCFPPHFFFF YLEPLEPNRL EPPCLLDHSS PTHFIKGYPK60
 RNC 63

(2) INFORMATION ON SEQ ID NO. 266:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 94 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

RRGSGSRSSM APVLASMLWM STAGTAMTST SLCTSRARSR FMPSSSSPTF TAWRCCCATR60
 TRVSTSTRTG ASLRMWCSCG GRCLLLWPTS APTF 94

(2) INFORMATION ON SEQ ID NO. 267:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 254 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

GDRKPLYHYG RGMNPADKPA WAREVKERTR MNKQONSPLA KSKPGSTGPE PPSQASPGP 60
 PGLPWAPKPY HKFMAFKSFA DLPHRPLLVD LTVEEGQRLK VIYGSSAGFH AVDVDGNSY120
 DIYIPVHIQS QITPHAIIFL PNTDGMEMLL CYEDEGVYVN TYGRIITKDVV LQWEMPTSV180
 AYICSNQIMG WGEKAIEIRS VETGHLGVF MHKRAQLKF LCEANDKVFF ASVRSGSSSQ240
 VYFMTLNRNC IMNW 254

(2) INFORMATION ON SEQ ID NO. 268:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 231 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

```
GKKHLVIPLT QELEPLSSVF HEDPVEVARL HRAOLNGFLT PAHYLVGADV GHRSRHLPL 60
QHHILNDAPV RVDVDTLVLV AQQLHAVGV GEEDOGMGRD LALDVHROVD VIAVPRVDIH120
SMEASTGAID DLEPLPLLYC QVQQRRAVGE VGKGLEGHEF VVGFGGPGEA WGPWGGGLGAG180
GLRPRAAWLA LGQGRVLLLV HPCSLFYLSG PGWFFVSGIHA PTIMVQGLPV P 231
```

(2) INFORMATION ON SEQ ID NO. 269:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 454 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

```
GAGCTSPGLW ARKAAARCLP TYPSPRAQPSN VGRRRRRRPPG LGALAAGVPA MAESVERLQQ 60
RVQELERELA QERSLQVPRS GDGGGGRVRI EKMSSEVVDS NPYSRLMALK RMGIVSDYEK120
IRTFEVAIVG VGGVGSVTAE MLTRCGIGKL LFLDYDKVEL ANMNRLFFQP HQAGLSKVQA180
AERTLRNINP DVLFEVHNIN ITTVENFQHF MDRI SNNGLE EGKPVLDVLS CVDNFEARM240
INTACNELGQ TWMSGVSEN AVSGHTQLII PGESACFACA PPLVVAANID EKTLLKREGVC300
AASLPTTMGV VAGILVQNVL KFLNFGTVS FYLGYNAMQD FFFTMMSKPN PQCDRNCRK360
QEEYKKKVA ALPKQVIQF EEEIHEDNE WGIELVSEVS EEELKNFSGP VPDLREGITV420
AYTIPKKQED SVTELTVEDS GESLEDLMK MKNM 454
```

(2) INFORMATION ON SEQ ID NO. 270:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

KLTVPKFNRN ENTFTCKIPA TPIVVGRLA AQTPSRFRVF SSIFAATTSG GAHAKQADSP 60
 GIISCICPET AFSLTPDSIH VCPSSLQAVF IVIRASKLST QLRTSTGFP SSNPPLLILS120
 MKC 123

(2) INFORMATION ON SEQ ID NO. 271:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 176 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

CSSEYVLLLE LYLILLDEVG RKVYSYWLVP PCHNQRVATY QCHILSAFQQ SHYLLHQHLL 60
 LLRQRYGFSH SRLQPPFVSM PSSGCROSNP PPLSSSSRCG PGRPLARRSS GPADSSPGQV120
 PAFAPGPAAA GAFQTPPWLG LRPPTLPARA FAAAFAPRCS AGPARGTWGG TSPLPS 176

(2) INFORMATION ON SEQ ID NO. 272:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 117 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

EARQAWTGAK GAGSLTFSSL QSGHLASGSQ SPESTKAPGT PPTPSYPGTP SRQLLWQWVQ 60
 PRPALPASSP CSRHQYLPR QAMSWLLSPA PSVPLDFSGA SPVWATLCFP HPRLPFR 117

(2) INFORMATION ON SEQ ID NO. 273:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 86 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

APALPPFAGN VLASQPSTIC SPRLLRGQPS LGHFLFPSSS APTQVIDPAD SFSLGKVGCC60
 LTSPSSPPPI HTHRHPTPG RLVSHM 86

(2) INFORMATION ON SEQ ID NO. 274:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 177 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

EARTLPAGGG RAGAYCRERR LAVLAWAGPT AITVAYLGSL GRMEWVCQG LWCFLVIGTL 60
 MPSAHFAKKK KLMTLLLEWLL SMLAWPPRVG GTSPELLAEG EQVLSYDPIH QAGVLSPSGH120
 HSSQRHGQFVG LGQGSEKGWQ EVPRSSQPRR GTNALNTSKL RDPKVSTPGS GLPPHRH 177

(2) INFORMATION ON SEQ ID NO. 275:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

QFPGPSVPEQ STSVSVTTSC LFPSSLHLLQF IYMLLLLVHF CLPYQAVNEG RNLVCFIH60
VPSAWHIVGL H 71

(2) INFORMATION ON SEQ ID NO. 276:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 102 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

FFFFFFFF FFFCLINMSI YLAPDGNTRS WQWENKGSLS QILPYYVDPK AGLGSKAHKP 60
PKQIFIEHLD YYRPSILLGT MGDVKEVISH MICLQGA6N SG 102

(2) INFORMATION ON SEQ ID NO. 277:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

GVIESRRVLS RGVIRIFKQ PNPGRGCPIL SALKKIPFPY LPASIMSVEE SNCGSFEGDG60
FFFPV 65

(2) INFORMATION ON SEQ ID NO. 278:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 65 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

FFFFFFFF FFLFNKYEHL FGTRWQYKIL AVGVVERFSL NTSILCRPKG RTWQQGSQTT60
QTNIIY 65

(2) INFORMATION ON SEQ ID NO. 279:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 489 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

LADSPFGSSP YEGNYGSFE NVSGSTDGLV DSAGTGDLSD GYQGRSFEPV GTRPRVDSMS 60
SVEEDDYDTL TDIDSDKNVI RTKQYLYVAD LARKDKRVL RKKYQIYFVNI ATIAVFYALP120
VVQLVITYQT VVNVTVNGDI CYYNFLCAHP LGNLSAFNNI LSNLGYILLG LLFLLIILQR180
EINHNRRALLR NDLCALECGI PKHFGFLFYAM GTALMMEGLL SACDHVCPNY TNFQFDTFSM240
YMIAGLCMLK LYQKRHPDIN ASAYSAYACL AIVIFFSVLG VVFGKGNFAT WIVFSLIHI300
ATLLLTQLY YMGWRKLDG IFRILHLVLY TDCIRQCSGP LYVDRMVLV MGNVINWSLA360
AYGLIMRPND FASYLLAIGI CNLLLYFAFY IIMKLRSGER TKLIPLLCTV CTSVVVWFAL420
FFFFQGLSTW QKTPAESREH NRDCILLDF DDHDIWHFLS SIAMFGSFLV LLTLODDLOT480
VQRDKIYVF 489

(2) INFORMATION ON SEQ ID NO. 280:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 182 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

APLCHRPVTL SCCGDESQHR CPALDGSRTA RSSLGLAWDS HGVAWNLAAL LCRGAGLLPW 60
 DPQMLAKLLL SSQCWGLPWA FVLWLSICPF ARGMEGTSP PFHALHFARP PPHNAPAWDL120
 RPLFPFILFL QGLVWGLNLC SVSGPQFSLG CPWLPSLPIP VSQDGGWGEI LGVGQLVPDF180
 WC 182

(2) INFORMATION ON SEQ ID NO. 281:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 536 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

ARPGCPAAIQ CWAAYVGLIP TARQSDRSMT QRSSGPLEV KRAQLLEDI DLVPLHSIQV 60
 VIQCQHQEG PERGDGEEV PDVVVVKEVE EDAPVVLPR LCRGFLPGA EEEEEEREAL20
 PDHGANDAE QGDELPLPT PELHDDVEGE VKEQVADANG QQVSGEIIA HDKPIGSRP180
 VDDVARDQHH HAVHVERPAA LPDAVCVEHV EDAAEDPRVQ FPPAHVIELA AEEQGGDDVN240
 DGEDDPERRV PFAKDHAQHR EEDDNGQAGV GTVGAGVDVR VPLLVELQHA ESGDHVHERC300
 VKLEIGIVGA HMIASTEQL HHQCGAHGVE KPKVFGDPTF QGTEVIAQQG PVVVDLPLQD360
 DEQEKQPQQD VPQVAEDVVE GAETIAQWVGA EEVVVADVLI PCDIHRLVG DHQLHHRKGI420
 EDSNGGNVPE VDLVLFQNT LVLPCQVSHI EVLLGANDIL VGIDVGQCQV VILLHRAHGV480
 HSGPSTYRFK GAALVTVREV PSASAVNQT IGRSRNLIKGA IVVTLIRGTA RKRISQ 536

(2) INFORMATION ON SEQ ID NO. 282:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 551 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

```
PLSSPSCCRY RRCRRLRPP LRSVVQPGPR TMSLSRSEEM HRLTENVYKT IMEQFNPSLR 60
NFTIAMGKNYE KALAGVTYAA KGYFDALVKM GELASESQGS KELGDVLFQM AEVHRQIQNQ120
LEEMLSKSFHN ELLTQLEQKV ELDSRYLSAA LKXYQTEQRS KGDALDKCQA ELKKLRKKSQ180
GSKNPQKYSD KELQYIDAIK NKQGELENTV SDGYKTALTE ERRRFCEFLVE KQCAVAKNSA240
AYHSKGKELL AQKPLWQQA CADPSKIPER AVQLMQQVAS NGATLPSALS ASKSNLVIDS300
PIPGAKPLPV PPELAPFVGR MSAQESTPIM NGVTGPDGED YSPWADRCAA QPKSLSPFQS360
QSKLSDSYSN TLPVRKSVTF KNSYATTENK TLFPSSSMAA GLERNGRMRV KAIFSHAAGD420
NSTLLSFKEG DLITLLVPEA RDGWHYGESE KTKMRGWFPF SYTRVLDSDG SDRLHMSLQQ480
GKSSSTGNLL DKDDLAIPPP DYGAASRAFP AQTASGFKQR PYSVAVPAFS QGLDDYGARS540
MSSADVEVAR F 551
```

(2) INFORMATION ON SEQ ID NO. 283:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 185 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

```
AGEAAGQPGS PFSHQLAKCF PLTQGYPRHL GHVTRGVYPQ EAAPQFWAAQ PLGLALQGPA 60
PHSARPCLEQ LGSSPGQTQV GQDQAAGAWM FSTQERTDDD RTGYMGRAGE ATRWAALQMW120
PSAEEGGRPV VGHCRLLQDV GKGLTLVRR LRIWPLPHRR CSWTALHSHP GPGRRRARPH180
CRASA 185
```

(2) INFORMATION ON SEQ ID NO. 284:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 518 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

```
SGGESGSHF IGAAHGPRSI VIQALGEGGH GHTVGPILLEA AGRLLGGEGPG GGAVIGGWDG 60
QVVVLQVEVAR AAALPLLQAH VQPVTIAIVQ DPGVGEGKPA PHLGLLTSLV VPAIAGLRHQ120
QGNEVTLLQA QEGAVVPSSV GEDGLHPHTA IALQAGCHGA RARQSLVLGG GIAVFWGHAI180
ARHGEVGVGV RELALRLRRR QGFGGLSLAV SPRAVVLAIR ACDAVHDGCA LLGRHPHHER240
CQLGGHRQGL GPRNGVGNQD VGLGGRQGAG EGGAVAGHLL HELHRLALDL AGVGTGLLPQ300
RQLLRQQLLA LGVVGRGVLG HGALLLHQEA EAPALLCQCG LVAVGHVILQ LALLVADGVD360
VLQLLVRVLL RILAAALALL KLLQLSLTLV QGVAFAPLLS LVFLQRSTQI PGVQLHLLQ420
LRKQLVVKRL QHFFQLILD L PVDFSHLEEN VSEFFGALL AGQLPHLHQG VKVAFGCIRH480
TCQCLLVILP HGDEVPEARV ELLHDGLIDI FREPVHLL 518
```

(2) INFORMATION ON SEQ ID NO. 285:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 217 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

```
VREAAARREQR YQEQGGEASP QRTWEQQQEV VSRNRNEQES AVHPREIFKQ KERAMSTTSI 60
SSPQPKLRS PFLQKQLTQP ETHFGREPAA AISRPADLP AEZEPAPSTPP CLVQEEEEAV120
YEEFPEQETF YEQPFPLVQQG GAGSEHIDHH IQGGGLSGQG LCARALYDYQ AADDTESISFD180
FENLITGIEV IDEGWWRGYG PDGHFGMFFA NYVELIE 217
```

(2) INFORMATION ON SEQ ID NO. 286:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 162 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

```

AGASGRLWLP SAFICLFSFS LASKGWWPPL FRMTLGNSEK RELFLAEFVT KVRVDHGGLA 60
AGNLSCWSLL CAPHSISLSL CLGYGKWGCR WPSSHGYSK TADTTCGSTR LTRCLQAPVC120
ASTSDFRKS NTEWPWPVVF PYFLSQLIRV SEEQICFWTK KK                               162
  
```

(2) INFORMATION ON SEQ ID NO. 287:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 173 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

```

LLACRGWPGR RWHEELNSGK VMYAFCRVKD PNSGLPKFVL INWTGEGVND VRKGACASHV 60
STMASFLKGA HVTINARAEK DVEPECIMEK VAKASGANYS FHKESGRFQD VGPQAPVGSV120
YQKTNAVSEI KRVGKDSFWA KAEKEEENRR LEEKRRAREK QRQWSRSAGS VSA           173
  
```

(2) INFORMATION ON SEQ ID NO. 288:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 597 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

EKCGQYIQKG YSKLKIYNCE LENVAEFEGL TDFSDFKLY RGKSDENEDP SVVGEFKGSF 60
 RIYPLDDPS VPAPPRQFRE LPDSVPQECT VRIYIVRGLE LQPQDNNGLC DPYIKITLGK120
 KVIEDRDHYI PNTLNPVFGF MYELSCYLPQ EKDLKISYVD YDTFTRDEKV GETIIDLENR180
 FLRSFGSHCG IPEEYCVSGV NTWRDQLRPT QLLQNVARFK GFPQPILSED GSRIRYGGRD240
 YSLDEFEANK ILHQHLGAPE ERLALHILRT QGLVPEHVET RTLHSTFQPN ISQGLQKQMWV300
 DVFPKSLGPP GPPFNITPRK AKKYILRVII WNTKDVILDE KSITGEEMSD IYVKGWIPGN360
 EENKQKTUVH YRSLDGEQNF NWRVFPFQDY LPAEQLCIVA KKEHEFWSIDQ TEFRIPEPLI420
 IQIWDNDKFS LDDYLGFLLE DLRHITIPAK SPEKCRDMI POLKAMNPLK AKTASLFEQK480
 SMKGWWPCYA EKDGARVMAG KVENTLEILN KEADERPAG KGRDEPNMNP KLDLPNRPET540
 SFLWFTNPCK TMKFIVWRRF KWVIIGLLFL LILLFVAVL LYSLPNYLSM KIVKPNV 597

(2) INFORMATION ON SEQ ID NO. 289:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 120 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

DQHSCEFKMSP DSKASHNPSF PKMGVESDME DETTAWMNLK PTKSCTSTSG PLKSGLLFTS 60
 SGLRGWSLST WKQGLCTAPS SPTFPRENER CGWMFSPRVW GHQALLSTSH PGKPRNTQCV120

(2) INFORMATION ON SEQ ID NO. 290:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 289 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

ETQVVIQRKL VIVPYLNDQP GWDSKFLVN TPEMLFFRND TELFGWKVVK RENKSPVKIP 60
FTIQRSVMDI CFLFVFFIAR NPAFDVDVTH FLSCDAFLVQ DNVLGVPPDH TQVVFLGFPGL20
CDVERRAWWP QTLGENIHPH LKFLSLGNVGL EGAQVQSPCFH VLADQPLSPE DVKSKPLFRG180
PEVLVQDFVG FKFIQAVVSS SISDSTPIFG KDGLWEAFES GDILKQLCWS QLISFGIDSR240
NTVLLWYAAV GPKAGKESVE QINNCFSYFF IPGKGVIID RNFQVFFLR 289

(2) INFORMATION ON SEQ ID NO. 291:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 201 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

GTGDGSKEIN IVWGIQVPIF HNGEPVSTNH EVARFPRI TS LASEGIIVPS TSTIRGMGVW 60
RASCDCRAD STSSIAQDRG PGLTIGHQAL GSLVWVGESW GQTWGEYLGQ PRWLGLDLRL20
QSWALSISEE VVKKRDPLFH FLNPLCLMVE DMFAHKLRTL EPLATERTQP LILAQFLRVGL180
GDELLHFLW VFAPHLGLF L 201

(2) INFORMATION ON SEQ ID NO. 292:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 171 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

SVIFFKIGFC EGRVLGRGGV PGSEAGSCVL SSSVWISLAA SLMSLRITCL CWVMPMLRLT 60
RRVRSLETPG LSSHRSRRMF CRFQQLSML TLRSKVTQPR RKNLLSGWGS ESATRIKPGYL20
LLQREMISAR EMLGAMLRMK REQVLCSSRG LHSSPAASLG FSHSSSLGFS F 171

(2) INFORMATION ON SEQ ID NO. 293:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 485 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

EKEKPKEEZW EKPKDAAGLE CKPRPLHKTC SLFMRNIAPN ISRAEIIISLC KRYPGFMVRA 60
 LSEPQPERRF FRRGWVTFDR SVNKEICWN LQNIRLRECE LSPGVNRDLT RVRNRINGIT120
 QHKQIVRNDI KLAAKLIHTL DDRTQLWASE PGTPLPLTSL PSQNPILKNI TDYLLIEVSA180
 EEEELLSSSG GAPPEPPKE GNPAEINVER DEKLIKVLDK LLLYLRIVHS LOYYNTCEYP240
 NEDEMPNRGC IIVHVGPMPP NRISHGEVLE WQKTFEKLT PLLSVRESLS EEEAQKMGKR300
 DPEQEVKVFV TSNTQELGKD KWLCLPSGKK FKGPFFVRKH IFNKHAEEKIE EVKKEVAFFN360
 NFLTDAKRA LPEIKPAQPP GPAQILPPGL TPGLPYPHQT PQGLMPYGP RPPIILGYGAG420
 AVRPAVPTGG PYPHAPYGA GRGNYDAFRG QGGYPGKPRN RMVRGDPRAI VEYRDLAPD480
 DVDF 485

(2) INFORMATION ON SEQ ID NO. 294:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 368 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

ESSGFQAIGR AEDDARSCWV KTSESTRPYQ LLRRRRPTLI TYRIFRHHRH KDTSSGDHLT 60
 CRLDPOAKDL KEGTQEEATK RQEAQVDPFR EGDQRTVIS WRGAVIEPEQ GTELPSRAEL120
 VPTKPLPPA RTQGTPHVHLN YRQKGVIDVF LHAWKGYRKF AWGHDELKPV SRSFSEWFG180
 GLTLIDALDT MWILGLRKEF EEARKNVSKK LHEKDVVDVN LPESTIRILG GLLSAYHLSG240
 DSLFLKRAED FGNRLMPAFR TFSKIPYSDV NIGTGVAHPP RWTSDSTVAE VTSIQLEFRE300
 LSLRTGDKKF QEAVEKVQKH IHGLSKKKG LVPMFINTHS GGVSPPTGVF HGGAPGADSL360
 LLSYLFER 368

(2) INFORMATION ON SEQ ID NO. 295:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 94 amino acids
 (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

ALRSPPRMRI VLSNALTSTS FSKCNFFDTH FLASSNSFLR PKIHMVSSAS ISVRPRPNHS60
LKDLDTGFSS SWPHANLRYF FHACRKTSIT PFWR 94

(2) INFORMATION ON SEQ ID NO. 296:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 94 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

LLRHPLPGFL KFFPQTQDPH GVQRVDQCET EAKPLTEGPG HRLQLVMAFC KLAVSFPCMQ60
EDVNHALLAI VQMHWCALCF GRWQGRLLGGH FCSS 94

(2) INFORMATION ON SEQ ID NO. 297:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 146 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

SGPLLACPAT LTGRMSEVRL PPLRALDDEFV LGSARLAAPD PCDFQRWCHR VINNLLYYQT 60

NYLLCFGIGL ALAGYVRPLH TLLSALVVAV ALGVLVWAAE TRALCAAAA ATLOPAWPQC120
LPSASWCSGS RAALAPSCSA SPGRCF 146

(2) INFORMATION ON SEQ ID NO. 298:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 152 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

TQRHSHPPFS MLIPKLGPGA RRSQILNPGP KLFQTPPYLP TQVKTLPNLE LRTQVFHAPV 60
 WMESGILTVG PLVQVIPTLT SPICLPALL RHFAHPNVP HHRQPRGEVG TGLSREWGVY120
 VSVAAATIKPV ASLMPKKKKK STGRKYSSSS RP 152

(2) INFORMATION ON SEQ ID NO. 299:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 172 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

RTTTTIFAA GRLLLLFWHE RCNRLYCCSN TNIYAPFPAE ACPHLTPWLS MVWNIGVRGK 60
 MPKQSWREAN GTGEGRDHLD QGSNSQDTRL HPHRGMEHLG SEFKIWQCLD LGWKVGVGLE120
 KLWSRVQDLR VPCSRPQFGD EHGEQWVGVS LGSQFEIGHG CSGLKPQFWG WM 172

(2) INFORMATION ON SEQ ID NO. 300:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 178 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

WFWRESYWQT IKVDLQVEHP YQFLLYAKQ LKGDKNKIQR LVQMAWTFVN DSLCTTSLQ 60
 WEPETIAVAV MYLAGRLCKF EIQWTSKPM YRRWWEQFVQ DVPVDVLEDI CHQILDLYSQ120
 GKQQMPHHTP HQLQQPPSPE PPTPLGPGCG CWASHLKEGK VVQPEPVEQC PVWPPKPK 178

(2) INFORMATION ON SEQ ID NO. 301:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

CISQDVCANL KYKNGPPNPC IGDGGSSLFK MSRSTFWKTS ATKSWIFTHK ENNRCLITPP 60
 ISCNSPHLLS LPPRCCLGPVV AGPPTSRGR LYSPNFWGNA LSGLQNQNKI GSL 113

(2) INFORMATION ON SEQ ID NO. 302:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

GGRPSNHRQA AAGWEAQEMG AVAADGGCDE ASVVFLVSKD PGFGGRCLPK RRPGLHLEQTA60
 PTISYTWVWR SILVFIQICTN VLDRTSLLLL 90

(2) INFORMATION ON SEQ ID NO. 303:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 158 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

TQVMVQSMFA PTDTSDEAV WKEAKPEDLM DSKLRVCFEL PAENDKPHDV EINKIISTA 60
 SKTETPIVSK SLSSSLDDTE VKKVMEECKR LQGEVORLRE ENKQFKEEDG LMRKTVQSN120
 SPISALAPTQ KEEGLSTRLL ALVVLFVIG VIIGKIAL 158

(2) INFORMATION ON SEQ ID NO. 304:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

VNKALFFISK ALGQSVNTRL SLMTSTSDAA TVQFLWASDS VHQSQGADGL DRTEDESSL 60
 GREWATWGLL CGADRTQHA GLQLFKGQHQ QARKGVILRE VIQHHVPRPT NV 112

(2) INFORMATION ON SEQ ID NO. 305:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

FKGKTCEMSS YINFFLHMVM INLNPMIWWI HQSNLPSCAC YLYKAIFPII TPTIKNKTTTR 60
AKSRVLRPSS FPGVANAEMG LLLCTVFLIR SPSSSLNCLF SSRSI 105

(2) INFORMATION ON SEQ ID NO. 306:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 126 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

RPPQRTLRS AQLGAAPAAL PQPLWELPRA HGSQRQPGPG EAADHAEQER EAAERPGSS 60
PEEGEGSGA FGGHTGHRAC ARCLGRGALG GRIPCGLLCQ LFRDGC PAD SEVQHHRHQH120
WQQLP 126

(2) INFORMATION ON SEQ ID NO. 307:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 240 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

NVGRCCERQA RAGAASLNAS LDGLHNALFA TORSLEQHQH LFHSLFGNFQ GLMEANVSID 60
 LGKLQTMISR KGKKQKKDLE APRKROKKEA EPLVDIRVTG FVPGALGAAL WEAGSPVAFY120
 ASFSEGTAAAL QTVKENTTYI NIGSSYFPEH GYFRAPERGV YLFAVSVEFG PCPGTGQLVF180
 GGGHRTPVCT TGQSGSGSTAT VFAMAELQKG ERVWFELTQG SITKRSLSGT AFGGFLMFKT240

(2) INFORMATION ON SEQ ID NO. 308:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 123 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

KAGIEGHRGS CLPERRAAGT WHRPCDPYVH QRLRFLLVPL PGSFQVFLLL LPFPAQHGLQ 60
 LPQVQADVGF HEPLEVPKEA VEEPLVLLQA ALSGEECVVE AVKGGVEGGG PGPGGLAAP120
 PDI 123

(2) INFORMATION ON SEQ ID NO. 309:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 84 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

PTTTLVIPLF FLSSRRKKQK DSFQTALCSL KCSFPKQAAS TGKARVVTPY FSEVLLFHGV60
 TLLSESKFRK QVLPADKNH TSFL 84

(2) INFORMATION ON SEQ ID NO. 310:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 128 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

```
CDRVPLFLSY WCAVADSWLT ASSVSHVKG I LSPQPTCAP PGPANCFNF FFFFFFFLVET 60
GPSVAQDGL ELLGSSNPT LASQSAEITG MSHAQPEQD DLNLINSTPK QQLSLSGQCQ120
GGLCEGKD                                     128
```

(2) INFORMATION ON SEQ ID NO. 311:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

```
WVAGRRHLLS VQTKSLQVLG LDLCVTPESQ CIRLYKKLV WFLSAKGKTC FLNLLSDNKV60
TPNKRRTSEK YGVTTWAFPV LAACFGKLQC RLQRAV                               96
```

(2) INFORMATION ON SEQ ID NO. 312:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

ISTSIAALWL PGGQDAGGGA LWPLCGSRGL CVSDRFFGNF RARLTSWKFK YSIALEF 57

(2) INFORMATION ON SEQ ID NO. 313:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 52 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

SAHQLQHCY QGVMRVAVP SGLCVVAEDS VSATVFRETS GRDSHLGNSN TQ 52

(2) INFORMATION ON SEQ ID NO. 314:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 43 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

NSRAIEYLNQ QDVSLARKFF GKRSLTQSPR LPHKGQRAPP PAS 43

(2) INFORMATION ON SEQ ID NO. 315:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 247 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

```
GSSGSRFEVV VVLEERRGGR GRGMGRGDGF DSRGKREFDR HSGSDRSGLK HEDKRGSGS 60
HNWGTVKDEL TESPKYIQKQ ISYNYSDDLQ SNVTEETPEG EEHHPVADTE NKENEVEEVK120
EEGPKEMTLD EWKAIQNKDR AKVEFNIRKP NEGADGQWKK GFVLHKSKE EAHAEVSMD180
HHFRKPANDI TSQLEINFGD LGRPGRGRGR GRGGRGRGRGR PNRGSRDTSK SASAPDVDDP240
EAFPALA                                     247
```

(2) INFORMATION ON SEQ ID NO. 316:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 75 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

```
FMKNKSLLEPL PISTFIWFSO IKFYFCPVLI LNSLPLIQSH LEWTLFLYLF NFILLIFSVC60
HMMMFETTRC FLSHI                                     75
```

(2) INFORMATION ON SEQ ID NO. 317:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 78 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

SFGILKHAKA LNRVRHKGTR VVLWHPVKPE LQMPLGHPHQ EQKHLTCRSC CHGLGAHHAAH60
 VHLVLPCRHV LGGQGLQN 78

(2) INFORMATION ON SEQ ID NO. 318:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 235 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

LHLGAQRALA PGLFRLQGM L RALLGRQLFR ARGPFVVRP LPRTTRLAVR HVWPPCDRPL 60
 RVGPGSPLPP GPLHMHLLPA PAHQGVLPGA RRQALLPALL PEALRLTARS ARPLPRRPRP120
 PGKAGSSRRP GLALRAGGPT HWRAPPLRY Y ESSGVKFRNG PARPKPTRPQ SGLHTDKNSR180
 AGLHSIPTLE GAPLLGEGPC NSSSESEARPG RPCSLRPHCS VHFFYLHKHT HSTSK 235

(2) INFORMATION ON SEQ ID NO. 319:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 478 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

GSRPPFCSPR ATGPRFAMED LDALLSDLET TTSHMPRSGA PKERPAEPLT PPSYGHQPQ 60
 TGSGESSGAS GQKDHLYSTV CKPRSPKPA AAPPFFSSSS GVLGTGLCEL DRLLQELNAT120
 QFNITDEIMS QFPSSKVASG EQKEDQSEDK KRPSLPSSPS PGLPKASATS ATLELDRLMA180
 SLSDFRVQNH LPASGPTQPP VVSSTNEGSP SPPEPTGKGS LOTMLGLLOS DLSRRGVPTQ240
 AKGLCGSCNK FIAGQVVVAL GRAWHPEHFV CGGCSTALGG SSFFEKDGAP FCPECYFERF300
 SPRCGFCNQF IRHKMVTALG THWHPEHFCC VSCGEPFGDE GFHEREGRPY CRRDFLQLFA360
 PRCCGCGQPI LDNYISALSA LWHPDCEFVCR ECFAPFSGGS FFEHEGRPLC ENHFHARRGS420
 LCATCGLPVT GRCVSALGR FHPDHFTCTF CLRPLTKGSF QERAGKPYCQ PCFLKLFG 478

(2) INFORMATION ON SEQ ID NO. 320:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 285 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

EQCLGVWTR LFREGAASGG EGEPSGLSAE ELQEAGLAVG LAGALLEGPL GERAQAEAGC 60
 EVVRVEAATQ GRHAAAGHRE ATRGAQRAAS CVEVVLQAQA ALVLEKAASR EGREAFADE120
 TVRVPERAER RDVVIQDGAL AALAARGEQL QEVPAVGAAL LALVETLISE GLPATDAAEM180
 LWVPVSAQGG HRLVSDGLVA EATSWREALK VALGAEGGSI LLEEAAASQG GGATASANEVL240
 GVPGAQSRH HLPNSRFIAG ATEAFGLGDN TPAAEVGLQQ PQHGV 285

(2) INFORMATION ON SEQ ID NO. 321:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

GLHLQPLLWR QSTEEEVREE GQALTEPKSC GAQGGAQHRG LTPCPTGNGL GLAQPKIPAL60
 SNSWRVDSVL ACLVSSDIFH TVEQNHQPCT DVTLCRRKP 99

(2) INFORMATION ON SEQ ID NO. 322:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 99 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

ETQSSQRLTC PRSLGLDLSL RLRLQNPHSI CYISQGWGQG SCEQKEKYQL LKGLGFVGRA60
 RQGQRGIQNK GASTSAWDGP IHSGRGCGVS FVLNRHLAS 99

(2) INFORMATION ON SEQ ID NO. 323:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 83 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

SNPKAPVSMW VKGPTMGTYT QEDESSLASE SDCLPQTTPQ NLLSLHPLH SOKTQAHIPG60
 PGVFACICID GNAGPAKAF YIK 83

(2) INFORMATION ON SEQ ID NO. 324:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 111 amino acids

(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:

VFPTVLRGVL VPSSVTSKPG LIVPIGDEGG MRRSHLQLLS VERTSGTEKN RGPHGSLEGR 60
GTRVGELIAE RRDVQRPSAP LSWDVNRIFP STPSLPPVLP LFFFPSIKRC I 111

(2) INFORMATION ON SEQ ID NO. 325:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 272 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

SSRASGITRA ARPCPAKNEG PSKAFVNCDE NSRLVSLTLN LVTRADEGWY WCGVKQGHFY 60
GETAAVYVAV EERKAAGSRD VSLAKADAAP DEKVLDSGFR EIKENKIQDP RLFAEEKAVAI20
DTRDQADGSR ASVDSGSSEE QGGSSRALVS TLVPLGLVLA VGAVAVGVAR ARHRKNVDRV180
SIRSYRTDIS MSDFENSREF GANDNMGASS ITQETSLGGK EEFVATTEST TETKEPKKAK240
RSSKEEAEMA YKDFLLQSST VAAEAQDGPQ EA 272

(2) INFORMATION ON SEQ ID NO. 326:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 241 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

TLVFGRLRTK PFRIPGFLQR KRRWQIQEIK PMGAHLWIP AALRNKVEAP ERWSPWCPW 60
 AWCWQWEPWL WGWPFGTGR TSTEFQSEAT GQTLACQTSR TFGNLEPMTT WEPLRSLRRH120
 PSEKKSLLP PLRAPQRPN PRRQKGHPRR KPRWPTKTSR SSPAPWPPRP RTAPRKPRRC180
 RRLLPAPMTI TFRIMSILGP SAPGDPTPCS NTCLGFSYCP QRRAGPLLSL IKAWPNCYSW240
 G 241

(2) INFORMATION ON SEQ ID NO. 327:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 121 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

AVVRVTWYKG EGITLPPVLT PALVRGESIP IRLFLAGYEL TPTMRDINKK FSVRYYNLV 60
 LIDEEERRYF KQEVVLWRK GDIVRKSMH QAALASQRF E GTTSLGEVRT PSQLSDNNCR120
 Q 121

(2) INFORMATION ON SEQ ID NO. 328:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 140 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

GETRVHSQQG GGIKAPSWDN FFREPGPLVK GLLGHVKQYL EQPRPWGYQV ERREGRRLLPC 60
 THLPWWAGFS LLGSTLPSPV HDTDPRASPC PRPSYRLLFQ DITDNPERME KGGAWVFAVS120
 GQKEVACGNL RSPHPRFFPKR 140

(2) INFORMATION ON SEQ ID NO. 329:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 127 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

VFPCHLVGAG PTPATTSGTA KGSTRCDYFG PCWQLRIPGT CSDPVSQSSE SQEPRMRALC 60
 SPSSKTQGSP PRKGAHVPR GWLPGCYLFY PTSAAESQGE TASHPKPLGF SREKNLSQKH120
 DLFSGCK 127

(2) INFORMATION ON SEQ ID NO. 330:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 418 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

GSTSTKNTKI SQACGVIVEL IKSCKMAGGA VLLAGPPGTG KTAALALAIQ ELGSKVPFCF 60
 MVGSEVYSTE IKKTEVLMEN FRAIGLRIRK ETKEVYEYEV TELTPCETEN PMGGYGKTIIS120
 HVIIGLKTAK GTKQLKLDPS IFESLQKERV EAGDVIYIEA NSGAVKRQGR CDTYATEFDL180
 EAEYYVPLPK GDVHKKKEII QDVTLDLDV ANARPGGGQD ILSMMGQLMK PKKTEITDKL240
 RGEINKVVNK YIDQGIAELV PGVLFFVEVH MLDIECTYL HRALESSIAP IVIFASNRGN300
 CVIRGTEDIT SPHGIFLDLL DRVMIIRTML YTPQEMKQII KIRAQTEGIN ISEELNHLG360
 EIGTKTTLRY SVQLLTPANL LAKINGKDSI EKEHVEEISE LFYDAKSSAK ILGLTRQG 418

(2) INFORMATION ON SEQ ID NO. 331:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

VPQCGLGANL PQVVQCLLTD VDSFRLGTD NDLFHFLWSI QHGPDYHHSV QRVKRDAVRG 60
 CDVLSASDDT VASVGCKDDG GSDRRLLQAV QVGEALNVQH VOLINKQHTR DQLSNALVDV120
 LVHHLINLPS KFCVDFCLLW LH 142

(2) INFORMATION ON SEQ ID NO. 332:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

LAHHGQDILS FLGPRISHIQ VMQGHILDDF FLFVHIPIFWQ GDILFSFKVE FCGIGITPAL 60
 PLHGPTVGFN VNHISFSYSL FLQTFKNAGV QFQLFGSFGC FESYOHMANG FAISSHGILCI20
 LTRS 124

(2) INFORMATION ON SEQ ID NO. 333:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 176 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

QAMGKKQKNK SEDSTKDDID LDALAAEIEG AGAAKEQEPQ KSKGKKKKKK KKQDFDEDDI 60
 LKELEELSLE AGGIKADRET VAVKPTENNE EFTSKDKKK KGQKGKKQSF DDNDSELED120
 KDSKSKKTAK PKVEMYSGSL TNFLKKLKGG LKNQIRSGMG QRSMRITVKK LKSVQE 176

(2) INFORMATION ON SEQ ID NO. 334:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 193 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

RFKIKKDKCT ESGNVLWEFN KLPKKAKGKA QKSNKKWDGS EEDEDNSKKI KERSRINSSG 60
 ESGDESDEFL QSRKGQKKNO KNKPGPNIES GNEDDDASFK IKTVAQKKA KKERERKKRD120
 EEKAKLRKLL EKELELTGKK DQSKQKESQR KFEETVKS KVTVDTGVI PA SEEKAETPTA180
 AEDDNEGDKK NER 193

(2) INFORMATION ON SEQ ID NO. 335:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

ETVAFARPF PSLSFPPPLS SFLFLIFRS FCLLHCHLLQ LWESLLSLQR QELLQYQSL 60
 WILQFLQIS FEIPFVYSDP FYLFLTLFL SASAVSLFLH LAFFSRAPSF LPSFGPLS 118

(2) INFORMATION ON SEQ ID NO. 336:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 230 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

LQRLPPGAE RPAHLCTGPG GEDGAGGRVP GTRPQRPPAL QRAEDGRQGG LRVAGTAGPP 60
 PGVPLRPGQG GSGHQEQGAS HPGSLDOGLT GAKRPOGCPA CGRRPPCVGG VPGSAHRPQP120
 EGAALRRGRS RLOQAGPCCC RVLWLRRCHP AGLPRRPPAA DPGARAAAGG RHVLCRSPLH180
 PGLRPPLPQW GLLRPEGGCL CVPVSRGILR TALREGAGGE VSGRGYLGL 230

(2) INFORMATION ON SEQ ID NO. 337:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 416 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

QDGSFPFLAD FNGFSHLELR GLHTFARDLG EKMALEVVEL ARGPSGLLLY NGQKTDGKGD 60
FVSLALDRRR LEFRYDLGKG AAVIRSREPVL TLGAWTRVSL ERNGRKGALR VGDGPRVLGE120
SPVPHTVLNL KEPLYVGGAP DFKSLARAAA VSSGFDGAIQ LVSLGGRQLL TPEHVLQRQVD180
VTSFAGHPCT RASGHPCLNG ASCVPREAAV VCLCPGGFSG PHCEKGLVEK SAGDVTDLAF240
DGRTFFVEYLN AVTESEKALQ SNHFELSLRT EATQGLVLWS GKATERADYV ALAIVDGHLQ300
LSYNLGSQPV VLRSTVPVNT NRWLRVVAHR EQREGSLQVG NEAPVTGSSP LGATQLDVG360
ALWLGLPEL PVGFALPKAY GTGFGVCLRD VVVGRRHPLHL LEDAVTKPEL RCPPTP 416

(2) INFORMATION ON SEQ ID NO. 338:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 241 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

NQHMKNNTAMA RPRYPGRRQR STFSHSELLS IAPRRRAWGVA EGYGHVQGGW AGPAEGQDTQ 60
IGPGLASAPQ QPGLAQAAARE QRAVPSSNI VWKSYWRRR PROGPEHTOE GAAQIGAWKG120
PVGSPGGRAP SDLSSFFLSG TRVPPDGARV IQEPGLLPGG DTVGQAQCKA GAQHLEAGVC180
VLRLPTPTSP PRCHLACPSL STRSVCSTAA WTEGRPGQQS LRPTLRQENH IKKRQVYKNR240
K 241

(2) INFORMATION ON SEQ ID NO. 339:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 79 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

LLQPOGEMPP GNPPMSTRGQ EATVLRTPEN LAGELFLVHP SLQLYLCPAD NVKDWSKVVL60
AYEPVWAIQT GKTATPQQG 79

(2) INFORMATION ON SEQ ID NO. 340:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 62 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

FFVGVQLQSCQ YQWPTQAHRP GRPCSSPSRY LQGRDTAGGK GEQERALQPG SPEYEERWPP60
AP 62

(2) INFORMATION ON SEQ ID NO. 341:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 80 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

SLLGCCSLAS TNGPHRLIGQ DDLAPVLHVI CRAEIQLAGR VNKKELSSQV LRSTKNGGLL60
PPSGHWGISR WHPLPLGLEKS 80

(2) INFORMATION ON SEQ ID NO. 345:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 257 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:

```

KNSQLEPRE NAKEEVKKEK GMGWVAAGAA QLLSLLSTST ASDSSVSSSS ACTSGLLPRR 60
RSPASPRSAH LHHLGGLLEHF HLAALDLDV EGEGLHLVDR GLGARVHHVV GREGFAQLVFL20
RRLQFLAPLG GHQARAQLVH ALLQGVPRLL QVFLGLEARL LQVLAGTHLG LLHLLGEGLL180
LEVVFAPQAL RLIRSARDSS ITSSTSTASS DESSSSAAASS SGRSPSPSSS PSFSGSASDS240
FSDLLMLSLA GSFTSSW                                     257

```

(2) INFORMATION ON SEQ ID NO. 346:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 237 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

```

KSRRRCQRRR ARSWARASGP RRTQRRWSFR RTRRWRLRL LRSPAQSVSS AGPAARGRLQ 60
EGLLQGEDGE DQGAYPEPBG EDAPQDQKGP GEDAAHPGEA HEQAGHAPGA RRAARETEDV120
AGQVAQILHA RPRGVRALQD RGLQGATLHL PRQEDPRGPG GSAQGHARDGG GGRSGGRPAT180
CGAGAAPTCT RCWRSPRSRT PCWWTRATAT ERPPLPTTF LAPSLEPLSH SLSARAG 237

```

(2) INFORMATION ON SEQ ID NO. 347:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 263 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

```

GRLPGYDPDR GFGASSAGAQ AAEEPSGAGS EELIKSDQVN GVLVLSLLDK IIGAVDQIQL 60
TQAQLEERQA EMGAVQSIQ GELSKLGKAH ATTSNTVSKL LEKVRKVSVN VKTVRGSRLR120
QAGQIKKLEV NEAELLRRRN FKVMIYQDEV KLPKLSISK SLKESEALPE KEHEELGE180
RPEEDAAALE LSSDEAVEVE EVIEESRAER IKRRACGAWT TSRRPSPRRR WRRPRCVPAR240
TWRRRASRPR KTWRRRGTPW RSA                                     263

```

(2) INFORMATION ON SEQ ID NO. 348:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 106 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

```

SSGSSRFSS GSRRRYASLY FCCAIEDQDN ELITLLEIHR YVELLDKYFG SVCELDIIFN 60
FEKAYFILDE FLLGGEVQET SKKNVLKAIE QADLLQEEAE TPRS GS                                     106

```

(2) INFORMATION ON SEQ ID NO. 349:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 78 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

LFLMPQNKVR MVICQEFFT VSYKKRVALF TVLCVKSLFK ARMEPLGYLL KNLFCFPPL60
 RSAAHFTAAS FLSMALPS 78

(2) INFORMATION ON SEQ ID NO. 350:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

TCLHGLYFHL YMLGWIKLCC DCDQHSQHS TVLSHRQLVV INVQRTKKKK GAASLGGITG60
 SGVKR 65

(2) INFORMATION ON SEQ ID NO. 351:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 196 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

LFGLPLRLQLG GVCHGHRPGL LLHQOHGGGA GAVQQPQREE EALHDPGQGS APAELCQFQQ 60
 HVPRFPLQQP QAVQEGGGAG AGQGLVLMQP GAGLQGVQPG DDGAPDLQHG DAAGDSHHDD120
 PAQELPAAEH RAQGGGPRP ALRGGARSNC RVCLVQMCPE APEGSHQLMP ASDPQQGWFA180
 AAAQGEFVSD PGGHHH 196

(2) INFORMATION ON SEQ ID NO. 352:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 361 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

SLASLSDSLQ VSVMATQDQS YSTSSTEEL EQFSSPSVKK KPSMILGKAR HRLSFASFSS 60
 MFHAFLSNNR KLYKKVVELA QQKGSYFGSL VQDYKVYSLE MMARQTSSTE MLQEIRTMMT120
 QLKSYLLQST ELKALVDPAL HSEEELEAIV ESALYKCVLK PLKEAINSCL HQIHSKDGSL180
 QQLKENQLVI LATTITDLGV TTSVPEVPMK EKILQKFTSM HKAYSPEKKI SILLKTCKLI240
 YDSMALGNPG KPYGADDFLP VLMYVLARSN LTEMLLNVEY MMELMOPALQ LGEGSYLLTT300
 TYGALEHIKS YDKITVTRQL SVEVQDSIHR WERRRTLNKA RASRSSVQPL HLRVVPARA360
 A 361

(2) INFORMATION ON SEQ ID NO. 353:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 161 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

VDGFLQGLQD TTVQGRLYNC FELLGVQGS VHQGLELQAL QQVALELGGH GANLLQHLRA 60
 GGLARHHLQA VHLVVLHQA KVRALVLRQL HHLVQLAVV GEESVEHAAE TGKAQVPVPSL120
 AQDHGGLLLH AGAARELLQL LRAAGGVGVV VGGHRRHPQA V 161

(2) INFORMATION ON SEQ ID NO. 354:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 218 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

```

SRGRGPKYVID VEQPFSCSTSL DAVVNYFVSH TKKALVPFLL DEDYEKVLGY VEADKNGEN 60
VWVAPSAPGP GPAPCTGGPK PLSPASSQDK LPPLPPLPNQ EENYVTPIGD GPAVDYENQD120
VASSSWPVIL KPKKLPKPPA KLPKPPVGP KPEKVFNGGL GREAASSVSA QPLLSPAGL180
GRGRGQSYRR SWEKRRGTGS MVSPTPGTSG LVPGRARW                218

```

(2) INFORMATION ON SEQ ID NO. 355:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 253 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

```

AGEGV DGLTQ ETPLKPVSQL PGPAGAPTGR RQQAEDPGSV MASALRPVRV PKPKGVLP SH 60
YYESFLEKKG PCDRDYKKFW AGLOGLTIYF YNSNRDFQHV EKLNLGAF EK LTDEIPWGSS120
RDPGTHFSLI LRNQEI KFKV ETLECREM WK GFILTVVELR VPTDLTLLPG HLYMMSEVL180
KEEARRALET PSCFLKVSRL EAQLLLERYP ECGNLLLRPS GDGADGVGH H AADAQRDARG240
PALQGEAGGA PST                253

```

(2) INFORMATION ON SEQ ID NO. 356:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

LTTASREVQE NGCSTSITYL GPLPLHLVMP DHVRPVVHLP RGDHRRRRRP RWAAAAGSRT 60
RGSAPGAVVP PAGSPSGSTR VSPVHGAPPL WPLQTSCIG AQEAGSSRSRG HGAPPPPLR 118

(2) INFORMATION ON SEQ ID NO. 357:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 223 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

DHTCGCAGNL QEAIMLRSGV TSQGIHPGSP WCCTPTQAZL IVGDQSGAIH IWLKTDHNE 60
QLIPEPEVSI TSARIDPDAS YMAAVNSTGN CYVWNLTGGI GDEVTQLIPK TKIPAHTRYAL20
LQCRFSPDST LLATCSADQT CKIWATSNFS LMTLSIKSG NPGESSRGWM WGCAFSGDSQ180
YIVTASSDNL ARLWCVETGE IKREYGGHQK AVVCLAFNCS VLG 223

(2) INFORMATION ON SEQ ID NO. 358:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 193 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

FFFFFFFF EQHLRVGLLL LPPRLSPRFG PAWPVNPVFG WPGHLHQGGQ LLAGTNKPFH 60
LAMVVVFSMD RGPETRAGRG REHTSLGVGT SLRPLSSFGE SADFPQCRL AQSRSVQPGLL20
GRALSHLDKQ LGAESPRAAW PSRSRRHRGP SGPVAQAGRG GSALTWVLRG SLQLPPAPGL80
SPEGSQASPA HCH 193

(2) INFORMATION ON SEQ ID NO. 359:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 251 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

PGCCMGPPSSC HHLHQAVPRG HRLAQHTVIE GQADNSLLVA AILSLDLSL HTEPGQVVR 60
GSSDDVLGVP REGAAPHAA GGLPGVAALD AQLRHQGEVG RPPDLARLIS RAGGEERGVL20
AEATLQGVAR VGRDLSLGDE LGHLVTNAPR QIPDIAVSGA IDSCHVAGVG IDVGGRDGDL180
GLRDQLLVV CFQVPDVDSF ALVTHDELCL GWGAAPGTFR VNALGGHTGP QHDCFLQVTS240
TSACMILTSS C 251

(2) INFORMATION ON SEQ ID NO. 360:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 50 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:
GNIPHSNLTD ASSPKRIKIV ACTQENILG RMKYVCLFFF KKNKGFWSNGE

50

(2) INFORMATION ON SEQ ID NO. 361:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 59 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

KGNQLYQGET RALGTMTRT AFILHHSDCF QSSNDCQATS QMTDNFCCSF LYKMLRQQA 59

(2) INFORMATION ON SEQ ID NO. 362:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 67 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

DKILLSPRME CSGMIMARCS LDLPGSHLSL PSSWDHRHVP PCPANFYFGR OKVSPCCCLGR60
FQTFGLK

67

(2) INFORMATION ON SEQ ID NO. 363:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 84 amino acids

(B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

MRRCIHPSHS LSGSRQTQSP LSHSASNGST TKVAQQMRR AAVVGESTEE TRLGRALGAA60
 GFTNKQLSEN TAQGEKRV M CLQN 84

(2) INFORMATION ON SEQ ID NO. 364:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 127 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

CAYRTEKWKs HTVPCsPEVK LVLTLALRAF SMSEPLGLGR KARVSahrHT SYLQDIDCLC 60
 RGSTGQPTAN TAASLVsASL LPVHPGDYSW INLPKNSAFI MSLFCSKTQN GSLPPRGRPS120
 HHCIpNR 127

(2) INFORMATION ON SEQ ID NO. 365:

(i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 114 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

PYVHSPAWSP WGLVGRILVSV HTDIPATERT LIVSAEVALG SQLQTQQPPW FQLLSFQYIL 60
ETTFGLIFLR TQHSLSCHFVS RKFMAPCHL EADQVITVSP TASTVCIWYI VQAP 114

(2) INFORMATION ON SEQ ID NO. 366:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 30 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

NLHSNIKVFF YNVPKISGPQ QAVEVPEVFFN

30

(2) INFORMATION ON SEQ ID NO. 367:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 44 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

KECMSEAQFL ATTLTKGNNC RGILQLINTQ HLLHTVFTDS NLVG

44

(2) INFORMATION ON SEQ ID NO. 368:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 34 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

NVDFRCKNML EIRFSAIKPN TTKIKKNVCQ KPNS

34

(2) INFORMATION ON SEQ ID NO. 369:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 147 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

QPSSLLHHCP YPYPPRHLLA TPLLKPQLLA GSPAHASLIS FLASPPQRASR QHGGPSQRAG 60
 TLSCLVELG GSSGGRLCH GSADPTNRRA EPQERGEPPA GDRRPLPEWG RVSLAESPGAL20
 EFRCPGSLGE WGEIPEKESS AHPKTEE

147

(2) INFORMATION ON SEQ ID NO. 370:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 244 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

NHSCWQGFQL MPASSPFLLA PKGPPGNMGG PVREPALSVA LWLSWGAALG AVACAMALLT 60
QQTQLQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS RKRRRAVLTK120
QKNDSDVTEV MWQPALRRGR GLQAQGYGVR IQDAGVYLLY SQVLFQDVTF TMGQVVSREG180
QGRQETLERC IRSMPSHPDR AYNSCYSAGV FHLHQGDILS VIIPRARAKL NLSPHGTFLG240
FVKL 244

(2) INFORMATION ON SEQ ID NO. 371:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 185 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

TPASWIRTPY FWACRPLPRL RAGCHITSVT SESFFCFWVS TALLFRDLSP LSQASRASL 60
CSGRLCQGY SPFWEGPPVP CSRLTLLRL CSSVCWVSRA MAQATAPRAA PQLNQRATES120
AGSLTGPPML FGGPLGASKK GDEAGMSWGP CQQLWFQEWG SKEVAGRVRV RAVVQKGRRL180
LRKEK 185

(2) INFORMATION ON SEQ ID NO. 372:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 148 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

VLYHCASRYR RRARQTCAPS YTRSADLPSR TTPVEDLLEL SRAFWVGADG GGRVRLGGT 60
 EAHEDGIPPE SMDHYADGHR PQHCHLGYRC HGRPQREGLP RCLKVPVNL SSVSVFPVTL20
 HRAGMEFNGC SGQTLVHGQT SLLWLQD 148

(2) INFORMATION ON SEQ ID NO. 373:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 135 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

CLPVRRLRQF EPKTPKVEAE FQSMGSRSLSQ PFESYITAPP GTAAAPAKPA PPATPGAPTS 60
 PAEHRLLTCT WSCRVLGSLG LMGAGGYVYW VARKPMKMGY PPSPTITQM VIGLSIATWG120
 INVMDPKGK AYRVV 135

(2) INFORMATION ON SEQ ID NO. 374:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 152 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

IPCLLCVSRG KGQRQKTDLS VVLSNNAVGL PFGVCHDNDT PGGNAEADDH LRNGPWRGV 60
 SHLAGLPCHP VHVPARPHQP QPRKHATAPA GLQQAFCWG GRRSGCSWGR RFGGGGGTG120
 RRSDIGLKRL GQPRPHALEL GLNLGRLWFK LA 152

(2) INFORMATION ON SEQ ID NO. 375:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

GAEQLRSCA MAVSQEGLDG EVKAPDARIF IPCANTAFTP DLQVLQQVLS SFTVSSPLFH 60
 SGFICYTPNL FSQSTPQSLP CWGQHRKRN LRKEKGNLQP AMDLMIP 107

(2) INFORMATION ON SEQ ID NO. 376:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

IPKNFYHNIH RSLYQLYLEV KQAWESIDCS ACPRVEALNK ATKTPFITDL TFQWPTGPGS 60
 QQVGHQANHL FPCASLCKSW SVPLARPSLV QDLGPQTKES RGLGFDPDRM VSL 113

(2) INFORMATION ON SEQ ID NO. 377:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

EGGPQAQPHS AVGSSLSSQI QVNLSFKNKG EPQTCTTRD NNTPWQEDHV LDCLRTATVR 60
 QEACCDPLCS MPLAQASSIP YHLPFMLFFG TTTLAKREYG QQRPRALLQY RHFEVGRQHMI20
 LHSK 124

(2) INFORMATION ON SEQ ID NO. 378:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

HKILLISRYR RNSVVTQAI LYTPMILQRK HPSLLLPLLW QLKICISSTL KRRKRNNLSL60
 IPKLPH 66

(2) INFORMATION ON SEQ ID NO. 379:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

PEKSPGAGPL LGGSPFFFFF YVSKSTEFIL KHSIKFESHE TKASLHYMLI LAKSKDQHTI60
 DIHDNVV 67

(2) INFORMATION ON SEQ ID NO. 380:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

FCIRFECLHV KTQLIYYFNI KPISFEAKLI LLFYKSNQDS FFRMLKAQCL RFMLAALLAL60
 LLPKMTKQN R 71

(2) INFORMATION ON SEQ ID NO. 381:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 107 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

MDGAQGRLLP VSSRHSNLAL LKPTSRDLTA PPEGASLMTV GGITAPRDVQ VWNPTWESV 60
 TLRGKROPAP VLQFRISWWG DDRGWLRLAL SNHGGPYKGR GVTRVCA 107

(2) INFORMATION ON SEQ ID NO. 382:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 143 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

EVENHTNLLS YSSRGQESKM VFTRLKSCQC GFVSPRRLWG RIQCLFQLLQ GPPHRLAPGL 60
LAIFTARSFL ASCADPRDSP SLIRAPMITQ GPPQPSTVIS PPRNPELKHR RRVPFATQGN120
TFPRPGVPNL DISGGCYSTH RHQ 143

(2) INFORMATION ON SEQ ID NO. 383:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 86 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

SHTHAQLSNH GGVEEPPLPL GVPKPGWSDS GALSPPGCKL KTPGGFQNAQ CLGHNLQQLN60
LNLQRDITAP QETPRGSQSA KPEETI 86

(2) INFORMATION ON SEQ ID NO. 384:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 123 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

LEPIRFQQKV MEKETEKRIE EIEDAAFLAR EKAKQDAEYY AAHRYATSNK HKLTPEYLEL 60
KKYQAIASNS KIYFGSNIPN MFDVSSCALK YSDIRTGRES SLPSKEALEP SGENVIQNKEL20
STG 123

(2) INFORMATION ON SEQ ID NO. 385:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 83 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:

DNSCVRYVEA QQKSHGTTSR NLSAVRFPVSL MTVCWLCQTL YLGKESPDNL GSFPWALSyr60
 GICNMEKIIF HFCSFNSINS LYK 83

(2) INFORMATION ON SEQ ID NO. 386:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

CLTFQCRQYL SIRLSSFMS SLEKNTRYRL DKTVAEKTIC VSDSWLYPPI SGAPRTIAGE60
 VEQMKCKFSV NLKSPYNDCS HLPFWATS 88

(2) INFORMATION ON SEQ ID NO. 387:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60
RDLLLLLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPs 105

(2) INFORMATION ON SEQ ID NO. 388:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 173 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

AQESFWQLCR GARTSKRKLK KLGMEQHCNE MCPFSSLFLP GAYKAQMYSD VWTNTKKKKK 60
KKKKKAFLSH RHKTQIIYCY EALFTNGQFL HFIAACERLP DGRFISLVLQ TSSQAIFYQK120
GENSCLSFLEK NAFLYLSIRH YTSELYKRPQ GTMSLVDTFH CSVAPFLAWE ASA 173

(2) INFORMATION ON SEQ ID NO. 389:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 105 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

TCEPFRNPQV GKDPTPSLRI ICLAITGSWK CFLGCVKINQ GGMKHIFLAT KLEFLREQMQ 60
RDLLLLLARLQ GPLWSHTEAV TGHKPRRARG SCAEAPGPLS GSFPs 105

(2) INFORMATION ON SEQ ID NO. 390:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 262 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

RCPRRGREMD SGCWLFGEF EDSVFEERPE RRSQPPASYC AKLCEPQWFY EETESSDDVE 60
 VLTILKKFKGD LAYRROEQYK ALQEYSSISE KLSSTNFAMK RDVQEGQARC LAHLGRHMEA120
 LEIAANLENK ATNTDHLTTV LYLQLAICSS LQNLEKTIFC LQKLISLHPF NPNWNGKLAE180
 AYLNLGFPALS AALASSQKQH SFTSSDKTIK SFFPHSGKDC LLCFFPETLPE SSLIFCGRDT240
 RNGRKIGKFC KCANLVGERG TG 262

(2) INFORMATION ON SEQ ID NO. 391:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 66 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

KPVPLSPTRL ARLQNFPIFL PFLVSLPQKI KELSGKVSQK HKRQSFPECG KKDILVLSLE60
 VKLCCF 66

(2) INFORMATION ON SEQ ID NO. 392:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 78 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

QAGGRVPWLN GLCWLLYFPS LQQSPAPPYA YPGEPDTEPD LPGHPFSWQN WLMTIFQRYW60
 NTPAVLSOTL VVCRPGLL 78

(2) INFORMATION ON SEQ ID NO. 393:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

TSLEGIDLQP SHLTIYTAAL KEKTPDFRRL SPRVSETADS RKVARGPRFV MRDNPGRGGD60
 HRGLQAPGWM KEGRGWGL 79

(2) INFORMATION ON SEQ ID NO. 394:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 72 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

VTPPPPSQIS SELPPSTAPP TKPPIPOPPS STPAFGDPYD HPRARGCPAL QIGAHGRPYG60
 SPRSPRREER DV 72

(2) INFORMATION ON SEQ ID NO. 395:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

PPPPPPPKFHP SFRLLQPPLQ NPPSPDLLHP PRRLTTPMIT PAPGVVPHYK SGPTGDLTGTV60
 RGLRDARRET SEVWRLFLQG CCVDCEVGGL KINSLEGG 98

(2) INFORMATION ON SEQ ID NO. 396:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

NWRQTVWQRV REGACAQESS RPASGCRFLR CAIGASAFSG DRGSAVATNT QPHTNHHTHK60
 WGQPHVQAF TNVISLVLYF 80

(2) INFORMATION ON SEQ ID NO. 397:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 309 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

YONSSTCKKG KVFPGKISVT VSETFDPEEK HSMAYQDLHS EITSLFKDVF GTSVYGGQTVI 60
LTVSTSLSPR SEMRADDKFV NVTIVTILAE TTSDNEKTVT EKINKAIRSS SSNFLNYDLT120
LRCDYVGCNQ TADDCLNGLA CDCKSDLQRP NPQSPFCVAS SLKCPDACNA QHKQCLIKKS180
GGAPEACACVP GYQEDANGNC QKCAFYGISGL CCKDKFQLIL TIVGTIAGIV ILSMIIALIV240
TARSNKTKH IEEENLIDED FQNLKLASTG FTLNLGAEGSV FPKVRITASR DSQMNPYPYSR300
HSSMPRPDY 309

(2) INFORMATION ON SEQ ID NO. 398:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 105 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

QALIASTTFN VIDSYLASEL OSLQTFTTSI QRGWQMSDGR KTFEARSLLV LTSPSVFLNT 60
LNNSLYIGWG EWRVPHSYDS NSQGGACCCV LNRDFASGCL WRPLS 105

(2) INFORMATION ON SEQ ID NO. 399:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 75 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

CFSCFVICSV SLCTLNIYPL CDKKKKKKKK SRTSTFDESQ PQPRKNGSWD KQLVVFVSKTQ60
IGHINATAFR SFDFO 75

(2) INFORMATION ON SEQ ID NO. 400:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

RKKAVCFMND LICFLDNTEK NNVLQAWWC VHLVPTIWEA EAGGSLEPRS LKLQCPVVAP60
 VNNCTPAWAT 70

(2) INFORMATION ON SEQ ID NO. 401:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

LVPQGSLLQT HPFVFFSFLE MRSRYVAQAG YQLFTGATTG HCSFKLLGSS DPPASASQIV60
 GTRCTHHHA 69

(2) INFORMATION ON SEQ ID NO. 402:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

PPLWVATVRN GCCHVFVWTLF ANRSLPGFGN TSITSLLLFC RDKTFEVARP RTSKSDSCYSA60
TVYTAHLSYS HVLSSLVRLF 80

(2) INFORMATION ON SEQ ID NO. 403:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

LTNMSDHLFG WLLLEMAVVM FSGLCQPTDP CQVLEILLP RCYFSAGIKL LRWPDPEHPR60
IPVTVLQYTL LIYFILMCF L 81

(2) INFORMATION ON SEQ ID NO. 404:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

VSHYPHSVSK PPKHQTKQMV VALTHSRLTS EFKWENTPYT TVIIPLWTLN IYFYLKILL60
KKKAHENRIN EQCIL 75

(2) INFORMATION ON SEQ ID NO. 405:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 328 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

```
RYLNMGNLLK VLTCTDLEQG PNFFLDFFENA QPTESEKEIY NQVNVVLKDA EGILEDLQSY 60
RGAGHEIREA IQHPADEKLQ EKAWGAVVPL VGKLLKFEYF SQRLAAPALRG LLGALTSTPY120
SPTQHLEREQ ALAKQFAEIL HTLRFDELK MTNPAIQNDF SYRRTLSRM RINNVPAGE180
NEVNNELANR MSLFYAEATP MLKTLSDATT KFSVENKNLP IENTTDCIST MASVCRVMLE240
TPEYRSRFTN EETVSFCLRV MGVVILLYDH VHPVGAFKAT SKIDMKGCIK VLKQPPNSV300
EGLLNALRYT TKHLNDETTT KQIKSMLQ                                     328
```

(2) INFORMATION ON SEQ ID NO. 406:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 115 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

```
YYIHLIINFL LRLCRLGIFK IKEKIWPLLK VCAQNFKKI PHVKVPSASA GDSVLVLSS 60
ARASRSQSR SCALLDRGG SAAALGGAPG PERGSGGSRT GSPSTPAPVA EPPQA 115
```

(2) INFORMATION ON SEQ ID NO. 407:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 100 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

QEPALALDAG WENMGYLLRL PEDLLMLLLT SEKIRKISLI CLLVEQLHPM PSLATSHLLD 60
AGLPLVFRGQ LLCMTASPPR CLLHLLILHS PDYKFFSQTL 100

(2) INFORMATION ON SEQ ID NO. 408:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 116 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

TVLRSHLPSS CLPCLSTHSV KEPRGATSPR LCFFTACGMG VSSATAGLRC FHQPORHLVL 60
HEEQTLRGWS GMGRSPGGQ ALVPSRFFSL APGVHTAQSA PGGWKPPCFR SLGSPP 116

(2) INFORMATION ON SEQ ID NO. 409:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 132 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

SPDERCSIRT SPFRACFASP RTVLRSEQEP LRPDFVSPPP AAWVCPVPL ASAASISLVA 60
TWSEMKSRHL EAGREWGRRP WEGRRWFQAG SRPWRLCTQ PSRHLVAGSH PALDHSGPHL120
RRVPALDQSR GH 132

(2) INFORMATION ON SEQ ID NO. 410:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 142 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

WKQRRPAVAL DTMPQAVGK QSLGEVAPLG SLTLCVERQG RHEEGRCEWS TVHPGISQPE 60
 SPPSLAAPFH SLWPTATEMS ACQDTWRRKK TRHQKCLFPQ EQIELLDQGH TRSGRHPAPC120
 AQQKETQFNV WLLCSRETAT LP 142

(2) INFORMATION ON SEQ ID NO. 411:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 244 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

KRRGVQRFW LVCTRRASPG AARSAPIAPA TGSGRRPNMD SAGQDINLS PNKGLSDSM 60
 TOVPVOTGVA ARTPAVEGLT EAEEEEELRAE LTKVEEEIVT LRQVLAAKER HCGELKRRLG120
 LSTLGELKQN LRSWHDVQV SSAYVKTSEK LGWEWNEKVQ SDLYKKTQET LSQAGQKTS180
 ALSTVGSALS RKLGDNRNSA TFKSFEDRVG TIKSKVVGDR ENGSDNLPSS AGSGDKPLSD240
 PAPP 244

(2) INFORMATION ON SEQ ID NO. 412:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 149 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

```

LGHFLEIPLSK FLRSFHIGAR DLHVMPAPGQ VLFQLPQGGG AQPPLELSTV PLLGCQDLAQ 60
SDNFLFHLGK LSPPELLLSL CQTLNSRSPG SHTCVDRNIR HGVRRQQTFR RIQVDILAGG120
VHVRAASGPC RGRYGRAGG AGRSSPRTH 149

```

(2) INFORMATION ON SEQ ID NO. 413:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 143 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

```

ALETCTSCQL LDRFCFSSPR VERPSLLSS PQCLSLAART WRRVTISSST LVSSALSSSS 60
SASVRPSTAG VRAATPVSTG TSMESDSRP LLGEFRLISW SAESMFGRRP DPVAGAMGAEL20
RAAPGEARRV HTSQRNCLTP RRF 143

```

(2) INFORMATION ON SEQ ID NO. 414:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 105 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

RGRGALWWAA KELRRTKKLS DYVGKNEKTK IIAKIQQRGQ GAPAREPIIS SEEQKQLMLY 60
YHRRQEELKR LEENDDDAYL NSPWADNTAL KRHFHGVKDI KWRPR 105

(2) INFORMATION ON SEQ ID NO. 415:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 386 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

AAELRDCGSR RISRSPSSNS HLSPRISLSG NLGPQTSRLG GPPSPSATWS VEWQLPRQQS 60
LPGRGSANLL PSVRSESAVL SDCVGGFFGR SSVRAWIAGP RCTPASPTRV LSLSWRLFNS120
ASLLLLATST SGSECRFPRS PRARERGIFD CERLLVRRSC WRSGDPRFAG PAGHAAGAFS180
TPQYLGGTAM VLLHVKGDE SQELLQAPGS TELEELTVQV ARVYNGRLKV QRLCSEMEEL240
AEHGIFLPPN MQGLTDDQIE ELKLDKEWGE KCVPSGGAVF KKDDIGRRNG QAPNEKMKQV300
LKKTIEEAKA IISKQVEAG VCVTMEVMD ALDQLRGAVM IVYPMGLPPY DPIRMEFENK360
EDLSGTQAGL NVIKEAEHC GGQPRS 386

(2) INFORMATION ON SEQ ID NO. 416:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 182 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

GVEKAPAAWP AGFAGRGSPD RQQLRRTNSR SQSGIPRSLA RGERGKRHSL PEVDVAKSNS 60
 EAEKSRQLK LRTRVGEAGV HRGPAIQART ELRPCKPPTQ SERTADSSERT DGRRFADPLP120
 GSDCCRGNCQ NTDQVAEGEG GPPNRLVWGP RFPLREIRGL RWELLOGERE IRREPQSRSS180
 AA 182

(2) INFORMATION ON SEQ ID NO. 417:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 467 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

HTLSRWTKHS IPRWNDART DTWSELDNR KIGQARNTLM DMRLSQVSDS VSGQTVVDFK 60
 GYLTDLNSMI PTHGGDNDI KCARLLLSV RETNPHHPA WIASARLEEV TGKLQVARNL120
 IMKGTEMCPK SEDVWLEAAR LQPGDTAKAV VAQAVRHLPQ SVRIYIRAAE LETDIRAKKR180
 VLRKALEHVP NSVRLWKAIV ELEEPEDARI MLRAVECCP TSVELWLALA RLETVENARK240
 VLNKARENIP TDRHIWITAA KLEENGNTQ MVEKIIDRAI TSLRANGVEI NREQMIQDAE300
 ECDRAGSVAT CQAVMRVAVIG IGIEEEDRKH TWMEDADSCV AHNALECARA IYAYALQVFP360
 SKKSVDLRAA YFEKNHGTRE SLEALLQRAV AHCPEAEVLW LMGAQSKWLA GDVPAARSIL420
 ALAFQANPNS EEIWLAAVKL ESENDEYERA RRLAKARTV PPPPGCS 467

(2) INFORMATION ON SEQ ID NO. 418:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 352 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

TPGRWGHCPR LGQQPPGPLV LIILGLQLHG CQPDLLTVGV GLEGQQQDAP CCRHIPCQPL 60
 GLGAHEPQRL CFGAVGHSPL QECFQGLPSA MVLLEVRGAQ PHTLLAGEHL QGVGVGDSCT120
 LQGIVGYTTV SILHPGMLFI FLLNPNPNHG THDGLAGGHT PSPVTFLGIL DPLLTVDLHT180
 VGPQRGDGVS DLLLHRLRVP IGFLQLSSRD PDMSCVRNVL PRLVQDLAGI FIGLQPCQSK240
 PELHAGGAAL HSSAQHDSSI FRFFQLNGCF PQANRVWNML EGFPKKNLLC TNVRFQLCGS300
 DVNPDRLWEM TDSLGYHGLG CVFRLQPGCF QPDITLGAH LRPLHDKVPS YL 352

(2) INFORMATION ON SEQ ID NO. 419:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 424 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

PFGAPFFLEF FFLTRDIKTF NEGGHSSEFF HMRPNPAPRR PAMATAQSEG VLDAAGHQPK 60
 DVPDLLLFG DVLGHGAPQL PMPRLCTLTA LPHLLLLLLS AMLQLKLVEE GPGIPQVRVN120
 LHSAVEPLFG LGDLPLTPKQ LGHGQEHMGV MLTLQGIHA LGPPLGPCLE EDGLRPQDTG180
 VGALLQRLGH ECICDVLQPR TVLQPHGLQP QPRVLWVLT RLFQNGPCSS KLPNLLQPR240
 EQKFGQCGVG TLLQPLVIGF PRLLHLLLLL LDPLLHHPQL GEVLIVPQGL LAQILGCPDV300
 VLHPLQLHRL HEHPGGGGTV RALLSSLRAR SYSSFSDDSF TAASQISSIL GLAWKARAPM360
 LLAAGTSPAS HLDAFMSHS TSALGQWATA LCRSASRDSR VPWFSSKYAA RSHTLFLLGW420
 TCRA 424

(2) INFORMATION ON SEQ ID NO. 420:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

GRTLPRGGGT VVWQGHGLEG WWAALSGSGF PAVGFLEWLL RLVIYFLSLP VTFGAPEYRL 60
 FSPWAVSLSC FLTLLPGLLC VHLRLAWSKQ VRPLLLYSLV LFWHLVKLA 109

(2) INFORMATION ON SEQ ID NO. 421:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 177 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

VSPSSSAAG TLFQGLCGAP DAPHPLSKIP GGRGGGRDPS LSALIYKDEK LTVTQDLFVN 60
 DGKPHIVHFQ YEVTEVKVSS WDAVLSSQSL FVEIPDGLLA DGSKEGLLAL LEFAEEKMKV120
 NYVFICFRKG REDRAPLLKT FSFLGFEIVR PGRPCVPSRP DVMFMVYPLD QNLSDSD 177

(2) INFORMATION ON SEQ ID NO. 422:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 114 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

ASRPYILELR EKDPFCRPLAH RGSSTVGEGB QEHHRGPGTM CLQHSWSGHL LNGILLSWV 60
 FIILGGSAGG GRRRRGEWVG GRVGGCGVAR AGRSLWAKSL SGRGRVPSSC LSER 114

(2) INFORMATION ON SEQ ID NO. 426:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 50 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

PFCSSSLAKLQ GIWGMWDLQF PAPASALSQV LTPAPASAPA PGRAPAPAAA

50

(2) INFORMATION ON SEQ ID NO. 427:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 114 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

EDKMRPGLSF LLALLFFLGQ AAGDLGDVGP PIPSPGFSSF PGVDSSSSFS SSSRSGSSSS 60
 RSLGSGGVS QLFNFTGSV DRGTCQCSV SLPDNNFPVD RVERWNSQLI VISQ 114

(2) INFORMATION ON SEQ ID NO. 428:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

EITMSCEFQR STLSTGKLLS GRETEHWQVP RSSTEPVKLE NNWDEPPLP KLRLELEPDL 60
 ELELKLELES TPGKELKPLG GIGGPTSPKS PAAWPRKNRR ARRNERPGLI LSS 113

(2) INFORMATION ON SEQ ID NO. 429:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 50 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:

AAAGAGARPG AGAEAGAGVN TWERAEGAG NWRSHIPQIP CSLAKEEQKG

50

(2) INFORMATION ON SEQ ID NO. 430:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 224 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

QTQKVVTSPF RITLHWLLPC AAHPDPLHKK GQENSGCAPA TAHSAPPGRS PPELRAGLQR 60
 LARAVLPVSR FSAPOPPAAS FSGPRVAPSE ESGPGTSSNS GRLALPRLRS LCPLGVARFR120
 CCRALARCCC SSSPRTAAWA RRAGSSSLAS PTSPTSALQ AHPGQPAAVF RHRIPEHAAA180
 QPAGPRDHEG GAGAGRRLLP AGHEAVPPGH QEVFVLALRP RLPR 224

(2) INFORMATION ON SEQ ID NO. 431:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 408 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

PALLGLPFIG SSLAPPTLQI CIKKAKKTLA VPQQRLLILP RVGAPRSCAR ACSASPALSS 60
 RCFASPRPSR RLPAPRGFES HPAKRAGPGQ ARTPAASFPF GSAPSAPSGS RAHDAAGPWL120
 AAAALPRLAL LPGLGARALP LWPARRLLQA QNCKPIPANL QLCHGIEYQN MRLPNLLGHE180
 TMKEVLEQAG AWIPLVMKQC HPDTKKFLCS LFAPVCLODL DETIQPCHSL CVQVKDRCAP240
 VMSAFGFPWP DMLECDRFPQ DNDLCIPLAS SDHLLPATEE APKVCEACKN KNDDNDNDIME300
 TLCKNDFALK IKVKEITYIN RDTKIILETK SKTIYKLVG SERDLKKSVL WLKDSLQCTC360
 EEMNDINAPY LVMGQKQGGG LVITSVKRWQ KGQREFKRIS RSIRKLQC 408

(2) INFORMATION ON SEQ ID NO. 432:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 323 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

VISFTTFISA KSFLQSVSIM SLSSSFLFLQ ASHTFGASSV AGRRWLLAR GMQRSLSWGK 60
 RSHSSMSGQG KPKADMTGAQ RSFTCTQSEW HGWMVSSRSS RQTGAKSEHR NFLVSGWHCF120
 MTSGIQAPAC SSTSMVSWP SRLGSRMFWY SMPWHSCLRA GMGLQFCACR RSRAGQGRAL180
 RAPSPGSSAR RGRAAAASQG PAASWARDPE GAEGAEPGKG EAAGVRCAPG PALFAGCDSG240
 PRKAGSRRLG RGAAGHRDGS AGEALQARAQ LRGAPTRGRS MSRCWGTVARV FLAFFMQIWR300
 VGGAREPEMK GNPFRAGHYF LGL 323

(2) INFORMATION ON SEQ ID NO. 433:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 333 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

```
RGRTWELFLA GRRVLVTGAG KGIGRGTVQA LHATGARVVA VSRTQADLDS LVRECPGIEP 60
VCVDLGDWEA TERALGSVGP VDLRGDCADM ELFLAGRRVL VTGAGKGIGR GTVQALHATG120
ARVVAVSRTQ ADLDSLVREC PGIEPVCVDL GDWEATERAL GSVGPDLLV NNAAVALLQP180
FLEVTKAEFD RSFEVNLRAV IQVSQIVARG LIARGVPGAI VNVSSQCSQR AVTNHVSVC240
TKGALDMLTK VMALELGPBK IRVNAVNTV VMTSMGQATW SDPHKAKTML NRIPLGKFAE300
VEHVVNAILF LLSDRSGMTT GSTLPVEGGF WAC 333
```

(2) INFORMATION ON SEQ ID NO. 434:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 210 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

```
APGHNLRHLD DRTQVHLKGS VKGLLGDLQE GLQQGDSGVV HQQVHGAHAA QRPLGGLPVT 60
QVHAHGFFYP ALADKAVKIR LSPAHSHHPR ARRVQRDLRA APYTFACPGD QHPAAREEQL120
HVGAVSAQVH GAHAAQRPLG GLFVTQVHAH GFYPRALADK AVKIRLSPAH SHHPRARRVQ180
RLDRAAPYTF ACPGDQHFAA REEQLPSCPT 210
```

(2) INFORMATION ON SEQ ID NO. 435:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 132 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

```
FFFFFFFFF GSRIRFIGGI GGRMSTAWGL RCVEGAQQAQ KPFSTGKVEP VVMPLRSLSR 60
KRMAFTTCST SANLPSGIRF SIVLALWGSL QVAWPMDEVIT TVGFTAFTRI LWGPSSRAIT120
LVMSMSRAPLV EQ 132
```

(2) INFORMATION ON SEQ ID NO. 436:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

KAKSWVPSPDF RFQELPENTR SQRVIFWSLF CRDSWEYGHF APRCGNESSR SGEAALADVQ60
 LAAPVSNQLH PDGVEDRGVG GLLPELHAAE PYLV 94

(2) INFORMATION ON SEQ ID NO. 437:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 70 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

FSGVCFAGIA GSMATLLHDA VMNPAEVVKQ RLQMYNSQHR SAISCIRTVM RTEGLGAFYR60
 SYTTPSPISC 70

(2) INFORMATION ON SEQ ID NO. 438:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

KAPNFSVLHT VRMQLIADRC CELYICKRCF TTSAGFITAS WSRVAILPAI PAKQTEENYP60
 LRSGVLRKFL EPKIRRNPLG SFLRSKMYIQ SAQVSTDS 98

(2) INFORMATION ON SEQ ID NO. 439:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 270 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

RSVVVRCLKM AAEPPQQQKQ EPLGSDSEGV NCLAYDEAIM AQQDRIQKEI AVQNPLVSR 60
 LELSVLYKEY AEDDNIYQK IKDLHKYYSY IRKTRPDGNC FYRAGFSHL EALLDDSKEL120
 QRFKAVSAKS KEDLVSGQGT EFTIEDFHNT FMOLIEQVEK QTSVADLLAS FNDQSTSDYL180
 VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVEPM CKESDRIHII ALAQALSVSI240
 QVEYMDRGEG GTTNPHIFPE GFRAQGLTLF 270

(2) INFORMATION ON SEQ ID NO. 440:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

RWRNRNLSRR SRSRWAATPK VLTWPFMMKP SWLSRTEFSK RLLCRTLWCQ SGWSSRSYTR 60
 SMLKMTTSIN RRSRTSTKST RTSARPGLTA TVSIGLSDSP TWRHCWMTAR SCGSGRLCLP120
 RARKTWCPRA SLNSQLRIST TRSWT 145

(2) INFORMATION ON SEQ ID NO. 441:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 210 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

```

IAPSRLKQKQK TLGSEALRED VRIGGAALAA VHVHLHDGHA EGLGQRNDVD VVALLAHGLH 60
LLLAELLDSP STLDEVLEEL ALALQVARGE QPQVDHKVVG GALVIEGGQQ VGORGLLLHL120
LNQVHERVVE ILNCFSEAL GHQVFLALGR HSLEPLQLLA VIQQCLQVGE SESPIETVAV180
RPGLADVRVL FVEVLDDLII DVVIFSILLV                               210

```

(2) INFORMATION ON SEQ ID NO. 442:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 322 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

```

NSERGRLOAM MTHLHVKSTE PKAAPQPLNL VSSVTLSKSA SEASPQSLPH TPTTPTAPLT 60
PVTQGSPVIT TTSMHTVGPI RRRYSCKYNV PISSADIAQN QEFYKNAEVR PPFTYASLIR120
QAILESPEKQ LTLNEIYNWF TRMFAYFRRN AATWKNAVRH NLSLHKCFVR VENVKGAVWT180
VDEVEFQKRR PQKISGNPSL IKMQSSSHAY CTPLNAALQA SMAENSIPLY TTASMGNP1240
GNLASAIREE LNGAMEHTNS NESDSSPGRS PMQAVHPVHV KEEPLDPEEA EGPLSLVTTA300
NHSPDFDHDR DYEDEFVNED ME                               322

```

(2) INFORMATION ON SEQ ID NO. 443:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

FGTRAPASHD DPFACEVYRT QSCPSAPESG IKCHPLQVRI GGFSTELTSY SNDPNRPPDS 60
 RHRPRLCHHN HQHAGGGTHP QAVLRQIQRA HFVSRYCAEP RIL 103

(2) INFORMATION ON SEQ ID NO. 444:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

SLSWSKSLGW LAVVTKDRGP SASGSGRGSS LTCTGCTACI GDLPGLLSLs LLLVCSIAFP 60
 SSSRIALAKL PRVGFMEAV VYRGILFSAI EACKAALRGV Q 101

(2) INFORMATION ON SEQ ID NO. 445:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 539 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

LDVQVKDDSR ALTIGALTLP LARLLTAPEL ILDQWFQLSS SGPNSRLYMK LVMRILYLD 60
SEICFPTVPG CPGAWDVDSE NPQRGSSVDA PPRPCHTPD SQFGTEHVLR IHVLEAQDLI120
AKDRFLLGGLV KKGSDPYVKL KLAGRSFRSH VVREDLNPRW NEVFEEIVTS VPGQEELEVEV180
FOKDLKDDF LGRCKVRLTT VLNSGFLOEW LTLEDVPSGR LHLRLERLTP RPTAAELEEEV240
LQVNSLIQTQ KSAELAAALL SIYMERAEDEL PLRKGTKHLS PYATLTVGDS SHKTKTISQT300
SAPVWDESAS FLIRKPHTES LELQVRGEGT GVLGSLSLPL SELLVADQLC LDRWFTLSSG360
QGQVLLRAQL GILVSQHSKV EAHSHSYSHS SSSLSEEPPEL SGGPPHITSS APELRQRLTH420
VDSPLEAPAG PLGQVKLTW YYSEERKLVS IVHGCRSLRQ NGRDPDPFYV SLLLLPDKNR480
GTKRRTSQK RTLSPEFNER FEWELPLDEA QRRKLDVSVK SNSSFMSRER DCWGRCSWT 539

(2) INFORMATION ON SEQ ID NO. 446:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 99 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

LLCLPAFVSL HHRLNMVSLK LGSKGACAL QPFLHTGPYS GLCLTKENR MFPLHLGLYP60
SGPLGRGPPEL AVSCFACTLF SLPPNSSGFS VSVPGQWQH 99

(2) INFORMATION ON SEQ ID NO. 447:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 112 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

VWIKLFTCT SSNSAAVGRG VRRSRKCRRL PDGTSSRVSH SSRKPLFKTV VRTLHLPRK 60
 SSLSKSLSKT STSSWPGTD VTITSKTSFQ RGLRSSRTTW LRKLRPANFS LT 112

(2) INFORMATION ON SEQ ID NO. 451:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 56 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

FFFFFVETGF RHVDETGLEL LASSDLPPQL LKVLGLYRHE PLSLALKRFS QRPSVR 56

(2) INFORMATION ON SEQ ID NO. 452:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 56 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

IRFGISCPGP GISLQEPLPL CWRHSFRIRR RREKRKCKGG RSFPGRITSV THMDPR 56

(2) INFORMATION ON SEQ ID NO. 453:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 57 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

VTEMVRPGKD LPPLHLFSL LLLILKCLQ QRGRGSCREI PGPGQEMPNI IYLTEGL 57

(2) INFORMATION ON SEQ ID NO. 454:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

ILAFWRAAPL WHHQILLCFP STWNSSNIRG CEGLAILLSW VHVSDRNGAA WERSPSFTFS60
LLPPPPYSKT VPPTGQGLL 80

(2) INFORMATION ON SEQ ID NO. 455:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

ARLPLLAARD RGQPGSVKDF KMAGRKLALK TIDWVAFIEI IPQNQKAIAS SLKSWNETLT 60
SRLAALPENP PAIDWAYYKA NVAKAGLVDD FEKKFNALKV FVPEDKYTAQ VDAEEKEDVK120
SCAEWVSLSK ARIVEYEKEM EKMKNLIPFD QMTIEDLNEA FPETKLDKKK YFYWPHQIEI180
NL 182

(2) INFORMATION ON SEQ ID NO. 456:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

AQSIAGGFSG KANLEVRVS FQDFRELAMA FWFWMISAK ATQSMVFRAS FRPAILGSFT60
 DPGCPRSSAA SNGSRA 76

(2) INFORMATION ON SEQ ID NO. 457:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

CPECVIQGPE LPPGLNFINS QLVGEANRDT FSCLINFLGK LHSSPQWSSD QMELSSSSSP 60
 SLSHILQSWP LREPTQHKI SHLLFLRHFP GQYIYPLARE PSAH 104

(2) INFORMATION ON SEQ ID NO. 458:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 223 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

RGAGGHQGES GRPEGWPPFF LHPRGRFQVP WLESVLIVVS NNIDEEALAR LAQEGSEVNV 60
IGIGISVVTC PQQPSLGGVY KLVAVGGQPR MKLTEDPEKQ TLPGSKAAFR LLGSDGSPML120
DMLQLAEEPV PQAGQELRVW PPGAQEPCTV RPAQVEPLL RCLQQLCE PLFSLAESRA180
LAQLSLRSL PEHRLRLSPA QYQVVLSERL QALVNSLCAG QSP 223

(2) INFORMATION ON SEQ ID NO. 459:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 157 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

VIRVVSSQPR SESQGDPAH RLFTACSLS DSTTWYAGL RSLCSGLSR LRDSWAKALD 60
SARDGSGSHS CPCWRQSRSS GSTWAGLTQ GSWAPGGHTL SSCPACGTGS SANCMSMSG120
DPSEPRSRKA ALLPGNVCF SSSVSFIRGW PPTATSL 157

(2) INFORMATION ON SEQ ID NO. 460:

- (i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 93 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
(A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

PPLFPHLLFL WGVVSDSCCF QSAPLRVSGG LPRTQTVHQG LQPLGQHHLV LCRAPQPPVL60
RAESAQQQLG QGSRLCQGW ERLTQLSLLEA EPQ 93

(2) INFORMATION ON SEQ ID NO. 461:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 328 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

FSLILCKHSI GDRKNYASAK LSELLPEEVE AEVKAAAEIS MGTEVSEEDI CNILHLCTQV 60
 IEISEYRTQL YEYLQNRMMMA IAPNVTVMVG ELVGARLIAH AGSLNLAKH AASTVQILGA120
 EKALFRALKS RRDTPKYGLI YHASLVGQTS PKHKGKISRM LAAKTVLAIR YDAFGEDSSS180
 AMGVENRAKL EARLRTLEDR GIRKISGTGK ALAKTEKYEY KSEVKTYDPS GDSTLPTCSK240
 KRKIEQVDKE DEITEKKAKK AKIKVKVEEE EEEKVAEEEE TSVKKKKKRG KKKHIKEEPL300
 SEEEPCTSTA IASPEKKKKK KKKRENE 328

(2) INFORMATION ON SEQ ID NO. 462:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

YNRNSFLIL VLSLFFLL FLWTSNCCAG TWFFLRKWF LNVFLFTPFL LLLHRCFFFF 60
 CHFFFLFFN FNFNLGFTGF LFSNFILFIY LFYFAFFRTG WKCGVTRRIV SLHFTVFVIF120
 FCFC 124

(2) INFORMATION ON SEQ ID NO. 463:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

SSFSLFFFFFF FFFSGLAIAV LVHGSSSESG SSLMCFLLPL FFFFTDVSS SSATFSSSSS 60
STLTLLLAFL AFFSVISSSL STCSILRFLE QVGSVESPEG S 101

(2) INFORMATION ON SEQ ID NO. 464:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 427 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

GGSSRRRHGGG YAAVALLVLL LLGPGGWCLA EPFRDSLREE LVITPLPSGD VAATFQFTR 60
WDSELQREGV SHYRLFPKAL GOLISKYSLR ELHLSFTQGF WRTRYWGPPF LQAPSGAELN120
VMFQDTVTVO DKSWKELSNV LSGIFCASLN FIDSTNTVTP TASFKPLGLA NTDHYFLRY180
AVLPREVVCT ENLTPWKLL PCSKAGLSV LLKADRLFHT SYHSQAVHIR PFCRNARCT240
ISWELRQTL S VVDAFITGQ GKWDWSLFRM FSRTLTEPCP LASESRVYVD ITTYNQONET300
LEVHPPPTTT YQDVILGTRK TYAIYOLLDT AMINNSRNLN IQLKWKRPPE NEAPPVFFLH360
AQRVSGGYGL QKGELSTLLY NTHPYRAFFV LLLDTVPWYL RLLHPLPACP GPAATPPFGD420
ADSAAGQ 427

(2) INFORMATION ON SEQ ID NO. 465:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 128 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

SPSILYGSCT CHSHKAFGGP DTGGHPSCRP HQVQSCGSGS KTLSLMWINL GRSSVMSSQG 60
 SSAPLTSST PPTQSLPLFP SNPWVWMTL TTTECAMLCC RGRWSAPKTS PPGRSSCPVV120
 PRQASLCC 128

(2) INFORMATION ON SEQ ID NO. 466:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 124 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

PQAWRLCRC CSARPVAPGA RRLVPCRTPT RQPAGGTCHH PAAFRGRSRH IPVPHALGFG 60
 ASAGRSVPLQ ALSQSPGAAD LQVFSTGAAP VIHTRLEDP ILGATLPAGP IRCRAVGLVP120
 RHCH 124

(2) INFORMATION ON SEQ ID NO. 467:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

FLHKTHNRAV EEAKEPFLCL CSRTERGFLA SVSLLVLPGL YQALRRGMET PHSGAWLGEG 60
 ERAGVLWASR GYNLSSLLGNV CFFVGSSPTR RGTQLYGTGI CVWSVL 106

(2) INFORMATION ON SEQ ID NO. 468:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 164 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

```
ISTKQTTHRL SQCKVESPDV SDYCLQMDTR SPSSDYTLK KPKEPLPPPL PQARPOSGAF 60
PYPASRPQTV REEPAGSRWP EGLSQSYRIG IKRAPLLPPQ PCCESCAGIN LRNSPERETG120
LMPWERSECE PMAPSLGLTN LPKYVKAEGD RDLAEGRKSF SSRN 164
```

(2) INFORMATION ON SEQ ID NO. 469:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 108 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

```
EIRGRPPLEFM PPLSCVDEFL QNRPHTECPG VKLSPPTCRT TAYKWTWVPQ RAQIIPSRSP 60
KNPCRLPFFPK PGPRVGRFHT PPQGLVQSGK NQQAHAQGRA SLSPTEA 108
```

(2) INFORMATION ON SEQ ID NO. 470:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 317 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

NMVOYYEVLG VQRHASPEDI KKAYRKLALK WHPDKNPNK EEAERKFKQV AEAYEVLSDA 60
 KKROIYDKYG KEGLNGGGGG GSHFDSPEF GTFRNPDV FREFFGGRDP FSDFFEDPF120
 EDFFGNRRGP RGRSRGTGS FFSAFSGFPS FGSGFSSFD TSTSFGSLGH GGLTSFSS180
 FGSGMGNFK S1STSTKMVN GRKITTNRIV ENGQERVEVE EDGQLSLTI NGVADDDALA240
 EERMRRGQNA LPAQPAGLRP PKPPRPASLL RHAPHCLSEE EGEQDRPGAP GPWDPLGVRS300
 RIERRWQEEE AEAERG 317

(2) INFORMATION ON SEQ ID NO. 471:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 123 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

SMPLVQLPSS FKLLSLLLLL PLATFFQSCC GRRGGPRARV PQVGFARPPP QRDSEARVSA 60
 ARQAGAASAG GGRQAGLAGR SGLSACAPQR GHRRRPHHLL LRTLTHLLQ LLLFLDRSRQ120
 FSL 123

(2) INFORMATION ON SEQ ID NO. 472:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 105 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

KIRSNQCLWS NFLPPSSSSL CFCFFLLPPS FNPAADAEGV PGPGCFRSVL LALLLRETVR 60
RVSQQRGRPG RLRRAEAGRL GWQGVLASPH ALLSEGIVVG HTIYC 105

(2) INFORMATION ON SEQ ID NO. 473:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 159 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

IVSERSLRSL WTAHWALPEM DSRIFYDDYP VVFLPAYENF PAWIPPHERV HHPDYNNELT 60
QFLPRTITLK KPFGAQLGFN IRGKASQLG IFISKVIPDS DAHRAGLQEG DQVLAVNDVDL20
FDIEHSKAV EILKTAREIS MRVRRFFPYNV HRQKERTVH 159

(2) INFORMATION ON SEQ ID NO. 474:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 75 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

PPTGRPPPEF FFFFFFFFIV FYFLGERLGG GRGENSVSLE SQKCMNLLVV QGWDKMAREV60
RWKIPKILFA TDFYN 75

(2) INFORMATION ON SEQ ID NO. 475:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

LGGLSSSDVK SQLSSRRLQ CDGSGQKLGQ LIVVVRVVYP LMRNPCWRI LIGRQENHRV60
 VIIRNPAVHL GQGPVGSPQR PQTPLTNSV WEPEADA 97

(2) INFORMATION ON SEQ ID NO. 476:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 274 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

GHLWRPAGGR LPRHHDQVCR AAEPHRGGGL CGHQRRLPHR PRVQEGWGLC PHESLHQVPA 60
 DREWHEPGAG CAADCEDPHR RFGACEPGAP PAARAAGLGR GTRHGNGDIL SFEDANRAMQ120
 TGVGTGIMAR GALLKPWLFT EIKEQRHWDI SSSERLDILR DFTNYGLEHW GSDTQGVKVT180
 RRFLEWLSF LCRYDPVGLL ERLPQRINER PPYYLGRDYL ETLMASQKRA DWIRISEMLL240
 GEVPPPTSPSC RSTRPTRTSS LRLSQGHFGA RRVQ 274

(2) INFORMATION ON SEQ ID NO. 477:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 256 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

AGPAPVQSGP HTRCRCPRGH GSRGRSQAGK LWCAPAGPRRP GTSTPSSSPV RTCGPLTDED 60
 VVRLRPECCK RLDIRGKLYL APLTTCGNLP FRRICKRFGA DVTCGEMAVC TNLLQGQMSE120
 WALLKRHQCE DIFGVQLEGA FPDMTKCAE LLSRTVEVDF VDINVGCPID LVYKKGGGCA180
 LMNRSTKFQQ IVRGMNQVLD VPLTVKIRTG VQERVNLAHR LPELRDWGV ALVTMGTSCT240
 HLRMPTAPCR LVSPGS 256

(2) INFORMATION ON SEQ ID NO. 478:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 165 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

NLLYSRPRPV PLGKPEATCT RWPCASARRR GGGHWPKEHL ADADPVGCLL AGHQRLQVVA 60
 AQVVGRLVD FLWEPLQQPH GIVPAQEGQP LEQKAPGLLH ALRVRAVQLQ AVVGEVPQDV120
 QALGRADVVP PLLLDLREEP RLEQGATGNH DPGDTS LHGA VGILK 165

(2) INFORMATION ON SEQ ID NO. 479:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 262 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

GSPMSPARAM QTLFVPEHGD HGAGVCSDDH HRGGHVPAEP LQAVCTVLHQ PAQPGAEERR 60
 CPVLRMPVA SETQCQATES QSRSLTPRLG PPTAWPCALR PAERFPPLPA QCLLHVQLQT120
 LFVPEHGDHG AGVCSDDHHR GGHVPAEPLQ AVCTVLHQPA QPGAEERRCP VLRRMPVALG180
 EHSVRQRNPR AAGLRPASAH RPPGRAALRP AGALPPLPAH LSVPAARDRP AAHHLAVRRG240
 GAPTLPGLD LQSGSPRGV GN 262

(2) INFORMATION ON SEQ ID NO. 480:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 270 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

AAQCLLVQC KRSLFQSMET TELEFVQIII IVVVTCLLSH YKLSARSFIS RBSQGERRED 60
 ALSSEGCLWP RRHSVRQRNP RAAVLRPASA HRPPGRAPFA QRSVFHRCQP NVSCTCNCKR120
 SLFQSMETIE LEFVQIIIV VVTCLLSHYK LSARSFISRH SQGRRREDAL SSEGCLWPSE180
 STVSGNGIPE PQVYAPPRPT ORLAVPFFAQ RERFHRFQPT YPVLQHEIDL PPTISLSDGE240
 EPPFYQGPWT FRVRDPEEL EIERGLGAET 270

(2) INFORMATION ON SEQ ID NO. 481:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 124 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

ATTSCCLHGPS SAGTARGGGE KMPCPKQDAC GPRAACQCAT ESQSRARSTPR LGPPTAWPCR 60
 PSPSGSASTA SSPPIRTCTST RSTCRPPSRC QTGRSPHETR APGSPRFGTP RRSWKLGNDW120
 VRRP 124

(2) INFORMATION ON SEQ ID NO. 482:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

RVLVSPLSL S MWRWKVEKDT VSILKLLRFS ERGRHLNRQV GFSVLSALGI WREMGLLSLC60
 TQEGHALKTV FVDQRRLYST GGIQMSLRGR EETWQADYI 99

(2) INFORMATION ON SEQ ID NO. 483:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 104 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

VLEEEKKHKGK QITSEPFELC FSFFPCLFESK IYLNLETQDI FLGNLLPMSE VASAASRQIP 60
 GNPEPQNVIP PGSAWDPVL SAGFTYQSHS SFSINTPKSS PNHH 104

(2) INFORMATION ON SEQ ID NO. 484:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

KLSTQCRPS LHTNMYVLLS ECHLLCTQCH DSKIKISVSN QNINQARNSW AQRGVRGLSY 60
TAVKQPTCSA HSQAESDWSC RQRGGGRVLC CPLLCMVSVV FQGGQLLSPN KTVNSLRTGP120
LPH 123

(2) INFORMATION ON SEQ ID NO. 485:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 303 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

LGRKP2SWVGG AGLEPSQSGS LSHHPAPQSD SAPTSPPIPG EPGPQREVDK WGGSLGRPES 60
SGHPGRTFAT CCHCAAVMAR SGSATPPARA PGAPPRSPPO RLVDQVSGPL RELRPRLCHL120
RKGPQGYGFN LHSKSRPGQ YIRSVDPGSP AARSGLRAQD RLIEVNGQNV EGLRHAEEVVA180
SIKAREDEAR LLVVDPETDE HFKRLRVTFP EEHVGEPLFS PVTNGTSPAQ LNGGSACSSR240
SDLPGSDKDT EDGSAWKQDP FQESGLHLSP TAAEAKKAR AMRVNKRAPQ MDWNRKREIF300
SNF 303

(2) INFORMATION ON SEQ ID NO. 486:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 149 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

APRRPRPRRR LEPCESTARS HRWTGTGSVK SSATSEPLPA CLGTLGPLEH GPWASACP 60
PQPQWTGGWS CHCFEISPSF GEPPSCPCFP GTGGLWQQR GRETQRCERE SETETEREREL20
RRERQRESE RARGSRGARA FAALPGPAD 149

(2) INFORMATION ON SEQ ID NO. 487:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 217 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

```

FLNGRRTTLQ STEAGGARGR LRPKVRAGGV PGSRDRQEGA QKLLKISRFL FQSICGARLL 60
TRMARAFSLA SAAVGLRWPR LSWKGSCEFQA LPSSVSLSEP GRSLRDEHAE PPLSWAGLVP120
LVTGDGRGPS TCSSVGVTRS RLKCSVSVGS TTSSRASSR ALMLATTSW RSPSTFCPFT180
SMRSRWARRP ERAAGEPGST ERMYPGGRDL SLCRLN?                               217

```

(2) INFORMATION ON SEQ ID NO. 488:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 298 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:

```

EIRAVGGGVC VDGMPGEG LGRCSHALIR GVPESLASGE GAGAGLPALD LAKAQREHGV 60
LGGKLRQRLG LQLELPPPEE SLPLGPLLGD TAVIQGDTAL ITRPWSFARR PEVDGVRKAL120
QDLGLRIVEI GDEATLDGT DVLFITGREFF VGLSKWTNHR GAEIVADTFR DFAVSTVPVS180
GPSHLRGLCG MGGPRTTVAG SSDAAQKAVR AMAVLTDHPY ASLTLPDDAA ADCFLRPLGL240
PGVPPFLLHR GGGDLPSNQE ALQKLSDVTL VVVSCESELEK AGAGLSSSLCL VLSTRPHS 298

```


(2) INFORMATION ON SEQ ID NO. 489:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 175 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:

```
AGHRYQGDIR ELLQCLLAVG QIPTSTVQEE RGHTRQPRTK KETVSSCVIW EGQGGIIVIC 60
QHCHCPDSSL GSVAACHNS ARSPHAAETA QVGGTRDWHG GDGEVPERVR HDLSSSVIGP120
FGEAYEKLP A GEENVSAIQR RVLVSYPHNS EPQVLQGFAD SIDLWPTSGA PGPRD 175
```

(2) INFORMATION ON SEQ ID NO. 490:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

```
LGPCPLGSRP CRQAAVPAAM TPQVAVLAAV APVVASVYLF APRAPFELWP DPEREGQPPH 60
LPPTPGSLGL PGSGHGSSGP APPPASPSHP HRLPLQLPLGF LSFLVSSPVS SGHPHSCRAV120
ISAGAPPPEO RVGEGGSPRL QASGTGSSGF 150
```

(2) INFORMATION ON SEQ ID NO. 491:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

FVKRTKQPRQ TLDAPCSALR LWGRCLLGEA VAQGVHCEAG PVDSAGGIHL ASGCLVSVYS60
DIAFCCHLSC GQRGVSWHEN IFFFKCGSF 89

(2) INFORMATION ON SEQ ID NO. 492:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

LTALLFEKCL LPSLGLITKF DHDHIVVSQS ALEIVSGLHE VAMGVWSTLK LYQSCITYFQT60
FLK 63

(2) INFORMATION ON SEQ ID NO. 493:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

DGSRMLCHYI QKQDNLKLNG CPLQSQQVQP HSARPELQPL PKGIFPTAST PSKEHQGFVS60
VVLFFLQITID IYS 73

(2) INFORMATION ON SEQ ID NO. 494:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 318 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:

KCATFWSFPR RQGGLGIAIS EEDTLGVII KSLTEHGVAA TGRLLKVGDO ILAVDDEIVV 60
 GYPIEKFISL LKTRKMTVKL TIHAENPDSQ AVPSAAGRAS GEKKNSSQSL MVPOSGSPEP120
 ESIRNTRSS TPAIFASDPA TCPPIPGCET TIEISKGRGT LGLSIVGSD TLLGAILIHE180
 VYEEGAACKD GRLWAGDQIL EVNGIDLKKA THDEAINVLR QTPQRVRLTL YRDEAPYKEE240
 EVCDTLTIEL QKKPGKGLGL SIVGKRNDTG VEVSDIVKGG IADADGRMLQ GDQILMVNGE300
 DVRNATQEA VAVIKVFP 318

(2) INFORMATION ON SEQ ID NO. 495:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 206 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

SAFAEMGSDH TQSSASKISQ DVDKEDEFGY SWKNIRERYG TLIGELHMIE LEKGHSGLGL 60
 SLAGNKDRSR MSVFIVGIDP NGAAGKDGR LQIADELLEIN GQILYGRSHQ NASSI IKCAP120
 SKVKIIFIRN KDAVNQMAVC PGNAVEPLPS NSENQNKET EPTVTTSDAA VDLSSFKNVQ180
 HSGAQGGGRG VVWLLSAKKI HSESS 206

(2) INFORMATION ON SEQ ID NO. 496:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:

TSWIIMAPSS VSEPTMLRP SPVRELEISM VVSQPGIMGQ VAGSEAKIAG VDOLLVFRMD 60
SGSGEPDCGT IRDWELFFFS PLAAPAAEGT AWESGFSAWM VSFTVIFAVF RRLINFSIG 119

(2) INFORMATION ON SEQ ID NO. 497:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

SAPSLIKCRS THVYPLSLIM FMSGSSRST LARMVPTST TSLSPRSSSS TSKLLTQSGP60
SLPQPPASRP F 71

(2) INFORMATION ON SEQ ID NO. 498:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 139 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

SRSPACGASE HGDGAMSLIC SISNEVPEHP CVSPVSNHVY ERRLIEKYIA ENGTDPINNQ 60
 PLSEEQIID I KVAHPIRPKP PSATSIPAIL KALQDEWDAV MLHSFTLRQS CRQPAKSCHT120
 LCTSTMPPAV SLPVSPRKL 139

(2) INFORMATION ON SEQ ID NO. 499:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

TTGRERGCRP CAGLFYCFLF LMKLDHCLQN PAQALLPIPF TVSLVRRAMT RQAASCWYRA60

CDSSWRVVC SGA E

74

(2) INFORMATION ON SEQ ID NO. 500:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

FSFFNETRSL LTKPCTSPPA HPLHSSLGSA SPVSQELQQN GCGTATTTSI ERQEGRGAVG60
 LVQGGFIVFF F

71

(2) INFORMATION ON SEQ ID NO. 501:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 284 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

EARGLATRTR SGAAAHAGDR FTDADDVAIL TVVKENARSP SSVTGNALWK AMEKSSLIQH 60
 SWQSLKDRYL KHLRGQEHKY LLGDAPVSPS SQKLKRKAE DPEAADSGEP QNKRTPOLPE120
 EEYVKEEIQE NEEAVKMLV EATREFEEVV VDESPPDFEI HITCDDDDPP TPEEDSETQP180
 DEEEEEEEEK VSQPEVGAAI KIIRQLMEKF NLDLSTVTQA FLKNSGELEA TSAFLASGQR240
 ADGYPIWSRQ DDIDLQKDE DTRREALVKKF GAQNVARRIE FRKK 284

(2) INFORMATION ON SEQ ID NO. 502:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 123 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

ETFSSSSSSS SSGCVSESSS GVGGSSSHIV ICISKSGGLS STTTSSNSRV ASTSIFLTAS 60
 SFSWISSFTY SSSGKSGVLL FCGSPLSAAS GSSSAFRLSF WEEGLTGASP SRYLCSWPRR120
 CLR. 123

(2) INFORMATION ON SEQ ID NO. 503:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 175 amino acids
 - (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

VFLRCGWIII THSYMFKIR RALIHNNLLK LPGGFHKHLF OCFFILLDFF LHILFFRQIW 60
SSLILWFPAI RGLRVLLRLP LELLGGGAHR RVPQQVLMML APQVLEVAVL QGLPRVLRER120
ALLHRFPQGV TGDGAGRAGI FLHVKGKGYV VRIREAIAIV RCRSAPRARR QAPGF 175

(2) INFORMATION ON SEQ ID NO. 504:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 78 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

CPPEKSLQMF QPLSSPDSHR KGTGFGLGIV FSLTFFKRRM WPLAFGSGMG LGMAYSNCQH60
DFQAPYLLHG KYVKEQE 78

(2) INFORMATION ON SEQ ID NO. 505:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 95 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

SKTSTLPVAI WTRQRLEHLQ GFLGWSITR ILSSRPHPD TGPTSCRAFT QTCSPPPA60
 FLSAGPRAPT PESLARAGNK SQVRKAGADA PDIAE 95

(2) INFORMATION ON SEQ ID NO. 506:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 156 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

AIPNPMPPEPK ANGHILLKK VSEKTIENPK PVPFLWLSGL DRGWNICRDF SGGHQLPGFY 60
 LHDRIQTPV PLPAELRLRH VPHPRQLQSS RPAPALRPLK VSRELETSR SGRQAQTLQI120
 SRDDPLLESL PVFSVGRQGD AVVWRLEVTI TLGCAY 156

(2) INFORMATION ON SEQ ID NO. 507:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 169 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

AASGMLGSWP ARTFHGACV SRRPSAPWKH TASGKDSPLD RFSEHGVSQE FWAGGLVAVL 60
 EMTSPSPWG TQEGPAGMCS LWVVGWCPGR GAGVROLVLV HAGVWCKHVC AVQRDACGES120
 RTPAPPKRG AVTSVCLFL IKTFPLFSYK FASCKQVHKD PPLVKSGFE 169

(2) INFORMATION ON SEQ ID NO. 508:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 155 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

TQNTGNRSF PGWRWCAALS TRVSLYSTYM FTPHTCVDEH QITHPSSTTG TPADYFQAAH 60
 SGRALLGAPR GGARGHLQHC HQAASPEFLG NTVLGKPKVR AVLPRGRVLP GCGGPAADTG120
 PRVEGPGRPA SKHARRSLGE PGSVASSLLS LRSPI 155

(2) INFORMATION ON SEQ ID NO. 509:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

ENRGNVLIKN KHKTLVTAPP FLGGAGVRLS PHASLCTAHT CLHHTPAWTS TRSRTPAFRQ 60
 GHQPTTHRLH IPAGPSWVPH GEGLGVISST ATRPPAQNSW ETPCSENRRS GLSFPEAVCF120
 QGAEGRRLTQ APGWKVLACQ LPSMPDAA 148

(2) INFORMATION ON SEQ ID NO. 510:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

NAYISGYERO FMTIQSNITL ADRETEVFHD LPSLPASLRQ NWIPTLVFFL PFTSFSLLYN60
VLRDQNSHQN RLFLR 75

(2) INFORMATION ON SEQ ID NO. 511:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 67 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

FRTEGLLLAL MTFWMLQLM TILILEERTL LIFSPIALLR RSTSYSESLH IPLVFLQAPE60
FLVQMLY 67

(2) INFORMATION ON SEQ ID NO. 512:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 101 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

IFFFFFFFFF PLRHLENNCR NPKELASNLE VVSEAAGWLD WAQPLSCLNR PRNGIMTMTR 60
TSILSSSHCV YYVFSFNKAF VPMALGLGGR LKECVVILSK M 101

(2) INFORMATION ON SEQ ID NO. 513:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 179 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

FGTMGGISDP DTLHIWKNS LPLRFWVNL KNPQFVFDID KTDHIDACLS VIAQAFIDAC 60
SISDLQLGKD SPTNKLKYAK EIPEYRKIVQ RYYKIQDMDT PLSEQEMNAH LAESRKYQNI20

EFNTNVMAAE IYKYAKRYRP QIMAALEANP TARRTQLQHK FEQVVALMED NIYECYSEA 179

(2) INFORMATION ON SEQ ID NO. 514:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 179 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

DRGAPALTPG HLHPLPPVPR SVSGMEAREL VRLPHLPSTA CTVPTHLLHN VOLVLLPRAP 60
CQAAKHKLK ERRPPARRLQ FRNSTSTLV QGALLELTFD WFLQLPKCY LHFPLTRRGS120
WPQTVSSSVR FLLGLRLLVE WAVPAPWGAL WASPGAGRVE GRDGGHRSWE ERLQEKERG 179

(2) INFORMATION ON SEQ ID NO. 515:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 200 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

SGDRWEGMEV PRGQGGGAPV SESSPSSCPR PSRLCSVTPS LSHRHGVEDQ VEAQWASISP 60
SSSLTNSPCV SGLTVALVDV VLHQSHLLK LVLQLCFFGR GVGLQRGHDL RPIPLGVLIN120
LCHGHIGVEL ILVFPRLGQ MGIHLLLAER RHVLDLLVVA LHDLPVLRNL LGVEELVGWR180
ILAQLQVRDG AGVDEGLRDD 200

(2) INFORMATION ON SEQ ID NO. 516:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 157 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

TSMEALLFRL FKLPATTLRC IGLRRPLVTH TLARKCEHKA SRLCHGGCCC TLEPCVGRHR 60
OWDLERKSS AKTGGLHGR RTAAARGGSE RPYLGHRRRD PDAGGLRGQD GEALQHRGW120
IPGSETLPGR GGHVPWPRPG RRPHPHMC GF WDSQSLA 157

(2) INFORMATION ON SEQ ID NO. 517:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 401 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

RTRCAGSVNT KPPGFVMAAA AARNHVVWG TETGILKGVN LQRKQANFT AGGQPRREEA 60
 VSALCWTGG ETQMLVGCAD RTVKHSTED GIFQGQRHCP GGEGMFRGLA QADGTLITCV120
 DSGILRVWHD KDKDTSSDPL LELRVGPGVC RMRQDPAHPH VVATGGKENA LKIWDLQGSSE180
 EPVFRANKVR NDWLDLRVPI WDQDIQFLPG SQKLVTCTGY HQVRVYDFAS PQRRFVLETT240
 YGEYPLTAMT LTPGGNSVIV GNTHGQLAEI DLKQGLLGC LKGLAGSVRG LQCHPSKPLL300
 ASCGLDRVLV IHRIQNPRGL EHKVYLSQL NCLLLSGRDN WEDEPQEPQE PNKVPLEDTE360
 TDELWASLEA AAKRKLGLLE QPQALQTRR RKKKRFGSTS P 401

(2) INFORMATION ON SEQ ID NO. 518:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 222 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

SWEKLYVLVP DGNPQVQVPI PHVLGPEHRF LRALQVPYLQ SILFPTCGNH MGVCNVLAHP 60
 THPRAHSQFQ ENVRGCVLVL VMPOSENPRI HTCDEGAVGL GEATERHALPA RAVSLTLEYAL20
 ILGAEVLHRP VRAAHQHLGL AAGAPTQGAH CLLAPRLSSG REVRRLFSLK IYFPQDPSLGI80
 ADPHMVPACS SSRHDKAWRL CVHTSGAACA SPAGVEVRCT AV 222

(2) INFORMATION ON SEQ ID NO. 519:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 86 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

DPRPVSLLTI ALLPRCHFLS SSVKYRLHLI SLNASTICVT PKDFWDFDET CEGEDTEKPV60
 ICKHLLLFPH HLWDISAVVS KWQIIN 86

(2) INFORMATION ON SEQ ID NO. 520:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

ISSVNYHMTI QAQYKLGHCI LCGWISVAVF LTSPKKRTSCR AELLVQAPDN DAPDFAFWGL60
 SLLLSRFLKL FAWPWHH 77

(2) INFORMATION ON SEQ ID NO. 521:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

CGNKSCKLQI TGFVSPPSQ VSSKSQKSLG VTQIVLALSD KMCSLYLTEE ERKWHLGSSA60
 RVSKETGLGS Q 71

(2) INFORMATION ON SEQ ID NO. 528:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 120 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

LTVLFFFFFF FTLESLGFT PSVGTLPSE APPSHGVGDS GPGNPSEWR GQWVSMYPA 60
LPHLFHGVEP QGQALICGEG SKQRRRPFRG GERAVAPRTP SPAHDIPKE TKIKPRGLST120

(2) INFORMATION ON SEQ ID NO. 529:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 90 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

PLLKGGKLSA ALTNLSFFFF FFFFFGKKPW LYSLCGDTVP FRGPSQPWGG GQWWAWESQR60
ASWRVRLHV FCSSPSFPWG PLPGSSTNMW 90

(2) INFORMATION ON SEQ ID NO. 530:

(i) SEQUENCE CHARACTERISTIC:
(A) LENGTH: 96 amino acids
(B) TYPE: Protein
(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

NKAPGPFYVG APLKYGMYVG REAVAQQSLS PDYQLWGGFQ GARSRLGSSS HRHVGGGRKY60
LQGGTVSEEQ DGRGFSACYG ILFKEMGVKP GTVAHA 96

(2) INFORMATION ON SEQ ID NO. 531:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 497 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

TPALVQRFRE GGSGAPEQAE CVELLLALGE PAELCEEFL AHARGLEKE LRNLEAELGP 60
 SPPAPDVLEF TDHGGSGFVG GLCQVAAAYQ ELFAAQGPAG AEKLAARFQ LGSRYFALVE120
 RRLAQEQGGG DNSLLVRALD RFHRLRAPG ALLAAAGLAD AATEIVERVA RERLGHHLQG180
 LRAAFLGCLT DVRQALAAFR VAGKEGPGLA ELLANVASSI LSHIKASLAA VHLFTAQEV240
 FSNKPYERGE FCSQGVREGL IVGFVHSMCQ TAQSFCDSPG EKGGA TPAL LLLSRLCLD300
 YETATISYIL TLTDEQFLVQ DQFPVTFVST LCAEARETAR RLLTHYVKVQ GLVISQMLRK360
 SVETRDWLST LEPRNVRAVM KRVEDTTAI DVQVGLLYEE GVRKAQSSDS SKRTFSVYSS420
 SRQQGRYAPS YTPSAFMDTN LLSNIQKLF5 ERIDVFSPVE FNKVSULTGI IKISLKTLAG480
 SVCGLRTFLA LCGLQQG 497

(2) INFORMATION ON SEQ ID NO. 532:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 153 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

CGSGWSWPHW PATRPGQGPP SQPREVLPAQ GGRLSGSPGR PPGDPAGGSP GARGPLVPRS 60
 PWQLRARQR PAGRPEPASA GSGGPAPAPA VSCHHHAPAPA PAAAPPAQNS GCFAAGRPP120
 ASRHLLGPGP QTAFGRPFPF GRGRPRSHCL HGR 153

(2) INFORMATION ON SEQ ID NO. 533:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 221 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

YDQALHLHVV GQPPPRRFFG LCTORAHGRH WELILHQKLF ISESEDVGDG GRLVVQAEAG 60
 EQQEQGRWCG TPLLPRVAE ALSRLAHRVD EAHDEALTDT LTAELTPEVG LVGEGHLFGG120
 EKVHCCQRLG NVAQDGAGHI GQQLGQARAL LPSHARCCQR LADVCQAAQE GRPETLQVVA180
 QALAGHSFHD LRGSVCEPGS GQQGPGSPQA PVEAVQRPHQ Q 221

(2) INFORMATION ON SEQ ID NO. 534:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 52 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

PSILIPMTPG GFFSVMVRK TGSTHRCSPA VYPLMRRI PC WRILIGRQET TG

52

(2) INFORMATION ON SEQ ID NO. 535:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 38 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

AGKKPPASHH KESGCPSRPS PTGHSTPPSD PLTDNSVW

38

(2) INFORMATION ON SEQ ID NO. 536:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

SGCVPSHEED SMLEDHRQA RNRRLVIIRN FVVHLGQAPL ATPHRPQIRS LTIQS

55

(2) INFORMATION ON SEQ ID NO. 537:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 113 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

TRGPRKRLRR SGRGGLRSW AGRERVLGTA LLGIYIVFPR IPGSGSEEAV TPYDRDLDS 60
RNSPQAPAGQ STTSSSFCC DGLSRGLKH TVSIDCIRFV QKPGQLTESH FLA 113

(2) INFORMATION ON SEQ ID NO. 538:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

EPADSQARGR QCLLLHQVQ GIWLKACIFF GHKLPEPLKW EARQFQTNLF STHRSTFKVC 60
 LLLLPVHPFS LQFFHSLTSE RVFGGSMVNK LTCMLQKKKK K 101

(2) INFORMATION ON SEQ ID NO. 539:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 198 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

YSLCSQCQVSA PLTLNRHRSR RKRKWWIAQL EPGDCYDCLO LCGHRASQPP QTLSLECGGT 60
 QCRFPGLSP RPSPCPPSSS GLLFYRFFLV SFLGLLFTG TAALGFLVTS ALLGSDGSAS120
 ASWDLGMGTM MASTQMSWKM APRKSPYRSR FSRKVGSGTS GGEKSRSEAM AQVACCLTSL180
 LTHHSLEPTP APPRRSPR 198

(2) INFORMATION ON SEQ ID NO. 540:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 147 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

KKNSSALIFL EEAADFQCQI SLRNGHFLRC FFLTESVDKL IKRLSHFKIT PKSSSTVFFF 60
 FSFCFKITNQ VRSPITSSSMN SFVTELLSVC SPHCALNTVS AAPVGPLFRK ESIFNTFTTIC120
 TPNWNLHMLTS YYKPTHPLQS SGTGHP 147

(2) INFORMATION ON SEQ ID NO. 541:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

KNDRFFWTSI PGLKGALIKL FTEHVAEKHI YGLMPLLEA QSTFFQVTPS TMANIVKGLY 60
 TLRPEWVQMA PTLFSKFIPN ILPPAVESEL SEYAAQQKF QRELIQNGFT RGDQSRKRAG120
 DELAYNSSSA CASSRGYR 138

(2) INFORMATION ON SEQ ID NO. 542:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 179 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:

KACIPSDQSG FRWLQLYFLN LFQTFSLRRW NLNFLNMLLK IRNFKENLYR MVLQGVTSFG 60
 RELGMSWLIY ARQHVVQVPGG TDSECIYAF LPEKRTHWSC RDCIQSTVGA AHTQELCHKAL20
 VGRGCGWIS: LVCNFKTKTA KKKNSAARLS GDFEWGQSF. SFIIRGCEER ASQAVTISA 170

(2) INFORMATION ON SEQ ID NO. 543:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 92 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:

IQFLEAAFAV FLHCMRFEGNE CRNLLWAFTF LCQFGFYCLN LMLTWRGDGS QCCCGASSES60
 VCGELCCADV AVGGQVRGSA PSWKKSCLRV YV 92

(2) INFORMATION ON SEQ ID NO. 544:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 99 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

KPNWHRKVNA HSKFLHSFPN RIQCKKTAKA ASRNCIYWPL PEQQAAMPAP WPFELDACCA60
 DVLTLMRMLG YGSDSEEIHL SYSSLERSSC VFNMKHFIW 99

(2) INFORMATION ON SEQ ID NO. 545:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 96 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

QSQNTKVFVP IRIYTDPLTK VLLIMQFASS PSSWLGSSEPI WHDRIKRTPS DMISSKKVPS60
 LLPDQQRPHQ HNTTLRIQIH CWFHNSTVPH LLSRSA

96

(2) INFORMATION ON SEQ ID NO. 546:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 108 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

GRDAGQSEPW LSTSGCCAWG GCAPGARGCW GPGPPSLGVG RKPGCVRVSAS SVPERWIAWS 60
 PRPSEASATF RGAPKSILTA RLWASAWRPQ HRGSQNERPW SSSMKTSG

108

(2) INFORMATION ON SEQ ID NO. 547:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 117 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

PGRRAKRAMA VYVGMRLRGR LCAGSSGVLG ARAALSRWQ EARLQGVRF SSREVDMMVS 60
 TPIGGLSYVQ GCTKKHLNSK TVGQCLETTA QRVPEREALV VLHEDVRLTF AQLKEEW 117

(2) INFORMATION ON SEQ ID NO. 548:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 117 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:

PLLLELGKGQ PDVFMEDDQG LSFWDPLCCG LQALAHSLAV KMLFGAPLNV AEASDGRGDH 60
 AIHLSGTEEA DTLQPGFLPT PREGGPGPQH PRAPGAQPPQ AQHPOVDSHG SLCPASR 117

(2) INFORMATION ON SEQ ID NO. 549:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 68 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

RLSGPAANPR GAAGWRAAGA QELGMSYKPM RPWLPSSTPW SARHPLGPGA PRFPDREACA60
 CAVRGCSV 68

(2) INFORMATION ON SEQ ID NO. 550:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

GHCSPARRTR TPQCQTGTV RAPGGAWQTR GCCWAARGAW VCRTSPTPGR QRHASRPLL60
 GWLRGRSA 68

(2) INFORMATION ON SEQ ID NO. 551:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

DTAAPHGARA RLPVREPGCP GPQGVPRPG GAAGQPGAHG FVGHPLLGA SGTPAGRSSG60
 VGCGAAQP 68

(2) INFORMATION ON SEQ ID NO. 552:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 32 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

SPISITETQQ FSNLIHTIT CLLRMALYLF SL

32

(2) INFORMATION ON SEQ ID NO. 553:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 33 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

ITLQPISQNM FLLNNTQLF YLCVLFMPDH QYQ

33

(2) INFORMATION ON SEQ ID NO. 554:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

SFYFGWSHYN ENKYNAILNR QVMVCIKLLL NCCVSVIDIG DQA

43

(2) INFORMATION ON SEQ ID NO. 555:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

CFTHWNVFPRLWMTSFLMERVQEGWKTGPKLSIPHMGFSIIFRPEAARPEVRLHLSALF60
 VLLLATLGLFLGTMCGCGMC EQKGG85

(2) INFORMATION ON SEQ ID NO. 556:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

FNDGKTWQLK KTLVTNGGFL LFFPHPPFCS HMPQPHMVPS RNPKVARSST KRADKCRRTS 60
 GRAASGLKMI EKPMWGM LSL NPGVFHPSWT LSIRKEVIHN RGKTFQ106

(2) INFORMATION ON SEQ ID NO. 557:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 109 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

NINYIEIIFL FLLISPLGPF HRLSPAQLAQ LAQLAHSPQV SRRHRALTMV GWHGVSNNAN 60
SSHHPHPHSP SQRPLVVGPA VFQKGLTCTN LRQTYAPFSV SLASPSWED 109

(2) INFORMATION ON SEQ ID NO. 558:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 50 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

LGIFVAYRNQ LGVPSLMRCS WKAIYARGGF TFVA??PFD? SAFKKLECN

50

(2) INFORMATION ON SEQ ID NO. 559:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 44 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

FRLPFLTWHF CSLQEPAWCT FSYEMQLESH LCKRWFHFCR SSIH

44

(2) INFORMATION ON SEQ ID NO. 560:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 45 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

RVNEWRSDKS ETTSCINGFP AASHKRRYTK LVPVSYKNAK LRMGV

45

(2) INFORMATION ON SEQ ID NO. 561:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 34 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

MRSRLPCEGL VARHPRELRV PSVRFWIDWP WVLTV

34

(2) INFORMATION ON SEQ ID NO. 562:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

VSTHGQSIQK RTEGTRSSRG CRATSPSHGN RLLIQESFPQ NPPRARFQGH PLGRQSRQQP60
FTEAMSQ 67

(2) INFORMATION ON SEQ ID NO. 563:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 50 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

APMASQSRSA LRARVAHAGA VPPALHTAID SSFRNHFLKT HQGLGSKGTR 50

(2) INFORMATION ON SEQ ID NO. 564:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 54 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

YSIIIFEQFFK CKSVSYSECV SEVIKDISQR YWPISLCNQR NSVSRLLLCV ICGS 54

(2) INFORMATION ON SEQ ID NO. 565:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 57 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

CTMVNVNDNTV SFLSSFLNVN LYLTQSVCLK LLRTFPNVTG PFPFVIRGIL EQDYCCV . 57

(2) INFORMATION ON SEQ ID NO. 566:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 49 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

EKCQPMSLIL LWPFFILIK SHRSHTTIIL KQNSSDYKKG WASNVGKCP

49

(2) INFORMATION ON SEQ ID NO. 567:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

GEGRVNPNPEG SKSRHWPDHP APWAPSPPQE QLFSPSQTS SIFTMTTFRE VSQASSRCPT60
IPSGGKRQEN SPRVPVMLLS PSQFRLSRTS YLQP 94

(2) INFORMATION ON SEQ ID NO. 568:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 89 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

GLTLKKGTFF RGPEIQADPN LTPCSRTOAH RPLNSNPTSP PPPPTPDLFI SWNAFQDWKS60
PQGSSEPILS PARISSMHPG HAFHISRNK 89

(2) INFORMATION ON SEQ ID NO. 569:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 89 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

DVLDLNLNWDG ESSMTGTAGE FSCLEPPEGI VGHLELAWET SLKVIVIKIE LVWEGMENS60
SCLGLGAQGA GWSGQCQLDLL PSGFHTRPS 89

(2) INFORMATION ON SEQ ID NO. 570:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

KSIASVIGY FHDFKWFYEE TESSDDVEVL TLKKFKGDLA YRRQEYQVEF NIWCLKWALV60
LSVMAYVNNNS VPS 73

(2) INFORMATION ON SEQ ID NO. 571:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 40 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

SADSQEIQRRL PGLQTTTRVSG RIQHMVLEVG SCFISYGICK

40

(2) INFORMATION ON SEQ ID NO. 572:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 60 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

NKSPLQAPYV EYLLILLSSV GQVSFEFLES QHFNITATC FFIKPLEIMK IAYYRVSYAF60

(2) INFORMATION ON SEQ ID NO. 573:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 318 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

GNLSLES LCN LYNWRYKNLG NLPHVQLLPE FSTANAGLLY DFQLINVEDF QGVGESEPNP 60
YFYQNLGEAE YVVALFMYMC LLGYPADKIS ILTTYNGQKH LIRDIINRRC GNNPLIGRPN120
KVTIVDRFQG QONDYILLSL VRTRAVGHLR DVERLVVAMS RARLGLYIFA RVSLFQNCFE180
LTPAFSOLTA RPLHLHIPT EPPFTTRKNG ERPSHEVQII KNMPQMANFV YNMYMHLIQT240
THHYHQTLLQ LPPAMVEEGE EVQNQETELE TEEEMTVQA DIIPSPTDTS CRQETPAFER300
ESRPGGEGAI ALGGLGCF 318

(2) INFORMATION ON SEQ ID NO. 574:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 67 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

KTPKPPQRNC PFPTGAALTL KGWSFLTAAG VCWTGYDVS LNSHGLFFCFQ LCFLLNFLT60
LFYHSRW 67

(2) INFORMATION ON SEQ ID NO. 575:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 155 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

SLMIMMCSLY QMHVVVYKV CHLGHIFYYL YFMRWSLSIL SSSWERFCWN YMQMGASCE 60
LTESWSQFET VLEEGYSGED IKSKSGSRHG HYQATDIPQM AHCPGSYQRK KNIVILLTLK120
SINSCHLWVS SNQWIVSTSS IDDVANKMLL AIICC 155

(2) INFORMATION ON SEQ ID NO. 576:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 57 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

DHLGFISTKM RTNHGVRKGS LEEHKNLKL GGYHYIISYF HRSDLAKLCI LSLLTFI 57

(2) INFORMATION ON SEQ ID NO. 577:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 48 amino acids
- (B) TYPE: Protein

- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

CSF CCILCKKTAN RGKRTLQIKT ILVSFPQR

48

(2) INFORMATION ON SEQ ID NO. 578:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 48 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

LYFFKTLKEK CVLFAASFVR RLPTEEGLY KLRPSWFHFH KDENKSWC

48

(2) INFORMATION ON SEQ ID NO. 579:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 48 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

GSFPNTMICS HLCGNETHMV LICKVLFPLL AVFLQRMQQK EHIFLSKF

48

(2) INFORMATION ON SEQ ID NO. 580:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 48 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

HCRIQLGLSP LVGREKTTQV MRNFYSFQEL EEQLLIKFA LVTKYFYS

48

(2) INFORMATION ON SEQ ID NO. 581:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 59 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

IMPRAPLYRI PLNCNYVLLK SQLVKEELMV SVFVGNTCNT AEFYKGFLLW WAGKKPLKS 59

(2) INFORMATION ON SEQ ID NO. 582:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

GTLRPRSSDV LPIYLCFTTC LSLTPNIFT YFSNSACHKF AASP

44

(2) INFORMATION ON SEQ ID NO. 583:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 46 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

NVDSQTHSL ALIPPLLSSS DIVNNDKQLL CTCFFMCCS HFIHMY

46

(2) INFORMATION ON SEQ ID NO. 584:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

LYMCIKCEQH IKKHSVHSSC LSLTISLLE RRGIRARLC V

41

(2) INFORMATION ON SEQ ID NO. 588:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

GKPLVLHATP LSRCPPLPLP TRSLILRPSL HSDPSFHHY LQRCSSYAPV YRGCPMTVP 60
 SQSNYSSEGP VVLSRAPLPR RGRPFQALPG WNWCRSLGC IVRPGVGVA LL 112

(2) INFORMATION ON SEQ ID NO. 589:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 76 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

GRSREAPAGW PKSTKPPSAR ENWFSPHPL SPGALCLFTP QEALSYVLLS IYRTPVSI160
 SRDVAIMRPS TGGARR 76

(2) INFORMATION ON SEQ ID NO. 590:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 97 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

AGLDQKEELR GVRQHQQGV RYTRGSSDTS SSPEGLGMAC HAGAMERVKA KPWDFKSNLT60
AKAPSSSGTP CRRAHNSYIS GDSGDNWGPI DGEKDVG 97

(2) INFORMATION ON SEQ ID NO. 591:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 63 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

NGARLTSQFQ LYQRNHFIQI SQHFQRNTNV YGRVNIRSEN PLEEISVSMF IISAFRGLPV60
WAK 63

(2) INFORMATION ON SEQ ID NO. 592:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 50 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

NGSFGTVGAV MSTWLHKNP YEIFTVKFNY TCVTADFGGR QGLGLFFYLS

50

(2) INFORMATION ON SEQ ID NO. 593:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 55 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

AYLFIFLKGK NTFTSSSSPE AQTLLYLTTT QLTPLCDHQG GVVRLKDDSG HMTSL

55

(2) INFORMATION ON SEQ ID NO. 594:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

- (iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

SGDVCTESHG GLSRVKEKEQ QELSLGRWRR GGIDQARWFP W

41

(2) INFORMATION ON SEQ ID NO. 595:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 47 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

FKVGLWKGDI VEGEAVLYT YKWTPTFING GQRSSDQVTV VQKVTVA

47

(2) INFORMATION ON SEQ ID NO. 596:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 44 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

SVLTTSQRLS SHFKSQIPTR AKVLLDLFHP FSTSLSTLA APSP

44

(2) INFORMATION ON SEQ ID NO. 597:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1651 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual
ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

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GAGCTGCCAA GCAGCCCACC TCCTGGGCTT CCCGAAGTGG CCCAGATGTC AACCTCCACT 60
GGCCTCCCTG ATACCCCCCG AGCTCCAGAA ACCAGGACCA ACTACCCAGT GGAGTGCACC 120
GAGGGGCTG CAGGCCCCCA GTCTCTCCCC TTGCCTATTG TGGAGCCGGT CAAAAACCCC 180
TGCTCTGTCA AAGACCAGAC GCCACTCCAA CTTTCTGTAG AAGATACCAC CTCTCCAAAT 240
ACCAAGCCGT GCCCACTTAC TCCCACCACC CCAGAAACAT GGGGGGGGGG GGGGGGGGGG 300
GCGCCGTCAT CTACTCCTTG TTCAGCTCAC CTGACCCCTT CCTCCCTGTT CCCTTCTCTC 360
CTGGAATCAT CATCGGAACA GAAATTCTAT AACTTTGTGA TCCTCCAGC CAGGGCAGAC 420
GAACACATCG CCCTGGGGGT TCGGGAGAAG CTGGAGGCCC TTGGCGTGCC CGACGGGGCC 480
ACCTTCTGCG AGGATTTCCA GGTGCGGGG CGCGGGGAGC TGAGCTGCCT GCAGGAGCGC 540
ATAGACCACT CAGCTTTCAT CATCCTACTT CTCACCTCCA ACTTCGACTG TCGCCTGAGC 600
CTGCACCAGG TGRACCAAGC CATGATGAGC AACCTCAGC GACAGGGGTC GCCAGACTGT 660
GTCATCCCTT TCCTGCCCCT GGAGAGCTCC CCGCCCCAGC TCAGCTCCGA CACGGCCAGC 720
CTGCTCTCCG GGCTGGTGCG GCTGGACGAA CACTCCCAGA TCTTCGCCAG GAAGGTGGCC 780
AACACCTTCA AGCCCCACAG GCTTCAGGCC CGAAAGGCCA TGTGGAGGAA GGAACAGGAC 840
ACCCGAGCCC TGGGGGAACA GAGCCAGCAC CTGGACGGTG AGCGGATGCA GCGCGCGCA 900
CTGAACGCGC CCTACTCAGC CTACCTCCAG AGCTACTTGT CCTACAGGC ACAGATGGAG 960
CAGCTCCAGG TGGCTTTTGG GAGCCACATG TCATTGGGA CTGGGGGCCC CTATGGGGTC 1020
AGAATGCCCT TTGGGGGCCA GGGGCCCCGT GGAGCCCCGC CACCCTTTTC CACTTGGCCG 1080
GGGTGCCCGC AGCCGCCACC CCTGCACGCA TGGCAGGCTG GCACCCCCCC ACCGCCCTCC 1140
CCACAGCCGC CAGCCTTTCC ACAGTCACTG CCTTCCCGC AGTCCCCAGC CTTCCCTACG 1200
GCCTCACCGC CACCCCTTCA GAGCCGAGGG CTGCAACCCC TCATTATCCA CCACGCACAG 1260
ATGTTACAGC TGGGGGTGAA CAACCACATG TGAACACAGA GAGGGTCCCA GGGCGCCGAG 1320
GACAAGACGC AGGAGGCAGA ATGACCGCGT GTCCTTGCCT GACCACCTGG GGAACACCCC 1380
TGGACCCAGG CTACGGCCAG GACCCCATAG AGCACCCCGG TCTGCCCTGT GCCTGTGGAL 1440
CAGTGGAAGA TAGGTCATC TGCCACTTTC AGGACATTGT CGGGGAGCCC TTCATTATTAG 1500
ACAAACGGGG CGCGATGATG CCTTGGCTTT CAGGCTGGTC AGAACTGGAT ACGGTGTTTA 1560
CAATTCCAAT CTCTCTATT CTGGGTGAAG GGTCTTGGTG GTGGGGGTAT TGCTACGGTC 1620
TTTTAATTAT AATAAATATT TATTGAATGC T

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1651

(2) INFORMATION ON SEQ ID NO. 598:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 3304 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

AAACCTCTT	GGCTGTCTGC	TGTCCAGGGA	GTCCGCACTC	CCTTCATTAT	AGCCTTGCTC	60
AGAGTGCAGC	GGCAGGCTTG	GGGATGGCCT	CGGAGAGGGG	ACCACAGAGC	ACCAGCTGCT	120
ATGGAACTTC	CTTCCTCACT	CAGCTTCCCA	CGTTGCCAGC	TGGGACAGGG	GAGATGGAGT	180
AATTTTGGT	TGGAAAGACT	TCACGCTTGG	CCGAATGAAA	GTCCCGCGCTG	TCTGTACAGC	240
TGATGCCCCG	GCAGCTGTCT	GAGCACCCTG	AATGGAATGA	GTCTATGCAC	TGCTTCCGGA	300
TCAGTGTGGG	GGGCTTCTCT	GTGCTGGCGT	CCATGACCAA	GGCCCGCGAG	CCCCGCTTCC	360
GCCCCCGCTG	GAAGGTGATC	CTGACGTCTT	TTGTGGGTGC	TGCCATCCTC	TGGCTGCTCT	420
GCTCCACACG	CCGGGCCCCC	GGCAGGCCCC	CCACCCACAA	TGCACACAA	TGGAGGCTCG	480
GCCAGGCGCC	CGCCAACTGG	TACAATGACA	CCTACCCCTT	GTCTCCCCCA	CAAAGGACAC	540
CGGCTGGGAT	TCCGTATCGA	ATCGCAGTTA	TGCGAGACCT	GGACACAGAG	CCAAACGCCC	600
AAGACGAAAC	CACCTGGCGA	AGCGACCTGA	AAAAGGGGCTA	CCTGACCTTG	TCAGACAGCT	660
GGGACAAAGT	GGCCGTGGAA	TGGGACAAAG	ACCATTGGGGT	CCTGGAGTCC	CACCTGGCGG	720
AGAAGGGGAG	AGGCACTGGG	CTATCCGACC	TGATTGTTTT	CAATGGGAAA	CTCTACTCGG	780
TGGATGACCG	GACGGGGGCT	GTCTACCCAG	TGGAAGGCAG	CAAAGCCGCT	CCCTGGGTGA	840
TTCTGTCCGA	CGGCGACGCG	ACCGTGGAGA	AAGGCTTCAG	GGCCGAATGG	GTGGCAGTGA	900
AGGACGAGCG	TCTGTACGTG	GGCGGCTCTG	GCAAGGAGTG	GACGACCACT	ACGGGTGATG	960
TGGTGAACAG	GAACCCGGAG	TGGGTGAAGG	TGGTGGGCTA	CAAGGGCAGC	GTGGACCCAG	1020
AGAACTGGGT	GTCCAACTAC	AACGCCCTCG	GGGCTGCTGC	CGGCATCCAG	CGCGAGCTAT	1080
ACCTCATACA	TGAGTCTGCC	TGCTGGAGTG	ACACGCTGCA	CGCTGTGTTT	TTCTCTGCCG	1140
GCCGCGCCAG	CCGAGAGCGC	TACAGCGAGA	AGGACGACGA	CGCAAGGGC	GCCAACTCGC	1200
TGCTGAGCGC	CTCCCTGATC	TTCCGGCACA	TGCGTGTGAG	CCGCTGCGG	GCGGTGGTCT	1260
CCACTCACGG	CTTCTCGTCC	TTCAAGTTCA	TCCCCAACAC	CGAGGACGAC	ATCATTTGGG	1320
CCCTCAAACT	CGAGGAGGAC	AGCGGCGAGG	TGCGCTCCTA	CATCATGGCC	TTCAAGCTGG	1380
ACGGGGCGCT	CTGTGTTCCG	GAGACCAAGA	TCGGAAGCGT	GAARATCGAA	GGCACTCGAG	1440
TCATTTAACT	CAAAACGGAA	ACACTGAGCA	AGGCCATCAG	GACTCAGCTT	TTATAAAAAA	1500
AAGAGGAGTG	CACTTTTGTT	TTGTTTTGTT	CTTTTTGAAA	GTGCGCTCTG	GTGGAGGTTG	1560
TGACAGGAGA	GCCCCATCCC	GGGCCCCATA	GTGGTGCGGG	CAGTGGACCC	CGCGGCCCAT	1620
CGAGGCCCGC	GGTCTGAAGT	GCTTTCCATG	TGCTCATCTG	TGGGTGATTA	CCGTCGCTCT	1680
AGGCATTGAG	TCAAGGCTTG	CCTAACTGGC	TGGGTGCTTT	CTTCCATCTG	ACCTCGTTTC	1740
TTTTCTTTCC	TATGTTCTTT	TGTTCACTGA	ATATCCCTAG	AGCTCTCTAC	ATATGTCAGG	1800
CCCTATGCTC	CACCTGAGGA	ACGCACTGAG	CATGAGGTGG	ACCTGTTTGC	TGGGAACCCC	1860
AGGTCAACCC	CTTTTCTTCC	CAAACCTGGT	GCCTTGAAGG	AATCAGGTCC	AGGCCGTGA	1920
ATCCTTGGGG	AAGAAAAATG	TTATGTTGCA	GGGTATTGCA	TGGTCACGAG	TAGGGGGCAG	1980
GCCCCGTGGG	GACACATCTG	CCCACAGCTG	CACAGGCCAG	GGGCACAGCG	ACATCTGCTG	2040
GGTTCAGGCG	CTCAGATAAA	ACCATCTCCG	CATCATATGG	CCAGTGACCG	CTTTCTCGCT	2100
TCAAGAAAAA	TCGTGGGCTG	TGCAGTACTT	TGAAGTTTTA	ATTATTAACC	TGCTTTAAAT	2160
AAAGACGTTT	CTTTCTTAT	AAAGTGGAA	ATCACACAG	AGCACAGCTC	GGGAGCTGCT	2220
TGTAGTTACC	CAGCCGCTCG	CAGCAGTGCG	GGAGATGTTA	AGGAAGCGGT	GGCGGCTGGT	2280
GAAGCAGTGT	TCACATGTCT	GCGTCTCTGG	CCAAATGGATA	CAAGATATAA	AAAAATGTGT	2340
CCTTTTTCTA	GGAACTGTCA	GAATCTCTCA	TGCTTTTCAA	GACTTCTGTG	AATGACTTGA	2400
ATTTTTTTAT	CCCTGGCTAG	GGTCTGTGAA	CGAGGCGTGT	CTCTTCCCTG	GGGTTTCTTT	2460
CCATGGCCTT	TATTTCTCCT	CTTCCAGTGG	GAGTTTTGCA	GGCTTCTCTC	TGTGGAACCT	2520
TCACGAGCGT	TGGCTGGGCG	TCGGCTTCGC	TGGAGTGTAC	TCCAGGGTGA	AGGCAGAGCT	2580
GGATTTTGAGA	CCGAGGCTAG	GCACGACCCA	GGCTGAGAAG	GGACGTTTCC	ATCATTCACA	2640
TGCGCCTCCC	CACAGCAACT	ACCTCACCCC	GACCCCCACC	CTCACTCCTA	CCCCCCCCCG	2700
CGATGCTCAG	GGGTGCCACG	TGGGGCCGGA	GGGTGCCGCG	TCTGGCTGTC	CCTGTCGCGG	2760
TCCTCACAAA	ACCTCTCCCC	CTTTGAAACT	CAAGCACAGC	TGCGAGGAGG	GCAGCGAGGA	2820
GGGAGCCCTT	TTCTCATGTT	GTCTCTTTCC	CCCGCTATGT	CATAGGTAGT	GGAGGAAGCG	2880
AAGGAAGTGA	ACGCTGAATG	TGACGCATTT	CTGAAGAGCT	CAGCTGTGCA	CGGGCAGTCA	2940
CTGGAAGCCC	CAAGTCTGTT	CTGACTTTTG	CTTGAGCTCT	CTTGACCCG	CCCTCTAGAT	3000
CATTGTCTCT	GATGTCCAGG	CTGGGTCTAT	TAAATAGAG	ATGCATTCAG	GAAGGTTGGG	3060
GGACTTGGGA	CTGTGGCTGA	ATTGAGACCT	TGCTGATGTA	TTCAATGTGAG	CACCTGAGTC	3120
ACAGCCGAGG	TGCCCCGSAAG	CAGCCTCTTC	GCATAGGCAG	TGATTTGCGA	TTACTTTAAA	3180
CTCACCCTTT	TTTTCTTCCC	TTCTGTGTGG	CTGTGTGTCAG	CATAATGATT	GTGTTTCTCT	3240
CCTATGGGAT	CCATCTGTTT	TGTAACCAAT	AAAGCGTCTG	AGGGAGTGTA	AAAAACAGAT	3300
GGAT						3304

(2) INFORMATION ON SEQ ID NO. 599:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 878 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

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GCGGCCGCGC CAGTCTCGCT TCATGACGCA GCGGGTGACC TTGCAGCAGA TCCAGGAGGT 60
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CCTGGAGTGC CTGCCCGGCA GCACGCAGAG CCTGTGCTGT CAGCGGGAGC AGCTCAGCAG180
CTGCAAACTG AGGAACAGCC TGGACTCCAG CGACTCCGAC TCGGCCCTGT AAGGGGGGCC240
GCCCGCGGGG GGGAGCGCGG CTTCCGCGGT CCGCGCGGGG ACCGGCGTGT GAACCCCGAG300
AGTGCCCGCG CCTGTCTCCC GGGGGACCCG CAAGGACCCG GGACCGCGCG TCCTCGCGCG360
CTCGGACTCC CGCCCCGCTG CGAACCAGTC GGTGCGCCCC TCGCCGCGCT CGCCCTGGCC420
CGGGAGCGCC GGGAGCGGGG CCGCTTTCCT CGTCCTTGTA AATGTTTATT TTTTAACTCT480
TCCCAGTCCG AACTCTGCTG TGAGTGTGTG CGGGGAGGCG CGCCCGCGCT GAGTCGGCGG540
CGGGTAGCCA CTCCATGCCC TTGTCCGATG GTTTGCAACT CCGATTTTGC ACACCGCTCC600
ACCGTGCCCC CCAGCGCACA CCCATTACA CTCACGCCAA CACTCTCGCT GAACACTTTT660
ATAATTGTTA GCGTGGCGG TTGGGACTTT GGGCGCAGCG CGGCTGCTAC TGCCTCTGGA720
GGATTGATAT TTATTTTTCG ATTGCCATGG CTGAAGGCAT TTATTTAACG ATCTTTTAC780
CTGGATATGT CTGTGAGGCT CCTGAAGGA GACAAATAAA GTCAATATAT TTGCACAGT840
CAAAAAAAAA AAAGAAAGAA AAGAGAAGGT TCGAGAAA

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878

(2) INFORMATION ON SEQ ID NO. 600:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2760 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

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CACCCAACTT GTGTGTGTGC CGCCCGGGCC TTNCCTCCAC AGNTCTNCTT NCTNCCGGCC 60
GGCACTTCTG TGAGCCCTTT NTTAGTTTAC AGGCACGGNT GGGGCCGGTC TGTGCTGGCG 120
NCTGCTGGCC ACTGAGGGGAC AGGGACACGT GCCACCTGCT CATCTCTGCC CTGAGGTCAC 180
CCCGTGTGGC CTCACAGTGC CCATCTCTCT CGAGTGGCCT CTCTGGCTGT GCAGCCCGCC 240
CACCCACAGC CTCACCCCTC CTGCGGGCTG CCAGAGGCCC CCTCCAGCAG GGCCTCTCTC 300
CGTNGCCCGA GCTTCACTCT CTCCCTCAGC ACCTGCCCCTG CTGGAGGCCC CAGCCCTCCG 360
TGGACAGCAG GGGCCACGTG GAGCCCGGGG CGCTCACCCG CCACCCAGTG CTGGCCGCTC 420
TCTTGGTGCC AAACCCCTTT CCCCACCCCA GAGACTGGGG AGCTGTGTCT GGTTCGTCTC 480
TTGCACTAAC CACATTTGTC ATCTCTAGGG CAGGCTGGGG CTGCGGGCTG AGGGGGACCG 540
CTGGCACCCC CCTTCCCTCC CTCTTGGTTC CCATTTCCAT CCATGACAGG TACAGCATCC 600
CAGGAGCCCG GCGTGAAGGG CTGGACCCGA GCCGCTGTG AACATCCCTC AGCCCCCTGT 660
GTCCCCCTTT GGGACTAACC ACTAACCTCA CCCCCAACT CCACGGGTGC CCCTAGCTGG 720
CCCAGAGCCG GCAGTGTGAG CCCAAGTCCG GGCTGGAGCC GAGGCCGGAG CAGCTGTCTG 780
GGAGTCAAGG CTCAGTAGC GTTTCCTCAT GGGGTGCTCC AGGGGGTGCC ACAGACCCAG 840
AGGCAGCCCA AGGGCCTGGA CACCCTCCC CAGGCAGGTG CTGCCCCAGG AGGACTGTCC 900
TCGGGAATGA ACCTCCCGCG GGCTTTGGAC TGAGTCCCTG GTGGCTCCGG TCTCCTCCCC 960
ATGAAGTTGGG AGCGAGGGCTC CCCAATGTGT CTTTGTGGCT TAGTGTACGA TGTTTGTCTG 1020
GTTTCCCGCG GTGGAGGGCA GAGCCACCCC ACATCAGAGT CGGACGTGCT ACCCCTCCCG 1080
GTCCCGGGCC TGGCCACGCC AGCCAGCCCC TCGAGGGTGC ATGCTGTGCG CAAGGCCAGG 1140
GGCAGCCAGA GGGCAGCTGG ATGGCCACGT GCAGGGGTCA AGGCTGGGGC CTGCAGTGGG 1200
GGCGGGCCCG AGCCCCAGCA GTTTACAGAC GCATGGCTCT TCCTCCCGCA CCGCCGGGCA 1260
GCTACCTGGA CCGGAAATGT CCTCATCCCC TCCTTGGGGC CAGGCTCTGC GCTGGCTCTC 1320
CTCTGTGAAC CCTCTCTTTC TTTGTGCTGG TGTCTGGGAC CAAAAGGGGG GAATATGGGA 1380
GGGCAGAGTG GGGAGGGGAG TCCATGGGCC TGGGGCCCCA AGCCGGGGGG TCTGAGCTCC 1440
CCAGGCATGA CCAACCTCA GTGGAGGGGC CAGCCACAGC CAACCTGCC AGTCTTTCCT CTGGGCTTGA 1500
CTGAGCCCCC CTGGGAGGCC CGCCACAGCC CAGCCTGCC AGTCTTTCCT CTGGGCTTGA 1560
CCCGCCAGGG GAGTTCTCCA GGCTTAGGGC CAGGAGAGAG GCCTGGCAC CCTGGCGTGG 1620
GTGCCCGCCA AACGCCCTGC GACCGCTACA GAAGCACAAC TGCTGTCCAT GGCCTGTGAG 1680
CTGCCTGCCA GGTGAATGGA CATAGCGTGA GAGGCGGTGA GGCAGGGGCT TCCAGCTCG 1740
TGCTGTCTCG GGACTCCTGA CCGTGGTGTG CGTGTGTGCC CGTCTGTGAC TTTCTACTCA 1800
CCAAAGTTGA AGAAAGGAAA CGGGGAAATC CAAAGGGGTG TCAAACCCCA CTTCCAGAGT 1860
TGGAGGGGAG CGCCTGCCAT TGGTTGTATT TTTGTTCTGA GTTTTGGGTG CCGTGTTCCT 1920
AACTACTGCA TCCCATGACC TCGCCACACC TACTGGGGCA TCTGGCTGTG GCCTGTGCTC 1980
ATGGCCAGCC CCACCTTCTC ACCCTGCACA GGGGGTCTTG CAGCCCCCAG GCCCAGAGCC 2040
TCGTTGGGAG GACAGGGTGG CCTTGGGGAG AAGAGGGAGG AGCCCAAGGG CTTACTCTAC 2100
TGAGAGTGCT CCCCAGCAGG CATCCACTAC CCCAGGGCCC CCACATGTG ATGGCAAGGT 2160
TGTAGTGAA TGGGCTCGGT TGGGAGCAGC CCCTGGCCCA TTGCCACACC ACCCATCTCA 2220
CTATGCAATT CGAGTTCCAA GCAACATTGT CTCTCGCCCT CTGCCCCAGCT CTGCCCCAGC 2280
CCTGAGAGGG GTGTTGAGGC AGCCCCCTTG ACCCCAGAAC CCCAGACAAG GGGGCGAGG 2340
GGGACCTAGG GCTCTCTCTG TGGGATCTTT GTTTTGTGTT TAACCATAT GGTGTGTAC 2400
TGACCACTTT CATATTTGTT ATATATATA TATATATATA TAATCTCCTT AAGACTCAGC 2460
CTCCTGGTTT ACCCCCCCGC CCTGGGCATC TGACCTCCCC CACCCAGATG TGATTTAACA 2520
TGCAGGAAGT GAGGCCTGAA CCATTTTGCA TTTCCCTCTC CTCAGCCTC TGTAGGGCCA 2580
CTGCTGTATG TACTGTCCGT GTGTTTTTTT GTTTTTTTT AACTGGGTTT GGGGGCTGAT 2640
TTTATTCTCT TTGGGGGCTT TTTTCTTGG CAAATACTAA AATGTCTGCT AATGTAATT 2700
CTGTGGTTTC TATTAGCTT GGGTTTCATG TTTTAAATAA AATTTTAAAA AGCAAAAAAA 2760

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(2) INFORMATION ON SEQ ID NO. 601:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1021 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

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GGCGGGGCGG CGAGAGCAGT AGGTGTTAGC AGCTTGGTCG CGACAGGGGC GCTAGGTAGA 60
GCGCCGGGAC CTGTGACAGG GCTGGTAGCA GCGCAGAGGA AAGGCGGGCT TTAGCCAGGT 120
ATTTCACTGT CTGTAGACAA GATGGAATCA TCTCCATTTA ATAGACGGCA ATGGACCTCA 180
CTATCATTGA GGGTAACAGC CAAAGAACTT TCTCTGTGCA ACAAGAACAA GTCATCGGCT 240
ATTGTGAAAA TATTCTCCAA GTACCAGAAA GCAGCTGAAG AAACAAACAT GGAGAAGAAG 300
AGAAAGTAAAC CCGAAAAATCT CTCCCAGCAC TTTAGAAAGG GGACCCCTGAC TGTGTTAAAG 360
AAGAAGTGGG AGAACCCAGG GCTGGGAGCA GAGTCTCACA CAGACTCTCT ACGGAACAGC 420
AGCACTGAGA TTAGGCCACAG AGCAGACCAT CCTCTGCTG AAGTGACAAG CCAGGCTGCT 480
TCTGGAGCCA AAGCTGACCA AGAAGAACAA ATCCACCCCA GATCTAGACT CAGGTCACCT 540
CCTGAAGCCC TCGTTCAGGG TCGATATCCC CACATCAAGG ACGGTGAGGA TCTTAAAGAC 600
CACTCAACAG AAAGTAAAAA AATGGAAAAA TGTCTAGGAG AATCCAGGCA TGAAGTAGAA 660
AAATCAGAAA TCAAGTAAAA CACAGATGCT TCGGGCAAAA TAGAGAAATA TAATGTTCCG 720
CTGAACAGGC TTAAGTATGAT GTTTGAGAAA GGTGAACCAA CTCAAACTAA GATTCTCCGG 780
GCCCAAAGCC GAAGTGCAAG TGAAGGAAG ATCTCTGAAA ACAGCTATTC TCTAGATGAC 840
CTGGAAGTAG GCCCAGTCA GTTGTCATCT TCTACATTTG ACTCGGAGAA AAATGAGAGT 900
AGACGAAATC TGGAACTTCC ACGCCTCTCA GAAACCTCTA TAAAGATGCG AATGGCCAAG 960
TACCAGGCAG CTGTGTCCAA ACAAGCAGC TCACCGACTA TACCAATGAG CTGAAGCCAG1020
G
1021

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(2) INFORMATION ON SEQ ID NO. 602:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 2889 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

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GATCAGGCGCT GTGGTCCAGC TCACTGCCAT TGAGATTCTA GCTTGGGGCT TAAGAAATAT 60
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AAGGGTGGAA  TCGGTTGGTGA TCAAAAACCT TAAGAAGACA CCCAACTTTC CAAGTTCTGCT 180
TCTCTTCATG  AAAGTGTCTT TGCCCAAGGA GGAATTGTAC ATGCCCCCAT TGGTGATCAA 240
GGTCACTCAG  CACAGGCAGT TTGGGCGGAA GCTGTGCTGC GGCCAGTGCA CCATCGAGGC 300
CCTGGACCGC  TTTGCTGTGT ACCCTTATGC AGGGAAGAG GACATCGTCC CACAGCTCAA 360
AGCCTCCCTG  CTGTCTGCCC CACCATGCGC GGACATCGTT ATCGAAATGG AAGACACCAA 420
ACCATCTACT  GCTTCTAAGC TGACAGAAAA GGAGGAAGAA ATCGTGGACT GGTGGAGTAA 480
ATTTGATGCT  TCCTCAGGGG AACATGAAAA ATGCGGACAG TATATTGAGA AAGGCTATTG 540
CAAGCTCAAG  ATATATAATT GTGAATAGA AAATGTAGCA GAAATTGAGG GCCTGACAGA 600
CTTCTCAGAT  ACGTTCAGT  TGTACCGAG  CAAATCGGAT  GAAAATGAAG  ATCTCTCTGT 660
GGTTGGAGAG  TTTAAGGGCT  CCTTTCCGAT  CTACCTCTG  CCGGATGACC  CCAGCGTGCC 720
AGCCCCCTCC  AGACAGTTTC  GGGAAATACC  TGACAGCGTC  CCACAGGAAT  GCACGGTTAG 780
GATTTACATT  GTTCGAGGCT  TAGAGCTCCA  GCCCCAGGAC  AACAAATGGC  TGTGTGACCC 840
TTACATAAAA  ATAACACTGG  GCAAAAAAGT  CATTGAAGAC  CGAGATCACT  ACATTCCCAA 900
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GCACCCAGCA  CTCGGGGCCC  CTGAAGAGCG  GCTTGCTCTT  CACATCTCCA  GCACTCAGGG1320
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CCAGGGA AAA  CTTCAGATGT  GGTGATGT  TTTCCCAAG  AGTTTGGGGC  CACCAAGGCC1440
TCCTTTCAAC  ATCACACCCC  GGAAGGCCAA  GAAATACTAC  CTGCGTGTGA  TCATCTGGAA1500
CACCAAGGAC  GTTATCTTGG  ACGAGAAAAG  CATCACAGGA  GAGGAAATGA  GTGACATCT1560
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CTCAGGCCAA  CAGGCAAGCT  TTGCATCAT  TTAATCTCTA  TTAATCTCTA  AGTATTAAAA 2520
CTAAAGTTTA  AATCATGTTT  TCAAAATAT  TTTCAAGGT  GGCTGGTTCC  ATTTAAAAAT2580
CATCTTTTAA  TATGTGTCTT  CGGTTCTAGA  CTTCAAGTTC  TGGAAATGCT  TAAATAGAA2640
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TGCAATTATA  AATCAGTTAG  AATAGTTAGA  ACAATCTCTA  TTTATGCCCA  CAACCATTC2760
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2889

(2) INFORMATION ON SEQ ID NO. 603:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 3638 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

AGAGTTTCAG TTTTGGCAGC AGCGTCCAGT GCCCTGCCAG TAGCTCCTAG AGAGGCAGGG 60
 GTTACCAACT GGGCCAGCAGG CTGTGTCCCT GAAGTCAGAT CAACCGGGAGA GAAGGAAGTG 120
 AGCTAAAACAT TGACACAGAG AAGTCGGCCT GAGTGGTGGC GCGCTCGGGA CCCACGAGCA 180
 ATGCTGTCTCT TCGTGTGAGC CTGCTGTCTG GCGGTCTTCC CAGCCATGTC CACGAAGAGT 240
 CCCATATTGT GTGCCGAGGA GGTGAATAGT GTGGAAGGTA ACTCAGTGTG CATCAGCTGC 300
 TACTTACCCAC CCACCTCTGT CAACCGGCAC ACCCGAAGT ACTGGTGGCG GCAGGGAGCT 360
 AGAGGTTGGCT GCATAACCTT CATCTCCTCG GAGGGCTACG TCTCCAGCAA ATATGTCAGGC 420
 AGGGCTTAACC TCACCAACTT CCGGAGAAAC GGCACATTGT TGGTGAACAT TGGCCAGCTG 480
 AGCCGACGATG ACTCTCGGGCG CTACAAAGTG GGCCTGGGCA TCAATAGCCG AGGCCCTGTC 540
 TTTGATGTCA GCTGTGAGGT CAGCCAGGGT CCTGGGCTCC TAAATGACAC TAAAGTCTAC 600
 ACAGTGGACG TGGGCGAAGG GGTGACCATC AACTGGCCTT TCAAGACTGA GAATGCTCAA 660
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 GGTTATGTGA ATCCCAACTA TACAGGAAGA ATAGCCCTTG ATATTGAGG TACTGGCCAA 780
 CGACTGTTCG GCGTGTGTCAT CAACCACTC AGGCTCAGCG ATGCTGGGCG GTCTCTCTGC 840
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 GAGCCCGAGC TGGTTTATGA AGACCTGAGG GGCTCAGTGA CCTTCCAGT TGGCCTGGGC 960
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 ATTAGCATGT CAGACTTCGA GAATCCAGG GAATTTGGAG CCAATGACAA CATGGAGGCG2280
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CCTAGGTTTT TCCTACTGTC CTCAGAGGCG TGCTGGTCCC CTCTCAGTG ACATCAAAGC2640
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 TTTCTGTGA GAGAACCTCA GGTACGGAGA AGAATAGAGG TCCCTCATGGG TCCTTGAAG2760
 AAGAGGGGAC CAGGGTGGGA GAGCTGATTG CAGAAAGGAG AGTCTGCGAG CGCCCTTCTG2820
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 TCTTCCCTCT TCTTCTTTCC TTACCATCAA AAGATGTATA TGAATTCATA CTAGAATTCA2940
 GGTGCTTTGC TAGATGCTGT GACAGGTATG CCACCAACAC TGCTCACAGC CTTTCTGAGG3000
 ACACCACTGA AAGAAGCCAC AGCTTCTTCT GCGCTATTTA TACTCACTGA GTCTTCT3060
 TTTACAGGGG GTGCTCACT CTGCCCCAT TGGGAGAGGT CATAAATAGT CTCTGAGTCT3120
 AAGGCGTTAG GGTGCTATGA TGATGAGCAT ACACACAGGC ATGTCAGCACT GAGCCTGGCC3180
 CAGAAGCGTT TTTCTCAAGG GCCTCAGTG AGATAAATTA GATTTGGCAT CTCTGTCTCT3240
 GGGCCAGGGA TCTCTCTACA AGAGCCCGCTG CCCCCTGTTT GGAGGCGACG TTTTGAAGTA3300
 AAGAGGAGGA GGGGTGTAGA AAAATGTAAA GAGGAGAGAT CTTTCCGAGG CGCCACCACT3360
 TCTGTCACTC ACATGTGACC AAGATAAAGG AAGTGGCCAAA CCGTCACAGA CCTGTGATT3420
 TGAAGAGTTC CAAAGTTGAAG GGAACCAAGG AAGTGTTTGA TGCTGTGACT TTTCTGACTT3480
 TCTCCAGAAA GCTAAAATTT AATTCTTTTT TTCTCTGAG TTCTGTACTT CAACCCAGCT3540
 ACAAGCTGGC ACTTGCTAAC AAATCAGAAA TATGACAATT AATGATTAAA GACTGTGATT3600
 GCCACAAAA AAAAAAAGG AGACGAAAAA AAAAAGGG

(2) INFORMATION ON SEQ ID NO. 604:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2775 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

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ATAGGTTTGG ACCTTTCTTG GTAGAATTAC TGCCTTAATT TTGTTCCACT GATACTAGAA 60
ACGGTCTGAT GTTAGAGCTG GAAGGGATCT GTAGTATCAC GCAGTCCGAT TCTCTAATTT 120
TCCACATGAG AAAATGAAGG TCCAGAGGAA GCAGAGACTT AACTCACAAA TCAGAAAAGC 180
GGTTCCTTGA GAACTGAGGC CATAGTGAGG ACTTTCCTGT TTCCACCATA CCACCTTGCC 240
AGTCCACACA AGAGGGAGGA TGATTTTGG GGGGCATACA CTGAGGATGG AGAAAGATGG 300
CATCAGAACT GCTGGGTGAA GTGGTGGCTT AACTGGACTT TGACAGCTGC CTTTGA AAAA 360
CCCCAAAAC AAACACACTG CATGTAATCA AAAGATGCTT ATACTAATAA TGACCTGTGC 420
TGTTCCCACT CAGTTGCTCT CTGTTTTCGA GAAGACATGA GAAGCTGCAA CATGACCTGG 480
ATGGAAATG GAGATCACA TTTTGTGTTG AGCCACTTC TGGCAGCAG ACCTGCTCCA 540
CCTTCCCAGA AGGCTGAAGT GCTCGTGTGC TGCACTCCAG TGGCATCTCT GCAGTGGTCA 600
GAGTGACCTG GTATAAGGGA GAGGGCATCA CCTTGCCTCC TGTGCTGACT CTGCGCTTC 660
CCCTACAGGA GAGTCCATCC CGATCCGGCT CTTCTGCGCC GGGTATGAGC TCACGCCAC 720
CATGCGGGAC ATCAACAAGA AGTTCTCTGT GCGCTATTAC CTCACCTTGG TGCTGATAGA 780
CGAGGAGGAG CGGCGCTACT TCAGCAGCA GGAAGTGGTG TTGTGGCGGA AGGGTGACAT 840
CGTACGGAAG AGCATGTCCC ACCAGGCGGC CATCGCCTCA CAGCGCTTTC AGGGCACCAC 900

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CTCCCTGGGT GAGSTGGGGA CCCCCAGCCA GCTGTCTGAC AACAACTGCA GGCAGTAGGC 960
CCCCAGGGGC GAGAAGATGC TGGGCACCCA CCCAGCACCC CCATCTACCA ACACAGCGG1020
CTGGGGGGCC GGGCGGACCT TGTGAGGCTC AGTTGACCCG TTACTTGCAC CCTGAAACA1080
AATCATGTTT TTGACTTAAA TTCTTTTCTC TGGAGAACCC AAGGGGCTTG GGGTGGGAAG1140
CAGTCTCTCC TTGGGATTCT GCGGCCGATG TGGGATAGAA GAGGTAGCAT CCTGGAAGCC1200
AGCCTCTCTG GGAACATGA GCCCCTTCC TCGGGGGGCT GCCTTGGCTC TTAGAGGAGG1260
GAGAGCAGAG AGCAGCATC CTTGGCTCCT GGCTCTCTGA GCTTCCTGAT ACAGGATCTG1320
AGCATGTCCC TGGGATTCTG AGCTGCCAAC AGGGCCCTGG GTAGTCACAT CTTTACTCC1380
CCTTTGCTGT CCCGGAGGTA GTGGCAGGAG TTGGGCCAGC CCCCACTAAG TGGCAGGGGA1440
AGACTCACGA TTGGGAAGCT ACCTCTTTGG GAATCTTGGG TGTGGTGATC TCAAGTTCCC1500
ACAGGCCATC TCCTTCTGCG CACTCACTGC TGGGACCCAG GCACTCCCTT TCTCCATCCT1560
CTCTGAGATT TCAGTAATGT CCTGGAACAG AAGCCTGTAG GATGSCCTTG GGCACGGAGA1620
AGCCCTGGGG TCAGTGTCTG GCACGGATGG CGGCAGTGTG GAACCCAGGA GGCTGAACCC1680
GGCCACCAC GGAAGATGAG TGCATGGCAA CCGCTCGCCT TCAGTGTGCT CCACCTGGTA1740
ACCCCAAGGT CTGGGCTGTT CTAGGTATTG CTTACGTGCG CCCAGCAAGC CCTTAACAAG1800
AGGGCCTGTT TCCTGAAGA ACCAATCCCA GGAAGGGGCC TTGATCCCTC CGCCTTGCTG1860
AGAGTGAACC CTCGTCTCTC CTCACCCCTC ATTTCAITTC TGGGAATTGG GGCTTAGTTT1920
CGAACCTTTG GCAAGGCTGT TCTTACTAAT GCCCAAGCCC CTTTACCCCT CTCCCTATAG1980
GTTACACAGG GGAGACCAGG GCCTCGGCAG AAGACTGCTG CCACACTTCC GAATCACTCT2040
GCTTGCCAAA TAGGTATCTT TCACCAAGTG ACTGACCCAA GTTTAGGACC ATTGGTATCG2100
TGTGTTTAAA AAACACATAT AAAAAAAGCT TTGTGAATAT TCTTGTATG CTAGAGAGGA2160
AGGTACTTCT CCCTCTACGG CTCCTGCGCTG GGGCCTATGG TAGTAAAGTT GTTTACTGTC2220
CTTTTCTGCG TTCCCTGGA AATGACAGGC ATTACTCTCC CATTGGCCTC CCTTCCCTTT2280
ATAGAAAGAC CAGAGAGGCC CCACTGGCCA AGAGGTACGG TATTTGGCAG TCTGAGTTCT2340
CAGTAATTTG GAAAGTTAAG GAGTTGGTTC CTGTGTCACC TTTCAAGTTAG TGTGGGAAGG2400
GAAGACTTCT GTTTCTCTGA GATCAGTGCA GTCTCAGGCC TTTGGCAGGG CTCACTGGATC2460
AGAGCTGAGA CTGGAGGGAG AGGCATTTCC GGTAGCCCTAG GAGGGCGACT GGGCGCAGCA2520
GAACCGAGGA AGGCAAGGTT GTTCCCCCA CGCTGTGTCC TGTGTTCAAG TGCGACACAC2580
AATCCTCATG GGAACAGGAT CACCCATGCG CTGCGCTTCA TGATCAAGTT TGGGGCTTAA2640
GTGGATAGGG GAGCAGAGTT CTGGGTCTCT TGCCCTTTCA GAGCATGAGG TCAGGCTCTG2700
TATCCCTCTT TTTCTAGCT GATATTCTAA CTAGAAGCAT TTGTCAAGTT CCCTGTGTGG2760
CCCTTCCCCC CAGAG

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2775

(2) INFORMATION ON SEQ ID NO. 605:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 944 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

- (iii) HYPOTHETICAL: NO

- (iii) ANTI-SENSE: NO

- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

```

GGGAGATGCC ACCGGGAAAT CCCCAATGT CCACTAGGGG GCAGGAGGCC ACCGTTCCTC120
GTACTCCGGA GAACCTGGCT GGAGAGCTCT TTCTTGTTCA CCCTTCCCAC CAGACTAAAA180
GGTCATCGCA GATAACGTGA AGGACTGGAG CAAGGTCGTC CTGGCCTATG AGCCTGTGTG240
GGCCATTGGT ACTGGCAAGA CTGCAACACC CCAACAGGCC CAGGAAGTAC ACCGAGAAGCT300
CCGAGGATGG CTGAAGTCCA ACGTCTCTGA TGCCTGGCT CAGAGCACCC GTATCATTTA360
TGGAGGCTCT GTGACTGGGG CAACCTGCAA GGAGCTGGCC AGCCAGCCTG ATGTGGATGG420
CTTCCTTTGG GGTGGTGCTT CCCTCAAGCC CGAATTGCTG GACATCATCA ATGCCAAACA480
ATGAGCCCCA TCCATCTTCC CTACCCCTCC TGCCAAGCCA GGGACTAAGC AGCCCAGAAG540
CCCAGTAAC TCCCTTTCCC TGCATATGCT TCTGATGGTG TCATCTGTCT CTTCTGTGG600
CCTCATCAA ACTGTATCTT CCTTTACTGT TTATATCTTC ACCCTGTAAT GGTGGGACC660
AGGCCAATCC CTCTCCACT TACTATAATG GTTGAACTA AACCTCACCA AGGTGGCTTC720
TCCTTGGCTG AGAGATGGAA GGCCTGGTGG GATTGTCTCC TGGGTTCCTT AGGCCCTAGT780
GAGGGCAGAA GAGAAACCAT CCTCTCCCTT CTTACCCGT GAGGCCAAGA TCCCCTCAGA840
AGGCAGGAGT GCTGCCCTCT CCCATGGTGC CCGTGCCTCT GTGCTGTGTA TGTGAACCAC900
CCATGTGAGG GAATAAACCT GGCCTAGGA AAAAAAAAAA AAAA

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944

(2) INFORMATION ON SEQ ID NO. 606:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 1939 base pairs

(B) TYPE: Nucleic acid

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

(A) ORGANISM: HUMAN

(C) ORGAN:

(vii) OTHER ORIGIN:

(A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

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CCAGTCAAGA ATCTCCCACT AAGCTTCAAA GTAGTGGATT ACAGCATGGC AACCATGCCA 60
GTAATTTGAA ATTTAGTAGA GAGGCTTTCG CTTAGTAGAG ATGGGTTTTT GCAGGCTGCT 120
CCCGAACTCC TGACCTCACC CCACCCGCGG CACCCGCCCC ATCGGGCCCC CAAAGTGCTG 180
GGGTACAGCG CTTAAGCCAC CAAGCCCGCG CGACCTTCTT CTATTTTTTC ATTCTCCTTT 240
CCAAAGCCAT GGCCATGCGC TCCTGTGTAC AGSTGCATAA ACACATCAGT GTGCCATCCC 300
TCACATGCAT GTCGTTCCCC ACCCTCTCTT CCCAGGGCTT CTCTTGGCTC CAGCGTTTCT 360
CTGGGACCC CTGCAGATAC AGCCTGTGCT GGACCCCGAG CCAGGGGTGAG GGCTCATTTCT 420
GCTCTGTCTT CCCCACTGCC TCAGTTTCCC CCAAAAGCTG ETTTCACGT CTTCTAGTAG 480
GGGGCCTCCC ATGGGGGCAA GGATCCCCCT TAGGATTCAA TCTTTCTCT TGGGCGAGTT 540
TTGGCTTTGA GTCCCCCAGG GATCAGGGTG AGAATGAAGA AGAGCTCAGT GAGCGGAATG 600
ACAGCAGCTG GGTGGGTGTT GTGGGGAGAG GCTGAGGGGA AGGCAGCTCT AAGACTGGGA 660
GTGGAGTTCC TGGAGGTGTG GGGAGGGGGG CGTGTTTTCA ATTTAGAAAA ATCTCAGCCA 720
GCTCGAGCCG AGAGAGAATG CGAAAGAGGA AGTTGGAAG GAGCGAGGAA TCGGGTGGGT 780
GGCAGCGGGG GCGCTCAGT CGCTGTCTCG CTTGTCCACC AGCAGCGGCT CCGACTCCTC 840
GGTGATCTCC AGCAGCGGCT GCACGTCGGG GCTGCTCCCG CGCCGAGGT CGCCGGCTC 900
CCCCCGCTCC GCGCCGCCCT CGTCGTCTGC GCGCGCCACC TCCACCATCT CGGTGGCCTT 960
GAGCACTTCC ACCTGGCCCT CGCGGATCTT CTTGACGTGG AAGGTGAAG GTGGCACCTT 1020
GTAGACCCG GTCTTGGAGC GCGCGTACAC CACGTGGTGG GCGCTGAAGG ATTTGCGCAAL080

CTTGTCCCG GACGTCTTCA GTTCTCGCG CGGCTCGGG GGCACCAAGC GCGTGCCCA1140
CTTGTTCATG CGCTTCTCCA GGGTGTGCGG CGTCTTCTCC AGGTTTTCTT TGGTCTTGAG1200
GCGCGTCTTC TCCAGGTTCT CGCGGGTACG CACCTTGGTC TTCTCCATCT TCTCCTTGA1260
GAAGGCCTTC TTGAAGTCGT CCACGCGCGG CAGGCCCTGC GCTTGATACG CTCTGCGCGG1320
GACTCCTCAA TAACCTCCTC AACCTCCACC GCCTCGTCCG ACGAAAGCTC CAGCGCGCT1380
GCGTCCTCCT CGGCGCGCTC GCCCTCGCCC AGCTCCTCGC CCTCCTTCTC TGGCAGCGCC1440
TCCGACTCTT TCAGCGATTG GCTGATGCTC AGTTTGGCGG CGAGCTTCA CTTCATCTTG1500
TAGATCATGA CTTTAAAGTT GCGCGCGCGC AGCAGCTCGG CTTGCTTGA CTCCAGCTT1560
TTGATCTGCC CCGCCTGGCG CTCGAGCGTG CCGCGCACGG TCTTACAGTT GACGCTGACC1620
TTGCGCACCT TCTCGAGCAG CTTGCTCACC GTATTGCTCG TGSTGGCGTG CGCCTTGCCC1680
AGCTTGTCTA GCTCGCCCTG GATGCTCTGC ACTGGGCCCT CCATCTCCGC CTGCGCTCC1740
TCCAGCTGTG CTTGAGTCAG CTGGATCTGG TCTAGGGCCC CGATGATTTT GTCCGAGAGG1800
CTCAGACCA GACGCGCGTT CACCTGGTCC GACTTGATCA GCTCTTCTGA GCCGCGCTT1860
GACGGCTCCT CCGCTGCCTG AGCCCCAGCG GAGGAAGCTC CGGGGCTCTG GCGATCGGG1920
TACCCGSGCA AGCGGCCG

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1939

(2) INFORMATION ON SEQ ID NO. 607:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1570 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

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GGCAGCAGGA AGTTAAGATC ATACATGCGG ATGTGCTGGT AACCTGCAAG AAGCAATCAT 60
GCTGCGGTCC GGTGTGACCT CCCAAGGCAT TCACCCCTGGG AGTCCCTGGT GCTGCACCCC 120
AACCCAGGCA GAGCTCATCG TGGGTGACCA GAGCGGGGCT ATCCACATCT GGGACTTGAA 180
AACAGACCAC AACGAGCAGC TGATCCCTGA GCCCGAGGCT TCCATCAGCT CCGCCCATAT 240
CGATCCCGAC GCCAGCTACA TGGCAGCTGT CAATAGCACC GGAAACTGCT ATGTCTGGAA 300
TCTGACGGGG GGCATTGGTG ACGAGGTGAC CCAGCTCATC CCCAAGACTA AGATCCCTGC 360
CCACACGCGC CGTACGCCCT CCACTGTGCG TTCAGCCCCG ACTCCACGCT CCTGCCACCC 420
TGCTCGGCCT GATTAAAGAG GTGCAAGATC TGGGAAGGACG TCCAACTTTC TCCTGATGA 480
CGGAGCTGAA GCATCAAGAG CGGCAACCCC GGGGAAGTCC TCCCGCGGCT TGGATGTGGG 540
GGCCTGCGCT CTCATCGGGG GACTCCCACT ACATCGTCAC TGCTTCCTCG GACAACCTGG 600
CCCGGCTCTG GTGTGTGGAG ACTGGAGAGA TCAAGAGAGA GTACGGCGGC CACCAGAAGG 660
CTGTGTGCTG CTTGGCCTTC AATGACAGTG TGCTGGGCTA GCCTGTGACC CCTGGGACN 720
TGCTGTGGTG AGGTGGTGGC AGCNTGGAGG GACCCATGCA GCACCCAGGT CAGAGCAGAC 780
CCNTNCCCTC NGCCNCGCCT GCGCCANGCT GGNACCTGAT GGCCCCCTGT GCGCCCTTGA 840
CCTGCTGGGC CAGGCTGNCC CTGGGACTCT CAGCCCCCAN GTTGCTTATC CANGATGTGA 900
CAGAGCTCGA CCCAAGCCAG GCTGCACACT CCTGGACNTG GGCTAGCCTG CACTGCCNTG 960
GGAAAGNTCN GCCGAGGGCC CANAAGCTGC TGAGGGGTNC TGAGGCTGGT GCCCACCCCC 1020
AAGCTAGTGT GTTCTCTGCC CCTCCCTGCC CGCGTTTCAG GGCCTCGGTC CATAGAGAAC 1080

ACCACACCCA TGCGCAGGTG GAAGGGTTTA TTAGTCCCTG CCAGCAGCTG TCCTCCCTGG 1140
CTCAGGTTGGC CTGGCCAGCC CACTGGATTG GGGACGGGCC AGGCTGGGCC AGGTCCGGGG 1200
TGCACTCTGG GAGGTAATAA AAGCAGACCG ACACGCAGAT GTTGCTCGGG AAAAAAAAAA 1260
AAAAAAAAAA AAAAAAAAAA CGCTGTCTCC GGGGGCCCTC TGCTCGCGCG GCCCAGTAGA 1320
TGGGGGTCTT CATGCACAGG CGCTGCACCA AAGCCCCCGC CTGGGCGGTA GCCACTTACG 1380
AGGCTCCCTT GCACATGCCAG CAGCTCCTGG GTGTGGTGGG TGTCTGGCTG GGGGACCCAA 1440
GCCTCTTGGA CTTTGGAGGT ATCCACCAGC AGCCGCAAGT CTCCCGATCA CTGTCTCTCA 1500
TCAGGCGGAG GAAGCAGACC TGGTGCTCCT CAGGGCGGTA ACAGATGCAG CCGCTCTGCC 1560
CGTCGAACAG
  
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1570

(2) INFORMATION ON SEQ ID NO. 608:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1768 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

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GCACAATCCC GGCTCACTGC AACCTCCAC TCTCGGGTTC AAGCGATTCT CCCGTCTCTA 60
CAAAGTATAC AAAAAAATTA GCCAGGCGAT GTGGTGCGTG CCTGTAAATCC CAGCTACTGT 120
GGAGGCTGGG GCACAGGAAT CCTTTGAAC TGGGAGGCAG AGGTTGCAGT GAGCTGAAAT 180
CACACTACTG CCCCCAGCC TGGGCAACAG AGCAAGACTC TGTCTCGAAA AAAAAAAAG 240
AAAAAATGA AGGAAAAGGA GGGTGAGTTA GCTGGAGTAG AATAGAGGTA TAGAATCGTT 300
CCTAAATAAC CGGCTGCATT GGTTCCTGG AGACTTGCTA AAAACCCAGA TTCCCAGGCC 360
CCACTTCTTG GTGCTCCTAA TTCAGTAGCA TCACAGTAGG GTTCCAGAAG CGGTATTTTT 420
AACAGCTCC CAGGTAATTC TGATGTGCAC CTAGATTGG AAATCACTGT GTTAAAAAAT 480
ATTGTGAGGT AAGTTGGTCA GTTAGGTTGG GCAGCTTTTA TTTCATTGCT AAGGGATTTG 540
GACTTGATGG TGTAATAAAG CATTAATTGA ACAATATTTT ATGGAGCCTG TACTATGTAC 600
CAGATGCAGA CTGTGCTAGC GGTGGGGAT ACAGTGATGA CTTGCTCTGC CTCTAGGTGG 660
CAGGGAGCCA TTTTGGGTTT TCGAACAGAA AAGTGACATA ATGAATGCTG AGTTCTTAGG 720
AAGATTAACT CAGGAGTAGT CTCAGGATG TACTGGAAGG AGAGAAGCTG AAACCCAGGA 780
GGCTGCTGTG TTTGCAGTTG GCTGCCAGT GCTACCTCTG CAGAGACAAT CAATGTCCCTG 840
AAGGTAGCTG GTATGTCTGT GTGCACTGAC ACGAGCCTTC CTACCAAGCC CCAGGGGGCTC 900
CATGCTGGAG AATGCACGTA GGGCTAGGGT GAGCACTAAC TTCACTTCAG GAGAGCAAGG 960
AACAGTGTGG CTCTTCCATT TTTCACTTCT GTAAGCACAT CACCCCTTTC TCCTCCCTTT 1020
GAGCTGTGTT CTCTGACAGC TGTTTGTGG TAAAGCCAGC AGCCCCTAAA GCAGCTCCCA 1080
GCCTTGTCTC CTCTGTGCTT TCCCCACCA CTGCTGCTGC ACGCCTCATT TGCTGGCCCA 1140
CTTTAGTGGT GGAACCATTA GAGGCTGACT GACTTAAAGG AGATTGAGTC TGCTCTGACC 1200
CGAGAGAGA GTGGGATGGA TGGATGCATC GTCTCATTTA GAAAGTGTGT CCTCTGACTC 1260
TAACACACTC TTCTCTCTTT CTTTACCGCC CTCCTGTGTG CGTCCCTTGG GGGGGCGTGG 1320
GCTAAACCCC TTCCGTCCCC CTTTCTCCTT CTCTCTCACA CTGTAGGCAC CACTTCTCTT 1380
ACAAATTAGG CTTTCTCTCT GCCTTGGGCT GAGTGAGGAA GAGGAGTGCT GTTCTGCCT 1440

TCTTAGCCCA GCTGGGCTCT ACCAGAGGCT ACTGTGTACC CATTTACCAT GCGTGATTGT 1500
TAACCTCAGG TGGGGGTAG CCAGGTATTG ACTGAATGTA TGTTCGTGCT GACCTGTGTT 1560
TTTTTCTGTA GGGACCAAG CAGTATCCTT ACAATAATCT GTACCTGGAA CGAGGCGGTG 1620
ATCCCTCCAA AGAACAGAG CGGGTGGTTC ACTATGAGAT CTGAGGAGGC TTCGTGGGCT 1680
TTGGGTCTCT TAACTAGGA CTCCTCATC CCTAGAAATT TAACCTTAAT GAAATCCCTA 1740
ATAAACTCA GTGCTGTGTT AAAAAAAA

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1768

(2) INFORMATION ON SEQ ID NO. 609:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1001 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cdna library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

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TAAGGAGACT GAAAGGTGAT TCATTTAGTG AGTAGCGATT ACAGAATTC TAAACAGTG 60
GGGGCGGGGG GGGCGGGGGG GAGGAGGGCT GGAATTGTCC TCCAGCGCAT ACAAGGTTGT 120
TGCTGCCAGA GAAATCCAGC AGGAAAGAGC AGCATTCTTT CACCTTTTCC GCCTCTGAAG 180
CGGAGGAGAA CTTCATTTC CAGCAGCCCT TAAGATTCCCT CCGCGCACTG CGTAGCGTCT 240
CCGGCATTCT GCTTCCGGC GCTCTGCCCT CCGGTGCGCT GTTTACGGCC AGTTTGAACC 300
AAAGACGCCC AANGGTTGAG GCCGAGNTTC CAGAGCATGG GGTCTCGGTT GTCCCGACCT 360
TTTGAGTCCT ATATCACTGC GCCTCCCGGT ACCGCCGCCG CGCCCGCCAA ACCTGCGNCC 420
CCCAGCTACA CCGGGAGCGC CGACCTNCCC CNAGCAGAAC ACCGCCNNGT TGAAGANCCCT 480
GCTGGAGCTG TCGNCGTNGC TTTCTGGGTT GGGGCTGATG GGGGNNCGGG CGGGTACGTG 540
TACNTGGGTG GCANCGGAAG CCCATGAAGA TNGGGATACC CCCCAGTNC CATGGACCNA 600
TTACNCGAGA TGGTCATCGN NGCCTCANGC NATTGCCACC TNGGGGTANT CGTTGTNCAT 660
NGGCAGACCC CAAAGGGAAN GGCCTANCCG CGTTGTTNG AAAGNTACCA CCANGTGAAT 720
NCTGTCTTCT GTCNCTNGT CCNNTTTNCC CCGTGACACA CAGAGCAGGC ATGGAATTTA 780
ATGGGNTGTT CTGGNACNAG ACACTTGTAC ATGGACAGAC ATCACTACTN NGTGGAATACT 840
NNACAAGACT GAAAAAGNAAA ATCGTATGTT GTCACTCNTC TGGCTANTGG AGTGTGTTGT 900
GCCTTCACAG ATTTACACAG AACCAATAAA TCCTCAGAG AAGTAAAAAA NAAAAAAA 960
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A

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(2) INFORMATION ON SEQ ID NO. 610:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 2515 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

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GGTGTTGGAAA CTACTGCAAA TAGTAGCACT TCACTGAGAT CTACAACCTCT TGA AAAAGAA 60
GTTCCTGTCA TCTTCATCCA CCTTTAAAC ACTGGATTAT TCCGGATAAA AATTCAAGGA 120
GCCACTGGAA AATTTAATAT GGTGATCCCT CTGTGGATG GGTATGTTGT CAGCAGGCGA 180
GCTCTTGGCT TTCTGGTGAG GCAGACTGTA ATTAACATTT ATAGAAAGAA GAGACTGGAA 240
AGTGA CTCT ACAGTCCCCC CATGTCCGCC GGAAACAGAA AATCAACGAC ATTGTCAACA 300
AGTACCGGAA CAAGCAGCTG GAGCCAGAGT TTTATACCTC ACTTTCCAG GAGGTTGGAC 360
TCAGAAGCTG CAGTTCCTTAG ACCACTGAAT TTCTAAGACT GTTGAACCTCC AGTTTGGGAA 420
CTATAACACA GCAGAACAGT TTGATAGGTC ATCACTGTAA AATAAATAAC AATCACTCC 480
CAAGAGCTTA CTGTTTAATC ACCAGAATAG AAGAACACA TTATAACCCA TTTGATAGAA 540
GACTTTGGGC TATCTAGTGA AATGGGCTCC CAGACACAA CTACTCCCTG CTGATAATGA 600
TGATATACAT TTTAGCCATA AACTTTCTTT TAAAGGTGAC AATTTTAGTT AAACATAAGC 660
CTTTTGAGGA GAAAGGGCTT TATGCATCTC AGTTAAACAC GTGCATTGGT AGTATCAACA 720
AATTTGCAAT ATAGAAGTTG AAGATAGTTT TTTNCTCAC TTTTtagGAG GCTGTATTCA 780
AAATTAATAA CTCGAATCT TACAGGACAT TTAAGGACT CATGTTGATA GCATGGAGGA 840
GAAGGAAAGA AGTCACAGCC TTCTACTCAG TTGATAGGTC TCTTGTCATC CAGCTGTAC 900
ACTGACAAAA AGAAAAGATG ATANCATGTT TTTTGTCTCA GATAAGAAAGC CTGACATTA 960
AAGATGTGCT ATTTTTTTCT CCACATTTC AAAAAAGTTC CTCTCATCA CTGCACAGAT 1020
CTGTCTGAAA GCCTCAGTTT CTGAGTGACC CAGGAACAGA TCAGAAATGG AGCATGGCCT 1080
TGTCCTTTAA TGGGGATGCA AATAAAGTTT GTGGGGTTAA AAGTTATAAG ACACGAGTGA 1140
TACCCCACTC TCTCCATTAT TGTCCAGCGG GGTGACATAA TGACAGGTTA AATATTTGTG 1200
ATTCATTGAT TAAATATTAT TTAAGAAAT GTAAAAAATA AAAAAGGTT GAAATATTAT 1260
TGTTTCTATC CATTTGCTCT TATTTAGGA CCAAGCAGCA AACTGCAGTA GTTTGTGAAG 1320
GATTTCTAAT TGGGGTTCAG GAATAGCCTC TCAACGCTAC TAATTAGAT CTCTCCAGAG 1380
GAACACTGAG ATTTCTCTAT AATTGACAAA CATGAGTGAC CACCTCTTTG GGTGGCTACT 1440
GTTAGAAATG GCTGTTGTCA TGTTTTCTGG ACTTTGCCAG CCAACAGATC CTTGCCAGGT 1500
TTTGAAATAA TTCTATTATC CTCCTGCTA CTCTTCTGCA GCGATAAATC TTTTGNAGAT 1560
GGCCAGAGCC AGAACATCCA AGGATTCCTG TTACAGTGCT ACAGTATACA CTGCTCATTT 1620
ATCCTATTCT CATGTGCTTT CTCTTTAGT AAGATTATT TAAGAAATA AGTGATATT 1680
AAAGTCCAAA GAGGAATGAT CACAGTTGTA TAAGGGGTGT TTTCCCACTT GAACCTCTG 1740
CTCAGCTCGAC TGTGGGTCAG AGCTACACCC ATCTGTTTGG TTTGATGTTT TGTGGGTTAA 1800
CTTAGCGAGT GGGGATAGTG TGAGACCTAA TTCCTGTGTC AATGTCTCTT TATCCGAGAA 1860
ATGTGCATTT TGTCATCTAT AAGCAAGAAA TATGGGCATA GCAGCTCTTG GTTTAAANGT 1920
TTGCCATAAC CTGTTCTATG TTGTTTTAAG CTCAGGTAAA GATAACCTCC NTCTTCTATT 1980
GACTCCAGGT TCCATTGAGG TTATAGTATT ATTCATAGT TGATTTTCTT TTAAGCTNG 2040
GGCAATAAAT TGATGTTTCC AGATGGTAAC ATGGGANGAG GGCATATAGG ATAAAGATNG 2100
AGCAAAATCT ACCCTAAAAA TGNTTCTAGT AGTTCAACAG AAGAAGATGA GGTTTAAATA 2160
CTTTCAAGGT AATTCTAGAT TGACATTTN GAGGGGAAAA TGGGCTCTTG TCTTAGTTGA 2220
AGTGAGCAGA GAANGGCTAT NAAATTAATA TGTAANCTTA CAGCATCTCA GAGGTTAAAA 2280
GACTCTGTC CAGATGTACT TCTTCAGTGT ATCAACTTCT TACTTTGGC 2340
ATAGTTAATT TCAGAAAAAT GTGCTGTATG TGTGTGTGTA TGAGGGTTGG TCTTGTGAT 2400
CCTTCAGTTA GCTCTAAATT CTGGCAACTC CTGTGATATC CCAATGATT TATACCATGA 2460

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(2) INFORMATION ON SEQ ID NO. 611:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 818 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

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TTTTTTTTT ATTTAAAGCC TGGATTGTAA CCAGATTTTC TTTTTCCTCC CTCTCAGCT 60
GTAGATATGA TATCTCCTTT CAGGGCCCCA GCTTAAGGGC AAAGTGAGTT AATGTGTAGAL20
CAAAGCGCAG GGACAAGAGA GAGTTAACAT CTAGACAGTG GAAAAAGCCA TGSTGTGTGG180
TTTCTGGGAA CCACCAACAC TTGCAGGTTT AGCTTTTTC CAGGGTTGAC TACAAGAAAG240
AAAACCATGT TTTTGCAAGA TTAATGTG GTTGAGTGTG CCTAAATTAA CCATCCCCAT300
TTTTATCATA TTTCCACCAT CACTTCAGGG TTTTAAGAGT CAGTGCTCAC CTGGGCGGAG360
CTGGTAGTAC ATTTTGCTTC TTAGAAAGCT AAGTCTGGG TTCCGTCTGA TTTTAGGTT420
CAGGAACTTC CTGAGAACAC CCGATCGCAG AGGTAATT TCTGGAGTTT GTTTGCAAG480
GATAGCTGGG AGTATGGCCA CCTGCTCCA CGATGCGGTA ATGAATCCAG CAGAAGTGGT540
GAAGCAGCGC TTGCAGATGT ACAACTCGCA GCACCGGTCA GCAATCAGCT GCATCCGAC600
GGTGTGGAGG ACCGAGGGGT TGGGGGCCCT CTACCGGAGC TACACCAGC CAGCTGACCA660
TGAACATCCC CTTCAGTCC ATCCACTTCA TCACCTATGA GTTCCTGCAG GAGCAGGTCA720
ACCCCCACCG GACCTACAAC CCGCAGTCCC ACATCATCTC AGCGGGGCTG GCCGGGGCCC780
TTGCCCGGGC GGCGAGGGGC CCCCTGGAGC TTTTAAGA

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818

(2) INFORMATION ON SEQ ID NO. 612:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 1024 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

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GCGGTCGGTA GTGCGGCGCT GTTTAAGAT GCGGCGGAG GAACCTCAGC AGCAGAAGCA 60
GGAGCCGCTG GGCAGCGACT CGAAGTGT AACTGTCTGG CCTATGATGA AGCCATCATG 120
GCTCAGCAGG ACCGAATTCA GCAAGAGATT GCTGTGCAGA ACCCTCTGGT GTCAGAGCGG 180
CTGGAGCTCT CGGTCCTATA CAAGGAGTAT GCTGAAGATG ACAACATCTA TCAACAGAAG 240
ATCAAGGACC TCCACAAAAA GTACTCGTAC ATCCGCAAGA CCAGGCCTGA CGGCAACTGT 300
TTCTATCGGG CTTCGCGATT CTCCCACCTG GAGGCACTGC TGGATGACAG CAAGGAGTTG 360
CAGCGGTTCA AGGCTGTGTC TGCCAAAGAG AAGGAAGACC TGGTGTCCCA GGGCTTCACT 420
GAATTCACAA TTGAGGATTT CCACAAACAG TTCATGGACC TGATTGAGCA GGTGGAGAG 480
CAGACCTCTG TCGCCGACCT GCTGGCCTCC TTCAATGACC AGAGCACCTC CGACTACCTT 540
GTGGTCTACC TCGCGGCTGCT CACCTCGGGC TACCTGCAGC GCGAGAGCAA GTTCTTCGAG 600
CACTTCTACG AGGGTGGACG GACTGTCAAG GAGTTCGCC AGCAGGAGGT GGAGCCCATG 660
TGCAAGGAGA GCGACCATAT CCACATCATT GCGCTGGCCC AGGCCCTCAG CGTGTCCATC 720
CAGGTGGAST ACATGGACCG CGCGAGGGG GGCACACCA ATCCGCACAT CTTCCTCGAG 780
GGCTCCGAGC CCAAGGTCTA CTTCTCTAC CGGCTGGAC ACTACGATAT CCTCTACAAA 840
TAGGGCTGGC TCCAGCCCGC TGCTGCCCTG CTGCCCCCTT CTGCCAGGCG CTAGACATGT 900
ACAGAGGTTT TTCTGTGGTT GTAAATGGTC CTATTTCACC CCCTTCTTCC TGTACATGA 960
CCCCCCCCCA TGTTTTATTA AAGGGGGTGC TGGTGGTGAA AAAAAAAAAA AAAAAAAAAA 1024
AAAA

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(2) INFORMATION ON SEQ ID NO. 613:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1322 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

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GCTGACCACG ACAATGTGTCT CCTCCTCTGC ACCTTCCAAG ACCTCCTTAA TAATGAACCC 60
ACATGCGCTCT ACCAATGGAC AGCTCTCAGT CCACACTCCC AAAAGGGAAA GTTTGTCCCA 120
TGAGGAGCAC CCCCATAGCC ATCCTCTCTA TGGACATGGT GTATGCAAGT GGCCAGGCTG 180

TGAAGCAGTG TGCGAAGATT TCCAATCATT TCTAAAACAT CTCAACACGTG AGCATGCGCT 240
GGACGATAGA AGTACAGCCC AATGTAGAGT ACRAATGCAG GTTGTACAGC AGTTAGAGCT 300
ACAGCTTGCA AAAGACAAG AGCGCCTGCA AGCCATGATG ACCCACTGCG ATGTGAAGTC 360
TACAGAACCC AAAGCGCGCC CTCAGCCCTT GAATCTGGTA TCAAGTGTCA CTCTCTCCAA 420
GTCGCGATCG GAGGCTTCTC CACAGAGCTT ACCTCATACT CCAACGACCC CAACCGCCCC 480
CCTGACTCCC GTCACCCAAG GCCCCTCTGT CATCACACCC ACCAGCATGC ACACGGTGGG 540
ACCCATCCGC AGGCGGTACT CAGACAAATA CAACGTGCCC ATTTCTGTCAG CAGATATTGC 600
GCAGAACCAA GAATTTTATA AGAACGCGAGA AGTTAGACCA CCATTATCAT ATGCATCTTT 660
AATTAGCGAG GCCATTCTCG AATCTCCAGA AAAGCAGCTA ACACATAATG AGATCTATAA 720
CTGGTTCACA CGAATGTTTG CTTACTTCCG ACGCAACGCG GCCACGTGGA AGAATGCAGT 780
GCGGCATAAT CTTAGTCTTC ACAAGTGTTT TGTGCGAGTA GAAAACGTTA AAGGGGCAGT 840
ATGGACAGTG GATGAAGTAG AATTCCAAAA ACGAAGGCCA CAAAAGATCA GTGTAACCC 900
TTCCCTTATT AAAAACATGC AGAGCAGCCA CGCCTACTGC ACACCTCTCA ATGCAGCTTT 960
ACAGGCTTCA ATGGCTGAGA ATAGTATACC TCTATACACT ACCGCTTCCA TGGGAAATCC1020
CACTCTGGGC AACTTAGCCA GCGCAATACG GGAAGAGCTG AACGGGGCGA TGGAGCATAC1080
CAACAGCAAC GAGAGTGACA GCGATCCAGG CAGATCTCCT ATGCAAGCCG TGCATCTCTG1140
ACACGTCAAA GAAGAGCCCC TCGATCCAGA GGAAGCTGAA GGGCCCCCTG CTTAGTGAC1200
AACAGCCAAC CACAGTCCAG ATTTTGACCA TGACAGAGAT TACGAGAGT AACCCAGTAA1260
CGAGGACATG GAGTGACTAT CGGGGCGGGC CAACCCCGAG AATGAAGATT GGAAGAAAG1320
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1322

(2) INFORMATION ON SEQ ID NO. 614:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 4458 base pairs
 - (B) TYPE: Nucleic acid
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 - (A) ORGANISM: HUMAN
 - (C) ORGAN:
- (vii) OTHER ORIGIN:
 - (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

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GCCCGGCGTT AACAAAGGGA GCCGATACCG ACCGGCGTGG GCGCGGAGCG GCGGGCCGCC 60
ACCGAGCGTG CTGAGCAACC GCAGCCTCCG CGGCCGAGAG TGCAGCGAGC AAGGGGACAA 120
AAAGTTCGCG AAAGCCCGCA CAACUAGCAC CACAGAGAGA AGGGAAGAAC GGCATCCAGC 180
CCACCAGAAA TGGACCGACA CACCTCAGCA TCTCCAAACC CCGCAGCACA CGTGACCATA 240
AACCAGCAAA GATGAGTTTT GATCATCCTG AGAAAAATGG GCCTTGGCCT GCAGACCCAA 300
TAAACCTTCC CTCCCATTGA TAATAGTGCT AATTCCTGAG GACCTGAAGG GCCTGCCGCC 360
CCTGGGGGAT TAGCCAGAAG CAGGCTTGTT TTCCTGCTCA GAACAAAGTG ACTTCCCTGA 420
ACACATCTTC ATTATGATTC ACACCAACCT GAAGAAAAAG TTCAGCTGCT GCGTCCTGGT 480
CTTCTTCTG TTTGAGTCA TCTGTGTGTG GAAGGAAAAG AAGAAAGGGA GTTACTATGA 540
TTCCTTAAAT TTGCAACCA AGGAATTCCA GGTGTTAAAG AGTCTGGGGA AATTGGCCAT 600
GGGGTCTGAT TCCCAGTCTG TATCCTCAAG CAGCACCCAG GACCCCCACA GGGGCCGCCA 660
GACCCTCGGC AGTCTCAGAG GCCTAGCCAA GGCCAAACCA GAGGCTCTCT TCCAGGTGTG 720
GAACAAGGAC AGCTCTTCCA AAAACCTTAT CCCTAGGCTG CAAAAGATCT GGAAGAATTA 780

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CCTAAGCATG ARCAAGTACA AAGTGTCTTA CAAGGGGCCA GGRCCAGGCA TCAAGTTCAG 840
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 AGGTTTTCCC TTCAATACCT CTGAATGGGA CGGTTATCTG CCAGAAAGAGA GCATTATGAC 960
 CAAGGCTGGG CCTTGGGGCA GGTGTGCTGT TGTGTCGTC GCGGGATCTC TGAAGTCTCTC 1020
 CCACCTAGGC AGAGAAATCG ATGATCATGA CGAGTCTCTG AGGTTTAAATG GGGCACCACAT 1080
 AGCCAACCTT CAACAAGATG TGGGCACAAA AACTACCATT CGCTCATGTA ACCTCTCAGTT 1140
 GGTTACCACA GAGAAGCGCT TCCTCAAGA CAGTTTGTAC AATGAAGGAA TCTTAATGT 1200
 ATGGGACCCA TCTGTATACC ACTCAGATAT CCCAAAGTGG TACCAGAATC CGGATTATTA 1260
 TTCTTTTAA AACTACAAGA CTTATCGTAA GCTGCACCCC AATCAGCCCT TTTACATCT 1320
 CAAGCCCCAG ATGCTTTGGG AGCTATGGGA CATCTTTCAA GAAATCTCCC TAGAGAGATT 1380
 TCAGCCAAAC CCCCCATGCT CTGGGATGCT TGGTATCATC ATCATGATGA CGCTGTGTGA 1440
 CCAGGTGGAT ATTTATAGT CCCTCCCATC CAAGCGCAAG ACTGACGTGT GCTACTACTA 1500
 CCAGAAGTTC TCGCATAGTG CCTGCACGAT GGGTGCCTAC CACCOCCTGC TCTATGAGAA 1560
 GAATTTGGTG AAGCATCTCA ACCAGGGCAC AGATTGAGGAC ATCTACCTGC CTGGAAGAGC 1620
 CACACTGCCT GGCTTCCGGA CCATTCACTG CTAAGCACAG GCTCCTCACT CTCTCCATC 1680
 AGGCATTAAA TGAATGGTCT CTGGCCACC CCAGCCTGGG AAGAACAATT TCTGTAACAA 1740
 TTCCAGCCTG CTCTTTTAC TCTAGGGGCC TCTGTACGA AGACCATGGG GACTTCAAGA 1800
 GCCTGTGGTG AGGAAATCAG GTCCAGCCTT CCTGTGAGCC AGACAGTTGA TGCCCCAGAA 1860
 GCCTCTCGCC ACACACATCG ACACATATCT AGCATTTCTT GCAGACAGCA TCTCTCCGCI 1920
 TCTCCACCTT GGTGATAGCA AGGTCTATCT CTCCCATCAG GGCTGCCAAA GCTGGGCTTT 1980
 GTTTTCCCA GCAGAAATGAT GCCATTCTCA CAACCCAATG CTCTATATTG CTTNAGAGT 2040
 TGCATTAAAA TGTGATTTT ACNNTTTTAA AGNAAATTCT NNCTTAAATT ACAATTGTGC 2100
 CCNATCGAGG GTGGNCTCTN NGGGGGGCAA TAGGGTGGTA CAGGGGATTG GAAACATCTT 2160
 CCGCGCTCCG AGAGAAAGT TGTCTCCGAG TCCATGCCCT CTGGAACGTG TTCTATCAGC 2220
 TCTGGTGTGT TGGGCTGTGC CTTAGACTGG GTGCTTATGA TAAAAGGTGT CTGGTTAAGC 2280
 CCCACTTTCT CTCTCCATGT GGAGATGGA GGTAGAGAAG GATACAGTGT CTATCTCAA 2340
 GTTGCTACGG TTCAGTGAAG GAGGCAGACA TCTGAACAGG NCAGGTAGGA TTCAGTGTGC 2400
 TCGTGCACCT GGGGATTTGG AGAGAGATGG TCTGTCTCTC TGTGTGCACC CAGGAGGGCC 2460
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 TGACTCTTAG AAGAGAGGAA GAAACATGCG AAGCAGATTA CATCTGAGCC TTTTGAATTG 2580
 TGTTTTTCTT TCTTCCCATG TTTATTTTCT AAGATCTACC TGAACCTAGN AGACTCAAGA 2640
 TATTTTTTAA GGAACCTCTC TACCATGCTC TAGGATAGCA TGTGCGCTCG CACGACAGAT 2700
 ACCAGGCAAT CCAGAGGCCAC AAAACGTGAT TCCTCCAGGC TCTGCTCTGC CTGACCGCTG 2760
 CCTGTGAGCT GGGTTTACAT ACCAGTCCCA TTCTTCTTT TCAATACCTA CCCCCAAATC 2820
 TTCTCTTAAC CACCATCTGT TTTTTTTTAG TTAAGCATT TTTTGTCTTA AAAGCATCT 2880
 GAGCCCAATT TCTTGAAGCT CACGGGCTTT TTGCTGAAGG TCTCTCAGGG TGATAGTGT 2940
 TGGCTCTCTG GACTTAAAGT CACTCTCAGN AGGTCAGAAC CTTNGGAGAT CAGAACTGAT 3000
 TCTCACCAGG TGTGAGAGGT GTGGNTANGC AGATTGCAAT GCTCTGCACC TTTTNCCTGT 3060
 CAAGTGAGNC AACTTNCAGG NCTCTCTGG NCAGAGGCTG GCCCATCTGA TTTTGCAGAC 3120
 ATGCTCTCCA GAGGNTTTT ACTAAGTCCC CTCTCCCTGN ATANGGGAAT CTGTGCTG 3180
 AGGACGCAN GCCTTNGGTT GTNGGANNGA GGTNAAAAAG CTTTGNACAA GGNATGAC 3240
 AGTNCATGCT GNTAGAGGCC AGGATTCCTA GACCCAGGGC TCTGCACTCT CAAGGCTGGC 3300
 CCATCTGTGT GATGGGGGCT TAATGTTTGG GCTCCAACTT AACCATCTCG GACTGGGCT 3360
 AACTCTTTAC TGCCAAATCC TCAGNCTTAT GTAGCNTAGA AAGGGCCCTG GANTGNAGA 3420
 CCGCTGGAT TTTCAAATTG ATGCTCCCAT ACTNGACTAG NCTGTGCCAC TNTGGGCAA 3480
 ATGCTCTTCC TGGAGCGCTG TTCCACACCT GTAAAGTGGG GATGATGATC TATCTCTACT 3540
 GCTTTTNGTG NAGGATTACA GGNNAAGACA CCTGTCTGG CTCTGTACCT GGCACGTAGT 3600
 ANGGTGCTGA GTTCATGCTG GTTCTCTTCC TGCTTTTAGT AGGGACCTGC TCTGTGAC 3660
 CACCTCGGCT GCATGCACCC TGCTGTGAGC GAGGCTAGTG TGGAAAGAGT CCTGTCTCA 3720
 GGGAAATTAAC TGTCTTATTG GGAGACAAAC ACTGTCTCTC TTTGAACACC CAGAAACCA 3780
 TGNCAAGACA GTGGACAACA CAGAACACGN CCTCTCTCCT CGCTGCTCTG AGCTNCCA 3840
 CTGATCTGCT TGGGGAATGG GCGGANACCG NTGGGCTGCT ATAGGACAAG 3900
 CCGCTTACCC CTCTCTGGGC CCATGAATTC CTGGCTTGGT TGTGTTCTG ATTTGACACA 3960
 CTGATTTTAA TCTTCGAATC ATGACACTGA GTGCGAGGGA GGTGGCACTC CGACAGCAGG 4020
 ACATACATGT TNGGTGTGAA GACTGGGACG ACATCGGGTA GAATCTAGTT TTTAAATTAT 4080
 ATTAATATAA AGGATCAAA TAAATTTAAAT APTGAATCTG ACTCCACAGA TCTTNNNN 4140
 AAGTGTCTGC CAGGCCAACA CTTTGGTAAA ATGCAAAATTA TGATATGGAC GTTATCATTG 4200
 GCTGTGTGAG GTTGTTCATA TTTGTGACAG TTAATTTAAA AATTATGACT TAATGTGCTC 4260
 TGTGCTCTAG GGGTCTGTCT TTCTTTGATA GCATCTTATT CATCTGGATC ATGGGACCTC 4320
 CTCTAATCTC TCCACCAATC AAATAAGCTA TTGCTATTGG TTTGGAGTTG AGATATCAGT 4380
 CTCGGAAACT TCTGAATAAT ACCCAAGGAT TATGTCAAA TTTAAAAATA 4440
 ATGTGTGTGT GTTCTCTT

(2) INFORMATION ON SEQ ID NO. 615:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 1562 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

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TGGAGGCGAGC TAGCGCGAGG GTGGGGGAGCG CTGAGCCGCG CGTCGTGCCC TGCCTGCCC 60
AGACTAGCGA ACAATACAGT CAGGATGGCT AAGAGGTGACC CCAAGAAACC AAAGGGCAAG 120
ATGTCCCGTT ATGCCCTTCT TGTGCAGACA TGCAGAGAAG AACATAAGAA GAAAAACCCA 180
GAGGTCCCTG TCAATTTTGC GGAATTTTCC AAGAAGTGCT CTGAGAGGTG GAAGACGATG 240
TCCGGGAAAG AGAATCTCAA ATTGTATGAA ATGGCAAAGG CAGATAAAGT GCGCTATGAT 300
CGGGAATGTA AGGATTATGG ACCAGCTAAG GGAGGCAAGA AGAAGAAGGA TCCTAATGCT 360
CCCAAAAGGC CACCGTCTGG ATTCTTCCTG TTCTGTTTCA AATTCGCGCC CAAGATCAAA 420
TCCACAAACC CCGCATCTCT TATTGGAGAC GTGGCAAAA AGCTGGGTGA GATGTGGAAT 480
AACTTAAATG ACAGTGA AAA GCAGCCTTAC ATCACTAAGA CGGCAAAGCT GAAGGAGAAG 540
TACGAGAAGG ATGTTGCTGA CTATAAGTCG AAAGGAAAGT TTGATGGTGC AAAGGTCCT 600
GCTAAGGTTG CCCGGA AAAA GGTGGAAGAG GAAGATGAAG AAGACGGGGG GGGGGGGGGG 660
GGGGGGGGGG GGGGGACGTA TAGTCGGGTC GGCTGGTGGA GTAGCCCAAA AGAAGGGGAG 720
CGCCGTAATT GACACATCTC TTATTTGAGA AGTGCTCTGT GCCCTCATT A GGTTTAATTA 780
CAAAATTTGA TCACGATCAT ATTGTAGTCT CTCAAAGTGC TCTAGAAATT GTCAGTGGTT 840
TACATGAAGT GGGCATGGGT GTCTGGAGCA CCTGAAACT GTATCAAAGT TGTACATATT 900
TCCAAACATT TTTAAATGA AAAGGCCACT TCGTGTTCTC CTCACCTCTG GCACCTTTGCT 960
GTTGGTGTGA CAAGGCATTT AAGATGTTT CTGGCATTTT CTTTTTATTT GTAAGGTGGT1020
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AAAAAGAAC AACAACCCGA GACAAACCCCT TGATGCTCCT TGCTCGGCGT TGAGGCTGTG1140
GGGAAGATGC CTTTGGGAG AGGCTGTAGC TCAGGCGGTG CACTGTGAGG CTGGACCTGT1200
TGACTCTGCA GGGGCGATCC ATTTAGCTTC AGGTTGCTCT GTTCTGTAT ATAGTGACAT1260
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TTTTTTTAAG TGGGATGTTT TTTAACTGT TGTGTTTTTA ACAAACTATA GAACCTTTCA1380
TTGTCAAGCA AGCAAGAGCT CACTGCATCA ATGAAAGTTC AAGAACCTCC TGTACTTTAA1440
CACGATTCGC AACGTTCTGT TATTTTTTTT GTATGTTTAG AATGCTGAAA TGTTTTTGAA1500
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AA

1562

(2) INFORMATION ON SEQ ID NO. 616:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 2278 base pairs
 (B) TYPE: Nucleic acid
 (C) STRAND: individual
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO
- (vi) ORIGIN:
 (A) ORGANISM: HUMAN
 (C) ORGAN:
- (vii) OTHER ORIGIN:
 (A) LIBRARY: cDNA library
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

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GGCAATTTC GTTAGTGCT GAAGGCTGT GCGCGCGGT GTCCCCATTC CCACGTGAAG 60
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AGCGGGGAGC CGGAAGTGGC TCGCGGAGGC TCAGAAGCTA GTCCCGGAGC CGCGCGTGTG 180
GCGCCTCGGA GCACGGTGAC GCGGCCATGT CCCTAATCTG CTCCTATCTC AAGCAATATC 240
CGGAGCACCC ATGTGTATCC CCGTCTCTTA ATCATGTTTA TGAGCGCGCG CTCATCGAGA 300
AGTACATTGC GGAGAATGGT ACCGACCCCA TCAACAACCA GCCTCTCTCC GAGGAGCAGC 360
TCATCGACAT CAAAGTTGGT CACCCAACTC GGGCCAAAGC TCCCTCAGCC ACCAGCATCC 420
CGGCGATTCT GAAAGCTTTG CAGGATGAGT GGGATGCAGT CATGCTGCAC AGCTTCACTC 480
TGCGCCAGAG CTCACAGCAA CCGCCCAAGA GCTGTCACAC GCTCTGTACC AGCAGCATGC 540
CGCCTGCCGT GTCAATTGCC GTCTCACCAA GGAAGTCACT GCTGCCGAG AAGCTCTGGC 600
TACCCTGAAA CCACAGGCTG GCCTCATTGT GCCCCAGGCT GTGCCAAGTT CCCAACCAAG 660
TGTTGTGGGT GCGGGTGAGC CAATGGATTT GGGTGAGCTG GTGGGAATGA CCCCAGAGAT 720
TATTGAGAAG CTTCAAGACA AAGCCACTGT GCTAACCACG GAGCGCAAGA AGAGAGGGAA 780
GACTCTGCCT GAGGAGCTGG TGAAGCCAGA AGAGCTCAGC AAATACCGGC AGGTGGCATC 840
CCACGTGGGG TTGCACAGTG CCAGCATTC TGGGATCCTG GCCTTGACC TCTGGCCGTC 900
CGACACCAAC AAGATCCTCA CTGGTGGGGC GGATAAAAT GTCGTTGTGT TTGACAAAAG 960
TTCTGAACAA ATCTTGCTCA CCTCAAAGG CCATACCAAG AAGGTCACCA CGGTGGTGT 1020
TCACCCCTCC CAGGACCTGG TGTTCCTGCT TCCCGCGAT GCCACTATCA GGAATTTGCT 1080
GGTCCCCCAAT GCCTCTTGCT TACAGGTGGT TCGGGCCCAT GAGAGTGTG GATGATCAGT 1140
CAGCCTTCAT GCCACTGGCG ACTATCTCT GAGCTCCTCC GATGATCAGT ACTGGGCTTT 1200
CTCTGACATC CAGACAGGCG GTGTGCTCAC CAAGGTGACA GATGAGACCT CTGGGTGCT 1260
TCTCACTGTG GCACAGTTC ACCCTGACGG ACTCATCTTT GGAACAGGAA CCATGGACTC 1320
TCAGATCAAG ATCTGGGACT TGAAGGAACG TACTAATGTG GCAACTCTCC CCGGCACCTC 1380
GGGCCCCCAT ACTAGCATCG CTTTCTCTGA GAATGGTTAC TACCTGGGTA CAGCGGCTGA 1440
TGACTCTCTG GTCAAGCTCT GGAATCTGCG CAAGTTAAGA ACTTTAAGAC TTGTCAGCTG 1500
GATAACAATC TTGAGGTAAA GTCACTGATC TTTGACCAGA GTGGTACCTA CTTGGCTCTT 1560
GGGGGACCGG ATGTCCAGAT CTACATCTGC AAACAATGGA CGGAGATTCT TCACTTTACA 1620
GAGCATAGCG GCCTGACCAC AGGGGTGGCC TTCGGGCATC ACGCCAAGTT CATCGCTTCA 1680
ACAGGCATGG ACAGAGCTCT CAAGTTCTAC AGCCTGTAGG CCCTGGCCCT TCTGATGGAA 1740
GCTGGGCCCT ATCTCAAGTG AGGGGTAGAA TTAGGTTTGT GGGGGGGGTG GGGGGAATCT 1800
ATGGGGGGAG GGGGCTCTGT GGGGTGGGAG ATTCAATCA TTTCACTCTG GTCTGAGTGG 1860
TGCCCTGAGA ACCATGTGGG CATGGACCAC CCTCATCAT GCAACTCCAG GCCCATCGGG 1920
AACGGATGTG GAAGGAAGAA CTGTCAACCT CTTAAGGCCC AGGGCTCGGAG CCGAGGGGCT 1980
CTCCCTTCCT GTCGTTCAAT GGACGTGGTG GTGGCTGTTC CACACCCATT TTGTTGCACT 2040
TCCGTGAGAG CAGGAGAGCG TGAGCCAAGG GAACTGTGAA GGGGATGGGC AGGAGGGCT 2100
GTGCAAGGGT TTGTAAGCAG TGATCTAGTT TCATTAATAA AAGAAAAACA TAACCATAAC 2160
CACCTCCCGG TGTCTGTCTG CACCAGGAGC ACCTGGGACT GGGGAAGTCA GGGGAGGGAG 2220
CACACACTGG GACACTGGCT TCCGGGAAGC CCATCTTCCT TTCCTTTTAC AGCTCTTA 2278

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(2) INFORMATION ON SEQ ID NO. 617:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 931 base pairs
- (B) TYPE: Nucleic acid
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Partial cDNAs produced from individual ESTs by assembling and editing

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGIN:

- (A) ORGANISM: HUMAN
- (C) ORGAN:

(vii) OTHER ORIGIN:

- (A) LIBRARY: cDNA library

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

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CAGGGGGCTG CAGCCCGCTT GCCAATCAGA GCGCGGCTGA GCGGCCCGCG AGCCAACCCC 60
CGAGGAGCGG CCGGCTGGCG TCCGCCCGCG CCAGGAGTTG GGGATGTCCT ACRAACCCAT120
CGCCCCCTGCT CCCAGCAGCA CCCTTGGCTC CAGCACCCCT GGGCCGCGGA CCCCGTCCC180
TACAGGAAGC GTCCCGTCGC CGTCGGGCTC AGTGCCAGGA GCGGCGCTC CTTTCAGACC240
GCTGTTTAAC GACTTTGGAC CGCCTTCCAT GGGCTACGTG CAGGCGATGA AGCCACCCGG300
CGCCAGGGG TCCAGAGCA CCTACACGGA CTGCTGTCA GTCATAGAG AGATGGGCAA360
AGAGATCGGG CCTACCTATG CTGGCAGCAA GAGGCCCATG GAGCGCTGA AGAGAGTAT420
CATCCATGCC CGGGCCCTAG TCAGAGAGTG CTGGCAGAG ACAGAGCGGA ACGCCCGCAC480
GTAACAGGAA GCGCCTCGGC CTCAGCGTCT GGACCTATCC GGCCACTGCA GAGCACCCGC540
TTCTCCCTGG CCTTCATCCC GAGTTGCACT AACCATCCTG GGCTTCCTGT CCGTGTCGCC600
TTGGTGGGTC CCTCCAGGA ACCAAGGAGT GGCCCTCCAG GTGGCAGCAC TAAGGACACC660
CCCCACACAC AAGAGTTAGC AGCAGGTTCC CCATGAGTCC CACCCATGAC CTGCCGACAG720
TGTGGCCAC CGGAACTTTT GTGGCCCTTA CCGCTCAGCC CTTCCAGCA CTTCTCCAC780
TTTGTCCTCGA GCGTCCTTCT CGCCAGCAGG GGGCACAGGC CTGGCACCTC CCGCTTGT840
GTCTGAGCC ATAGTGACTC TTTTATCTGT GTGCTTTTG CTAAATATGC CTTTTTATA900
TTAATAAAAG ATGATTTGGA GTTGTGCTCT C

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931

(2) INFORMATION ON SEQ ID NO. 618:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 447 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

ELPSSPPFGL FEVAPDATST GLPDTAAPE TSTNYPVECT EGSAGPQSLP LPFILEPVKNP 60
 CSVKDQTPLO LSVEDTTSPN TKPCPTPTT PETWGGGGGG APSSTPCSAP LTPSSLFSS120
 LESSSEQKFY NFVILHARAD EHIALRVREK LEALGVDPGA TFCEDFQVPG RGELSCLQDA180
 IDHSAFIILL LTSNFDCLRL LHQVNQAMMS NLTRQGSPOC VIFFLPLESS PAQLSSOTAS240
 LLSGLVRLDE HSIQIFARKVA NTFKPHRLQA RKAMWRKEQD TRALREQSQH LDGERMQAAA300
 LNAAYSAYLO SYLSYQAQME QLQVAFGSHM SFGTGAZYGV RMPFGGQGPL GAPPFFPTWP360
 GCPQPPPLHA WQAGTPPPPS PQPAAFPQSL PFPQSPAFPT ASPAPPQSPG LQPLIIHHAQ420
 MVQLGLNNHM WNQRGSQAPE DKTQEAZ 447

(2) INFORMATION ON SEQ ID NO. 619:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 205 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

ADAGGGTTERS LLSLPPELIV LPGTDGAAPG GFWEHPHIWD WGA LWGQNAL WGPGAPGSPA 60
 TLSHLAGVPA AATPFARMAGW HPPTALPTAS SLSTVTALPA VPSLPYGLTR TPSEPRAAATP120
 HYPPTDGTGA GAEQPHVEPE RVPGARQDA GGRMTACPL TTWGTPLDPG IGQDPFIEHPG180
 LPCALWTVED EVICHFDIV REPFI 205

(2) INFORMATION ON SEQ ID NO. 620:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 409 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

KSRLSVTLMP VQLSEHPewn ESMHSLRISV GGLPVLASMT KAADPRFRFR WKVILTFEFG 60
 AAILWLLCSH RPAPGRPPTH NAHNWRLGQA PANWYNDTYP LSPFQRTFAG IRYRIAVIADI20
 LDTEPTAQDE NWRSDLKKG YLTLSDSGDK VAVEWDKDHG VLESHLAEGK RGMELSDLIV180
 FNGKLYSDDD RTGVVYQIEG SKAVPVVILS DGDGTVEKGF KAEWLAVKDE RLYVGGGLGKE240
 WTTTGDVVN ENPEVVKVVG YKGVVDHENW VSNYNALRAA AGIQPPANLI HESACWSDTL300
 QRWFFLPERR SQERYSEKDD ERKGANLLLS ASPDFGDIIV SHVGAVVPTH GFSSFKFIPN360
 TDDQIIVALK SEEDSGRVAS YIMAFITLOGR FLLPETKIGS VKYEGIEFI 409

(2) INFORMATION ON SEQ ID NO. 621:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 249 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

KLSPDGLAQC FRFELNELDA FVFHASDLGL RQGEAPVQRE GHVVGGSAA VLLGFEGHND 60
 LVVGVGDELE GREAVSGDHR PDVAHSDVAE VRGGAQQQVG ALALVVLLAV ALLAGAAQGE120
 EPALQRVTPA GRIMDEVSWR LDAGSSFGQV VVGHFVLVWH AALVAHHLHP LRVLVHHITR180
 SGRPFLAQAA HVQTLVLHQC PFGLAEFLHG AVAVGQNHFG HGFAAFDLVD DRRPVIHGE240
 FPIENNQVG 249

(2) INFORMATION ON SEQ ID NO. 622:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 255 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

AAAPVSLHDA AGDLRRDPGG GGGGGVPHGG GEGQEVVPRE PGVPAPQHA E PVAAGAAQQ 60
 LQTEEQPGLQ RLRLGPVRGA ARGGDARVRG PRGDRRVNPE SARALLPGDP QGPGTAAAPRA120
 LGLPFRCEPV GAFLAALALA RERRERGRFP RPCKCLFFNS SQCELCCECV RGGAPALSRR180
 RVATPCPCPM VCNDSFAHRS TVPPSAHPFT LPTLSLNTF IIVRGRWDF GRSAAATASG240
 GLIFIFALRW LKAFI 255

(2) INFORMATION ON SEQ ID NO. 623:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 196 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

INAFSHRNAK ININFPDAVA AALRPKSQRP RLTIKVFSE SVGVSVNGCA LGGTVERCAK 60
 SELQTIGQGH GVATRRRLSA GAPPRTHSQQ SSHWEEKLNK HLQGRGKRPR SRRSRARASAI20
 ARGAPTGSQR GGSPSARGAA VPGPCGSPGS RARALSGFTR RSPRGPRTRA SPPRAAPLTG180
 PSRSRWSPGC SSVCS 196

(2) INFORMATION ON SEQ ID NO. 624:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 242 amino acids
 (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

VESHRRANTH TTVRSPETAR GWKPWPHRLS RYVHSPGRQP HGHGQHLQFC SGRRAFGGHP 60
RQGARASLLA LGLENSPGGS SPEERLGLRL VAGPPRGAQN VSQAGPEAEA PPLRFGHAWG120
AQTPRLGAPG FWTPLPLTPS HIPFFWSQTP AQRKEGFTEE GQGRAWFPQGG DEDISGPGSCL80
RLLEEEPCV CKLLGLAARF TAGPSLDPCT WPSSCPLAAP GLGTGIEPRG LGWLQGRDR240
EG 242

(2) INFORMATION ON SEQ ID NO. 625:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 216 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

GLVMPGELRR PGLGPQAHGL PSPLCPPIFP LFGPRHQHKE RRGSRQKARA EPGPREGMRT 60
FPVQVAAGCS GRKSHASVNC GWWRPAPLQG PALTARGHP AALNLPLALA QASSLEGWAG120
WARAGTGRGS TSDPDVGNLC PPRREAQOTS YTKAKSTIGE PRSHFMGRAP RFGGPGSKAR180
GRFIPEDSPP GAAPAWGVSV RPLGCLSVCG TFWSTP 216

(2) INFORMATION ON SEQ ID NO. 626:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 299 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

PGISVSVDKM ESSPFNRRQW TSLSLRVTAKELSLVNKNKS SAIVEIFSKY QKAAEETNME 60
 KKRSNTENLS QHFRKGTLTV LKKKWENPGL GAESHTDLSL NSSTEIRHRA DHPPAEVTS120
 AASGAKADQE EQIHPRSLRL SPPEALVQGR YPHIKDGEDL KDHSTESKKM ENCLGESRHEL180
 VEKSEISENT DASGKIEKYN VPLNRLKMMF EKGEPTQTKI LRAQSRASAG RKISENSYSL240
 DDLEIGPGQL SSSTFDSEKN ESRRNLELPR LSETSIKDRM AKYQAAVSKQ SSSPTIPMS 299

(2) INFORMATION ON SEQ ID NO. 627:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

DSAPSPGFESH FFFNTVRVPF LKCWERFSVL LLFFSMFVSS AAFWYLENIS TIADDLFLT60
 RESSLAVTLN DSEVHCRLLN GDDSIILSTDT EIPG 94

(2) INFORMATION ON SEQ ID NO. 628:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 765 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

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IRPVVQLTAI EILAWGLRNM KNFQMASITS PSLVVECGGE RVESVVIKNL KKTNPFPSSV 60
LFMKVFLPKE ELYMPPLVIK VIDHRQFGRK PVVGQCTIER LDRFRCDPYA GKEDIVPQLK120
ASLLSAPPCR DIVIEMEDTK PLLASKLITEK EEEIVDWSK FDSASSEHEK CGQYIQKGS180
KLKIYNCELE NVAEFGELTD FSDTFKLYRG KSDENEDPSV VGEFKGSFRI YPLPDDPSVP240
APPRQFRELP DSVPQECTVR IYIVRGLELQ PQDNNGLCDP YIKITLGKKV IEDRDHYIPN300
TINPVFGRMY ELSCYLPQEK DLKISVYDYD TFRDEKVGGE TIIDLENRFL SRFGSHCGIP360
EEYCVSGVNT WRDQLRPTQL LQNVARFKGF PQPILSEDSG RIRYGGRDYS LDEFANKIL420
HQHLGAPEER LALHILRTQG LVPEHVETRT LHSTEQPNIS QGKLQMWVDV FPKSLGPPGP480
PFNITPRKAK KYLLRVIIWN TKDVIDEKS ITGEEMSDIY VKGWIPGNNE NKQKTDVHYR540
SLDGEENFNW RFVFPFDYLP AEQLCIVAKK EHFWSIDQTE FRIPPLLIQ IWDNDKFSLD600
DYLGFLELDL RHTIIPAKSF EKCRLDMIPD LKAMNPLKAK TASLFEQKSM KGWVPCYAEK660
DGARVMAGKV EMTLEILNEK EADERPAGKG RDEPNMNPKL DLNRPETSF LWFNTNCKTM720
KFIVWRREKW VIIGLLFLLI LLEFVAVLLY SLPNYLSMKI VKPNV 765

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(2) INFORMATION ON SEQ ID NO. 629:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 289 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

- (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

```

ETQVVIQRKL VIVFYLNDQP GWDKFRVLN TPEMLFFRND TELFGWKVVK RENKSPVKIP 60
FTIQRSMVDI CFLFVFFFIAR NPAFDVDVTH FLSCDAFLVQ DNVLGVPDDH TQVVFGLFPG120
CDVERRAWPW QTLGENIAPH LKFSLGNVGL EGAVQSPCFH VLRDQPLSPE DVKSPLFRG180
PEVLVQDFVG FKFIQAVVSS SISDSTPIFG KDGLWEAFES GOILKQLCNS QLISPGIDSR240
NTVLLWYAAV GPKAGKESVF QINNECFSYFF IPGEGVIIID RNFQVFFLR 289

```

(2) INFORMATION ON SEQ ID NO. 630:

- (i) SEQUENCE CHARACTERISTIC:
- (A) LENGTH: 824 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

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RVSVLAAASS ALFPVAPREAG VTNWPAAGCVP EVRSTGEKEV AKTLHRRSRP EWCGARDPPA 60
MLFLVLTCLL AVFFAISTKS PIFGPEEVNS VEGNSVSITC YYPPTSNNRH TRKYWCRQGA120
RGGCITLISS EGYVSSKYAG RANLTNFPEN GTFVFNIAQL SQDDSGRYKC GLGINSRGLS180
FDVSLVSSQG PGLLNDTKVY TVDLGRTVTI NCPFFTENAQ KRKSLYKQIG LYPVLVIDSS240
GYVNPNTYGR IRLDIQGTGQ RLFSVVINQL RLSDAGQYLC QAGDDSNSENK KNADLQVLKP300
EPELVYEDLR GSVTFHCALG PEVANVAKFL CROSSGENCD VVVNTLKGRA PAFEGRILLN360
PQDKDGSFSV VITGLRKEDA GRYLCAHSD GQLQEGSPIQ ANQLEVNNEES TIPASPTVVK420
GVAGGSAVL CPYNRKESKS IKYKWLWEGA QNGRCPLVD SEGWWKAQYE GRLSLLEEPG480
NGTFTVILNQ LTRSDAGFYW CLTNGDTLWR TTVEIKIEG EPNLKVPGNV TAVLGETLKV540
PCHFPCFESS YEKYWCWNWN TGCQALPQSD EGPSKAFYNC DENSRVLSLT LNLVTRADEG600
WYWCQGVKQH FYGETAAVYV AVEERKAAGS RDVSLAKADA APDEKVLDSG FREIENKAIQ660
DPRLFAEKA VADTRDQADG SRASVDSGSS EEQGGSSRAL VSTLVPLGLV LAVGAVAVGV720
ARARHRKNVD RVSIRSRYTD ISMSDFENS EFGANDNMGA SSITQETSLG GKEEFVATTE780
STTETKEPKK AKRSSKEEAE MAYKDFLLQS STVAAEAQCG PQEA 824

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(2) INFORMATION ON SEQ ID NO. 631:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 267 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

```

ADIAGPRCLP LFNCHIDGCS LSIEVALLHS TPVPALISPG HQVQGGQDKP AVLVTVHEGL 60
AGAFVLAQGG LAARVIPLAP VFLVRGEFAW KVTGDLESLS QHSRDIPWYL EVWFSEFNL0120
LHGQPPESIA VGQTPVEAGV PARGELVEDDS EGAVAWLLQQ GEALVVLGLN PPLAVHQQGA180
AAILGPFPEP PVLDAFAFLT VVGAEGHGRA SCHPLHSGA AGNRGLLIDE ELFGDORRAF240
LQLTRMGST QVAPCILLPQ ACDHHTT 267

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(2) INFORMATION ON SEQ ID NO. 632:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 140 amino acids

(B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

GETRVHSQQG GGIKAPSWDW FFREPGPLVK GLLGHVKQYL EQPRPWGYQV ERREGARLPC 60
THLPWWAGFS LLGSLPPSV HDTDPASPC PRPSYRLLFQ DITDNPERME KGGAWVPAVS120
GQKEVACGNL RSPHPRFPKR 140

(2) INFORMATION ON SEQ ID NO. 633:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 127 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

VFPCHLVGAG PTPATTSGTA KGSTRCDYPG PCWQLRIPGT CSDPVSQSSE SQEPRMRALC 60

SPSSKTQGSP PRKGAHVQR GWLPGCYLFY PTSAAESQGE TASHPKPLGF SREKNLSQKH120
DLFSGCK 127

(2) INFORMATION ON SEQ ID NO. 634:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 140 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

HHQKHMQKKG SYWASGLLSP WLGRKGREDG WGSFLGIDDV HEFGLEGSTT HKEATHIRLA 60
 GQLLAGCP SH RASINDTGAL SHRIRDVGLQ PSSELLVYFL GLLGCCSLAS TNGPHRLIGQ120
 DDLAPVLHVI CDDLLVWVEG 140

(2) INFORMATION ON SEQ ID NO. 635:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 101 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

KVIADNVKDW SKVVLAYEPV WAIGTGKTAT PQAQAEVHEK LRGLWLSNVS DAVAQSTRII 60
 YGGSVTGATC KELASQPDVD GFLVGGASLK PEFVDIINAK Q 101

(2) INFORMATION ON SEQ ID NO. 636:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 329 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

DSIFPLWAVL ALSPPGIRVR MKKSSVSGMT AAGVVWGEA EGKAALRLGV EFLEVWGGGR 60
 VFNLEKSQPA RAECECERGS SEGARNVGVG SGGRSVAVAL VHQHGVRLLG DLQQRVHVGA120
 APAPOVAGLP PLRAALVVVG AHLHHLGLE HFHLALADLL DVEGEGWHLV DRGLGARVHH180
 VVGREGFAQL VPRRLQFLAP LGGHQARAQL VHALLQGVPR LLQVFLGLEA RLQVLAGTH240
 LGLLHLLLE GLLEVHHAPO ALRLIRSARD SSITSTSTSTA SDESSSSAAA SSSGRSPSPS300
 SSPSFSGSAS DSFSDLLMLS LAGSFTSSW 329

(2) INFORMATION ON SEQ ID NO. 637:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 263 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

GRLPGYPDRR GPGASSAGAQ AAEEPSGAGS EELIKSDQVN GVLVLSLLDK IIGAVDQIQL 60
 TQAQLEERQA EMGAVQSIQ GELSKLGAH ATTSNTVSKL LEKVRKVSVN VKTVRGSRLER120
 QAGQIKKLEV NEAELLRRRN FKVMIYQDEV KLPKLSISK SLKESEALPE KEGEELGEGE180
 RPEEDAAALE LSSDEAVEVE EVIEESRAER IKRRACGAWT TSTRPSPRRR WRRPRCV240
 TWRRRASRPR KTWRRRGTPW RSA 263

(2) INFORMATION ON SEQ ID NO. 638:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 205 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

SGDLRLLVDT SKVQEAHVPS QDTHHTQELL AVQGSIVSGY RPPGGFGAAP VHEDPHLLGP 60
 ASRGAPETAA FFFFFFFF EQHLRVGLLL LPRLSPRPG PAWPVNPVPG WPGHLHQGGQ 120
 LLAGTNKPFH LAMVVVFMSD RGPETRAGR REHTSLGVGT SLXTPQQLKG PRXXFFXAVQ 180
 ASPXPGVCSL AWVELCHIXD KQXGG 205

(2) INFORMATION ON SEQ ID NO. 639:

- (i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 171 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

PVTPRDXPGA GGGXKEGPMQ HPGQSRPXPL AXPAEXWXLM APCGALTCWA RLXLGLSAFX 60
 LLIXDVTELD PSQAASHSWT ASLHCXGKCK PRAXKLLRGX EAGAHPQASV FSAPPCPRFRI20
 ASVHREHHHH GQVEGFISPC QQLSSLVQVA WPAHWIGDGF GWARSGAQSG R 171

(2) INFORMATION ON SEQ ID NO. 640:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 161 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

ISRNEGVLVR GPKSPRSLR SHSEPPALVL WRDRLVPGT DYCKDTALVP TEKNTGQEH 60
 TFSQYLATPH SELTITHGKW VHSSLWSDPA GLGRQEQHSS SSLSPRQRES LNCKRSGAYT120
 VREKEKGGRK GFSRPRPRDA HREGGKEREK SVLESEATLS K 161

(2) INFORMATION ON SEQ ID NO. 641:

(i) SEQUENCE CHARACTERISTIC:

- (A) LENGTH: 127 amino acids
- (B) TYPE: Protein
- (C) STRAND: individual
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

CAYRTEKWKs HTVPCSPVVK LVLTLALRAF SSMEPLGLGR KARVSAHRHT SYLQDIDCLC 60
RGSTGQPTAN TAASLVASL LPVHFGDYSW INLPKNSAFI MSLFCSKTQN GSLPPRGRPS120
HHCIPNR 127

(2) INFORMATION ON SEQ ID NO. 642:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 136 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

WGxGRVVRVxG WxRKPFMEKxGI PPEXHG?ITA DGHxRLxXLxP PxxGxRCxxAD PxxGxGLxALF 60
KxxPPxEXxCL LxxPPxxPVT HRAGMEFNGx FWxxTLVHGQ TSLLxGYxTR LxxKIVCCHS120
SGxWSVCGLH RFHRNQ 136

(2) INFORMATION ON SEQ ID NO. 643:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 132 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

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LSGLGLMGxR AGTCTWVAXE AHEDxDTPrV PWTxYxRWSS xPxAIATxGx SLxxGRFQRE120
XPxRVVxxXT TX 132

(2) INFORMATION ON SEQ ID NO. 644:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 131 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

GVETTANSST SLRSTTLEKE VPVIFIHPLN TGLFRIKIQG ATGKFNMVIP LVDGMIVSRR 60
 ALGELVRQTV INICRRKRLE SDSYSPFMSA GNRKSPTLST STGTSSWSQS FILHFSRRLD120
 SRTAVLRPLN F 131

(2) INFORMATION ON SEQ ID NO. 645:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 645:

LTNMSDHLFG WLLLEMAVVM FSGLCQPTDP CQVLEILLP RCYFSAGIKL LXVARPRTSK60
 DSCYSATVYT AHLSSYSHVLS SLVRLF 86

(2) INFORMATION ON SEQ ID NO. 646:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 96 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 646:

KAPNPSVLHT VRMQLIADRC CELYICKRCF TTSAGFITAS WSRVAILPAI PAKQTPENYP60
LRSGVLRRKFL EPKIRRNFL SFLASKMYQ LRPGEH 96

(2) INFORMATION ON SEQ ID NO. 647:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 92 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 647:

SSACRCTTRS TGOQSAASGR CGGPRGWGPS TGATPRLTM NIPFQSIHFI TYEFLQEQVN60
PHRTYNPQSH IISGGLAGAL AAAARGPLDV LR 92

(2) INFORMATION ON SEQ ID NO. 648:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 280 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 648:

AVGSAALFKD GGGGTSAAEA GAAGQRLRSV NCLAYDEAIM AQQDRIQKEI AVQNPLVSER 60
LELSVLYKEY AEDDNIYQK IKDLHKYSY IRKTRPDGNC FYRAFGFSL EALLDDSKEL120
QRFKAVSAKS KEDLVSGFT EFTIEDFHNT FMDLIEQVEK QTSVADLLAS FNDQSTSDYL180
VVYLRLLTSG YLQRESKFFE HFIEGGRTVK EFCQQEVEPM CKESDRIHII ALAQALSVS1240
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(2) INFORMATION ON SEQ ID NO. 649:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 244 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 649:

DHLQPQKNLC TCLAPGRGGQ QGSSGLEPAL FVEDIVVSRP VEKVDLGLGA LREDVRIGGA 60
 ALAAVHVHLH DGHAEGLGQR NDVDVVALLA HGLHLLLAEL LOSPSTLDEV LEELALALQV120
 ARGEQFPQVDH KVVGGALVIE GGQQVGDRGL LLHLLNQVHE RVVEILNCEF SEALGHQVFL180
 ALGRHSLEPL QLLAVIQQCL QVGESESPIE TVAVRPLGAD VRVLFVEVLD LLLIDVWIFS240
 ILLV 244

(2) INFORMATION ON SEQ ID NO. 650:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 424 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: ORF
- (iii) HYPOTHETICAL: yes
- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 650:

LTTCVSSSA PSKTS LIMNP HASTNGQLSV HTPKRESLSH EEPHSHPLY GHGVCCKWPGC 60
 EAVCEDFQSF LKHLNSEHAL DDRSTAQCRV QMQVVQLEL QLAQDKERLQ AMMTHLHVKS120
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 PIRRRYSOKY NVPISSADIA QNOEFYKNAE VRPPPTYASL IRQAILESPE KQLTLNEIYN240
 WFTRMFAYFR RNAATWKNVA RHNLSLHKCF VRVENVKGAV WTVDEVEFQK RRPQKISGNP300
 SLIKNQSSH AYCTPLNAAL QASMAENSIP LYTTASMGNP TLGNLASAIR EELNGAMEHT360
 NSNESOSSPG RSPMQAVHPV HVKEEPLDPE EAEGPLSLVT TANKSPDFDH DRDYEDPYN420
 EDME 424

(2) INFORMATION ON SEQ ID NO. 651:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 117 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 651:

STNAGCTAVR ATACKRQRAP ASHDDPPACE VYRTQSRPSA LESGIKCHSL QVRIGGFSTE 60
 LTSYSNDPNR PPSDRHPRPL CHHNHQHAHG GTHPQAVLRQ IQRAHFVSRY CAEPRIL 117

(2) INFORMATION ON SEQ ID NO. 652:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 426 amino acids
 (B) TYPE: Protein
 (C) STRAND: individual
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN
 (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 652:

PEAGLFGCSE QSDPFPHIFI MIHTNLKKKF SCCVLVLLF AVICVWKEKK KGSYYDSFKL 60

QTKEFQVLKS LGLKAMGSDS QSVSSSSTQD PHRGRTLGS LRGLAKAKPE ASFQVWNKDS120
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 QDVGTKTTR LMNSQLVTTT KRFKDSLNL EGIILVWDFS VYHSDIPKMY QNPDPYNFFNN300
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 FRTIHC 426

(2) INFORMATION ON SEQ ID NO. 653:

- (i) SEQUENCE CHARACTERISTIC:
 (A) LENGTH: 139 amino acids
 (B) TYPE: Protein

(C) STRAND: individual
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 653:

RCVQGSHEVL SRKTSLLAN PPGAAGPSGP QELALLSMGG KVVWVCRPRP IFLRMKTHL 60
CWEMVICAAG FGDAEVCRSI SGGDLAVLPF SLWCWLCGLC GTFCPLARCT LGRGGCGCSA120
RSVAAARSAP TPGVIGSLC 139

(2) INFORMATION ON SEQ ID NO. 654:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 243 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 654:

WRQLARGWGA LSRASCPALP RLANN TVRMA KGDPKKPKGK MSAYAFFVOT CREEHKKKNP 60
EVPVNFAEFS KKCSEKWKTM SGKEKSKFDE MAKADKVRID REMKDYGPAK GGKKKKDPNA120
PKRPPSGFFL FCSEFRPKIK STNPGISIGD VAKKLGEMWN NLNDSEKQPY ITKTAKLKEK180
YEKDVADYKS KGKFDGAKGP AKVARKKVEE EDEEDGGGGG GGGGGTYSRV GWWSSPKEGE240
RRN 243

(2) INFORMATION ON SEQ ID NO. 655:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 110 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 655:

TEQESRRWP FGSIRILLLL ASLSWSIILH FPIIAHFICL CHFIKFRFLF PGHRLPPLRA 60
LLGKFRKIDR DLWVFLLMFF SACLHKEGIS GHLALWFLGV TFSHPDCIVR 110

(2) INFORMATION ON SEQ ID NO. 656:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 356 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 656:

VGCSHAAQLH SAPELQTTRQ ELSHALYQHD AACRVIARLT KEVTAAREAL ATLPQAGLI 60
VPOAVPSSQP SVVGAGEPMD LGELVGMTPE IIQKLQDKAT VLTTERKKRG KTVPEELVKP120
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(2) INFORMATION ON SEQ ID NO. 657:

(i) SEQUENCE CHARACTERISTIC:

(A) LENGTH: 240 amino acids

(B) TYPE: Protein

(C) STRAND: individual

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

(vi) ORIGIN

(A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 657:

LAQIPELDRG VISRCSQVVT ILREGDASDG ARVAREVVGHI STFLQVPDLD LAVHGSCSKD 60
ESVRVELCTG ERAAGGLICH LGEHTPCLDV RESPVLIIGG AQEIVASGMK AEACHSTLMG120
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(2) INFORMATION ON SEQ ID NO. 658:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 658:

EHNSKSSPIN IKRAYLAKDT QIKESLWLRT QGREVPGLCP CWARRRLGTK WEKWEGLSG 60
RGHKSSGGQH CRQVMGGTHG DLAANSCCGG VSLVLPGGP LLGSRWGPTK GHRTGSPGWL120
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(2) INFORMATION ON SEQ ID NO. 659:

- (i) SEQUENCE CHARACTERISTIC:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: Protein
 - (C) STRAND: individual
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ORF

(iii) HYPOTHETICAL: yes

- (vi) ORIGIN
 - (A) ORGANISM: HUMAN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 659:

RLWTATHGLR AGDEATRPPG LPEHLHGPAV SHRGDQGRDF AYLCWQQRH GAPEERYHPC 60
PGPSQRVPGR DRAERFHV TG SASASASGPI RPLQSTRFSL AFIPSCNHP GLEVLCPVLG120
PLQEPASGPP GGSTKDTFPQ QELAARSF 148

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PCT/DE99/01258

Claims

1. A nucleic acid sequence that codes a gene product or a portion thereof, comprising

a) a nucleic acid sequence, selected from the group Seq. ID Nos. 1-88, 90-96, 98-120, 123-140, 142-144, and 597-617,

b) an allelic variation of the nucleic acid sequences named under a)

or

c) a nucleic acid sequence that is complementary to the nucleic acid sequences named under a) or b).

2. A nucleic acid sequence according to one of the sequences Seq. ID Nos. 1-157, 597-617, or a complementary or allelic variant thereof.

3. Nucleic acid sequence Seq. ID Nos. 1-157 and 597-617, characterized in that they are expressed elevated in pancreas tumor tissue.

4. BAC, PAC and cosmid clones containing functional genes and their chromosomal localization according to sequences Seq. ID Nos. 1-157 and 597-617 for use as vehicles for gene transfer.

5. A nucleic acid sequence according to claims 1 to 4, wherein it has 90% homology to a human nucleic acid sequence.

6. A nucleic acid sequence according to claims 1 to 4, wherein it has 95% homology to a human nucleic acid sequence.

7. A nucleic acid sequence comprising a portion of the nucleic acid sequences named in claims 1 to 6, in such a sufficient amount that they hybridize with the sequences according to claims 1 to 6.

8. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4500 bp.

9. A nucleic acid sequence according to claims 1 to 7, wherein the size of the fragment has a length of at least 50 to 4000 bp.

10. A nucleic acid sequence according to one of claims 1 to 9, which codes at least one partial sequence of a bioactive polypeptide.

11. An expression cassette, comprising a nucleic acid fragment or a sequence according to one of claims 1 to 9, together with at least one control or regulatory sequence.

12. An expression cassette, comprising a nucleic acid fragment or a sequence according to claim 11, in which the control or regulatory sequence is a suitable promoter.

13. An expression cassette according to one of claims 11 and 12, wherein the DNA sequences located on the cassette code a fusion protein, which comprises a known protein and a bioactive polypeptide fragment.

14. Use of nucleic acid sequences according to claims 1 to 10 for producing full-length genes.

15. A DNA fragment, comprising a gene, that can be obtained from the use according to claim 14.

16. Host cell, containing as the heterologous part of its expressible genetic information a nucleic acid fragment according to one of claims 1 to 10.

17. Host cell according to claim 16, wherein it is a prokaryotic or eukaryotic cell system.

18. Host cell according to one of claims 16 or 17, wherein the prokaryotic cell system is E. coli, and the eukaryotic cell system is an animal, human or yeast cell system.

19. A process for producing a polypeptide or a fragment, wherein the host cells according to claims 16 to 18 are cultivated.

20. An antibody that is directed against a polypeptide or a fragment that is coded by the nucleic acids of sequences Seq. ID Nos. 1-157 and 597-617, which can be obtained according to claim 19.

21. An antibody according to claim 20, wherein it is monoclonal.

22. An antibody according to claim 20, wherein it is a phage display antibody.

23. Polypeptide partial sequences according to sequences Seq. ID Nos. 158-596 and 618-659.

24. Polypeptide partial sequences according to claim 23, with at least 80% homology to these sequences.

25. A polypeptide that is known from a phage display and that can bind to the polypeptide partial sequences according to claim 23.

26. Polypeptide partial sequences according to claim 23, with at least 90% homology to these sequences.

27. Use of polypeptide partial sequences according to sequences Seq. ID Nos. 158-596 and 618-659 as tools for finding active ingredients against the pancreas tumor.

28. Use of nucleic acid sequences according to sequences Seq. ID Nos. 1-157 and 597-617 for expression of polypeptides that can be used as tools for finding active ingredients against the pancreas tumor.

29. Use of nucleic acid sequences Seq. ID Nos. 1-157 and 597-617 in sense or antisense form.

30. Use of polypeptide partial sequences Seq. ID Nos. 158-596 and 618-659 as pharmaceutical agents in gene therapy for treatment of the pancreas tumor.

31. Use of polypeptide partial sequences Seq. ID Nos. 158-596 and 618-659 for the production of a pharmaceutical agent for treatment of the pancreas tumor.

32. Pharmaceutical agent, containing at least one polypeptide partial sequence Seq. ID Nos. 158-596 and 618-659.

33. A nucleic acid sequence according to claims 1 to 10, wherein it is a genomic sequence.

34. A nucleic acid sequence according to claims 1 to 10, wherein it is an mRNA sequence.

35. Genomic genes, their promoters, enhancers, silencers, exon structure, intron structure and their splice variants, that can be obtained from cDNAs of sequences Seq. ID Nos. 1-157 and 597-617.

36. Use of the genomic genes according to claim 33, together with suitable regulatory elements.

37. Use according to claim 36, wherein the regulatory element is a suitable promoter and/or enhancer.

38. A nucleic acid sequence according to claims 1 to 7,
wherein the size of the fragment has a length of at least 300 to
3500 bp.

09/674266

526 Rec'd PCT/PTO 30 OCT 2000

Sequence Listing

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<400> 22

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<213> homo sapiens

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<211> 1021

<212> DNA

<213> homo sapiens

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 <212> DNA
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 <211> 286
 <212> DNA
 <213> homo sapiens

<400> 26

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 <212> DNA

<213> homo sapiens

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<211> 548

<212> DNA

<213> homo sapiens

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<211> 493

<212> DNA

<213> homo sapiens

<400> 29

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<210> 30

<211> 1063

<212> DNA

<213> homo sapiens

<400> 30

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<210> 31

<211> 472

<212> DNA

<213> homo sapiens

<400> 31

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<210> 32

<211> 2568

<212> DNA

<213> homo sapiens

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<211> 1106

<212> DNA

<213> homo sapiens

<400> 46

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<211> 1370

<212> DNA

<213> homo sapiens

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<212> DNA

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<212> DNA

<213> homo sapiens

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<211> 1398

<212> DNA

<213> homo sapiens

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<400> 52

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<212> DNA

<213> homo sapiens

<400> 57

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<211> 1510

<212> DNA

<213> homo sapiens

<400> 58

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<210> 59

<211> 1188

<212> DNA

<213> homo sapiens

<400> 59

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1188

<210> 60

<211> 2208

<212> DNA

<213> homo sapiens

<400> 60

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<210> 61

<211> 283

<212> DNA

<213> homo sapiens

<400> 61

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gtactccgga gaacctggct ggagagctct ttctgttcca ccttccctc cagctgtat 180
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gggcatttgg tactggcgaag actgcaaac aac 283
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<210> 62

<211> 184

<212> DNA

<213> homo sapiens

<400> 62

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<211> 1780

<212> DNA

<213> homo sapiens

<400> 63

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<212> DNA

<213> homo sapiens

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<212> DNA
<213> homo sapiens

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<400> 65

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<400> 66

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<212> DNA
<213> homo sapiens

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<211> 426
<212> DNA
<213> homo sapiens

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<400> 70
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<210> 71
<211> 1417
<212> DNA
<213> homo sapiens

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<400> 71
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<400> 72

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 <212> DNA
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<400> 75

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<211> 2513

<212> DNA

<213> homo sapiens

<400> 76

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<210> 77
 <211> 1962
 <212> DNA
 <213> homo sapiens

<400> 77

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 <211> 788
 <212> DNA
 <213> homo sapiens

<400> 78

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 <212> DNA
 <213> homo sapiens

<400> 80

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 <212> DNA
 <213> homo sapiens

<400> 81

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1284

<210> 82

<211> 1335

<212> DNA

<213> homo sapiens

<400> 82

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<213> homo sapiens

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<213> homo sapiens

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<212> DNA

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<210> 92

<211> 1111

<212> DNA

<213> homo sapiens

<400> 92

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<210> 93

<211> 657

<212> DNA

<213> homo sapiens

<400> 93

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<210> 94

<211> 863

<212> DNA

<213> homo sapiens

<400> 94

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<210> 95

<211> 1015

<212> DNA

<213> homo sapiens

<400> 95

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<210> 96

<211> 2532

<212> DNA

<213> homo sapiens

<400> 96

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<210> 100
 <211> 757
 <212> DNA
 <213> homo sapiens

<400> 100

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<210> 101
 <211> 1262
 <212> DNA
 <213> homo sapiens

<400> 101

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<210> 102
 <211> 1281
 <212> DNA
 <213> homo sapiens

<400> 102

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<210> 105

<211> 1040

<212> DNA

<213> homo sapiens

<400> 105

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<210> 106

<211> 1336

<212> DNA

<213> homo sapiens

<400> 106

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<210> 107
 <211> 812
 <212> DNA
 <213> homo sapiens

<400> 107

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<210> 108
 <211> 2681
 <212> DNA
 <213> homo sapiens

<400> 108

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<211> 1407

<212> DNA

<213> homo sapiens

<400> 109

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<210> 110

<211> 1376

<212> DNA

<213> homo sapiens

<400> 110

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<210> 111

<211> 854

<212> DNA

<213> homo sapiens

<400> 111

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<210> 112

<211> 1681

<212> DNA

<213> homo sapiens

<400> 112

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<210> 113
<211> 852
<212> DNA
<213> homo sapiens

<400> 113

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<211> 1739
<212> DNA
<213> homo sapiens

<400> 114

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 <212> DNA
 <213> homo sapiens

<400> 115

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<210> 116
 <211> 1483
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<400> 116

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<210> 117

<211> 1347
 <212> DNA
 <213> homo sapiens

<400> 117

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 <212> DNA
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<400> 118

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<210> 119

<211> 1355

<212> DNA

<213> homo sapiens

<400> 119

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<210> 120

<211> 1816

<212> DNA

<213> homo sapiens

<400> 120

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<210> 125

<211> 250

<212> DNA

<213> homo sapiens

<400> 125

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<210> 126

<211> 1202

<212> DNA

<213> homo sapiens

<400> 126

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<210> 127

<211> 1014

<212> DNA

<213> homo sapiens

<400> 127

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<210> 128

<211> 1171

<212> DNA

<213> homo sapiens

<400> 128

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<210> 129

<211> 353

<212> DNA

<213> homo sapiens

<400> 129

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<210> 130

<211> 205

<212> DNA

<213> homo sapiens

<400> 130

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<211> 211
<212> DNA
<213> homo sapiens

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<400> 131
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211

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<210> 132
<211> 867
<212> DNA
<213> homo sapiens

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<400> 132
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<211> 257
<212> DNA
<213> homo sapiens

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<400> 133
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257

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<210> 134
<211> 204
<212> DNA
<213> homo sapiens

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<400> 134
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<210> 135

<211> 245

<212> DNA

<213> homo sapiens

<400> 135

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cccatcttccc ttgttaatca gaggaaattct gtttcaagat tatgtgtgtg tgtgatctgt180
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<210> 136

<211> 1637

<212> DNA

<213> homo sapiens

<400> 136

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tctattttta tcacaatgac ctttagagag gtctcccagg ccagctcaag gtgtcccact 180
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1637

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<210> 137

<211> 260

<212> DNA

<213> homo sapiens

<400> 137

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tacagacgac aagagatca ggtagaattc aacatatggt gcttgaagtg ggctcttgg180
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260

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<210> 138
 <211> 957
 <212> DNA
 <213> homo sapiens

<400> 138

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tgacttccag ctcatatatt ttgaagattt tcaaggagtg ggagaatctg aacctaatcc180
tacttctctt cagaattctg gagaggcaga atatgtagta gcacttttta tgtacatgtg240
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<210> 139
 <211> 760
 <212> DNA
 <213> homo sapiens

<400> 139

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aatcagcagt tgttcttcaa gttcctgaaa gctataaaag tttctcatga cttgagtggt180
tttttccctg ccaccagag gagaaagccc ttgtagaatt ctgcagtggt acaagtgttc240
cctacaaaaa ctgaaacctat cagctctctt ttaacaagtt ggctttttaa aagcacgtga300
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gacttatatt ctccaaaact ttgaaagaaa aatgtgttct ttttgcgtga tctttgttaa420
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acaaagatga gaacaaatca tgggttttag aaaggatcct tagaagaaca caagaatttg540
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aataaaactg agtaagtaat gaaaaaaaaa aaaaaaaaaa

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760

<210> 140
 <211> 280
 <212> DNA
 <213> homo sapiens

<400> 140

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tgctgtcttc cctaaagtga aatgttgatt cctgtcaaac acacagccta gccctgattc180
ctcctcttct ctcaagcagt gatattgtca acaatgataa acaactacta tgtactgagt240
gtttttttat gtgctgtctca cactttatca acatgtatag

```

280

<210> 141
 <400> 141
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<210> 142
 <211> 461
 <212> DNA
 <213> homo sapiens

<400> 142

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cacaagaagc  cttatcctac  gtccctctct  ccatctatcg  gaccccgagt  tccatcacta  180
ctccagagaa  tgtagctatt  atgcgcccgt  ctacaggggg  tgcccagaca  tgacggtgcc  240
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gcgtggcagc  ccattccaag  cccttccggg  ctggaactcg  tgctggagga  gcctcggtgt  360
tatctacgc  cctgggtttg  gtgttcctc  actcctctga  gctcttctt  ctgatcaagg  420
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<210> 143
 <211> 436
 <212> DNA
 <213> homo sapiens

<400> 143

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aaatgtaaaa  gtattttttc  ctttaagaaa  gataaaaagg  taagcctaaa  ccttgccggc  180
caccgaagtc  agctgttacg  catgtgtagt  taaatttcac  tgtaaatatt  ctataagggt  240
tcttgaatg  gagccaggtt  gacatcacag  ccccaactgt  accaaaggaa  ccatttcatt  300
caaatagacc  aacatttcca  aagaacacgc  aatgtctatg  gcagagtgaa  cataagggtc  360
gaaaatcttc  tggagaagaa  ttcggtatca  atgtttataa  tctctgcatt  taggggtttg  420
ccagttttgg  aaaaaa                                     436
```

<210> 144
 <211> 287
 <212> DNA
 <213> homo sapiens

<400> 144

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gttcagaaaa  gtcaactgtg  cctgagtaga  gtcaaggaga  aggagcagca  agagtgagct  180
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gggattttaa  gtgagaggac  aaccgttggt  atgttgtgag  cacagaa                                     287
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<210> 145
 <211> 555
 <212> DNA
 <213> homo sapiens

<400> 145

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tgacgtgggt  gatccctcac  atcaagaagg  agagccccc  cctcaatgat  tacccgggct  360
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cctcgcggtg  ctggtt                                     555
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<210> 146
 <211> 1790
 <212> DNA
 <213> homo sapiens

<400> 146

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atactgtgga tggtagggaa gaaaagtctg cttctgattc ttctggaaaa cagtctactc 600
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<210> 147
 <211> 2357
 <212> DNA
 <213> homo sapiens

<400> 147

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<210> 148
 <211> 907
 <212> DNA
 <213> homo sapiens

<400> 148

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<210> 149
 <211> 1987
 <212> DNA
 <213> homo sapiens

<400> 149

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cagcaacacc	atccagtcca	tcatggccat	tgtcaaaagcc	atgggcaacc	tgcagatcga 180
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tgtgtctacgg	accgcgttaa	agacacgggg	gatcgtggag	acacacttca	ccttcaagga 480
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Val 65	Gly	Ala	Val	Leu	Ser 70	Val	Ser	Ser	Val	Pro 75	Ala	Lys	Gln	Cys	Pro 80
Pro	Leu	Cys	Thr	Arg 85	Phe	Leu	Pro	Glu	Phe 90	Ala	Gly	Thr	Gln	Leu 95	Lys
Ile	Leu	Arg	Phe 100	Leu	Val	Pro	Leu	Glu 105	Gln	Ser	Pro	Val	Leu 110	Glu	Gln
Ser	Thr	Leu 115	Gln	His	Asn	Asn	Gln 120	Thr	Arg	Val	Gln	Thr 125	Cys	Gln	Asn
Lys	Ala 130	Gln	Val	Arg	Ser	Thr 135	Arg	Pro	Gln	Pro	Ser 140	Gln	Val	Gly	Ser
Ser 145	Arg	Gly	Gln	Lys	Asn 150	Leu	Lys	Ser	Tyr	Phe 155	Gln	Pro	Ser	Pro	Ser 160

Cys	Pro	Gln	Ala	Ser 165	Pro	Asp	Ile	Glu	Leu 170	Pro	Ser	Leu	Pro	Leu 175	Met
Ser	Ala	Leu	Met 180	Thr	Pro	Lys	Thr	Pro 185	Glu	Glu	Lys	Ala	Val 190	Ala	Lys
Val	Val	Lys 195	Gly	Gln	Ala	Lys	Thr 200	Ser	Glu	Ala	Lys	Asp 205	Glu	Lys	Glu
Leu	Arg 210	Thr	Ser	Phe	Trp	Lys 215	Ser	Val	Leu	Ala	Gly 220	Pro	Leu	Arg	Thr
Pro 225	Leu	Cys	Gly	Gly	His 230	Arg	Glu	Pro	Cys	Val 235	Met	Arg	Thr	Val	Lys 240
Lys	Pro	Gly	Pro	Asn 245	Leu	Gly	Arg	Arg	Phe 250	Tyr	Met	Cys	Ala	Arg 255	Pro
Arg	Gly	Pro	Pro 260	Thr	Asp	Pro	Ser	Ser 265	Arg	Cys	Asn	Ser	Ser 270	Ser	Gly
Ala	Gly	Pro 275	Ala	Glu	Pro	Met	Glu 280	Ala	Trp	Gly	His	Leu 285	Ala	Trp	Ser
Pro	Leu 290	His	Met	Ile											

<210> 159

<211> 131

<212> PRT

<213> homo sapiens

<400> 159

Glu 1	Thr	Leu	Arg	Glu 5	Lys	Gln	Glu	Ala	Ala 10	Gln	Gly	Arg	Gly	Ala 15	Gly
Leu	Arg	Ser	Cys 20	Ala	Gly	Val	Thr	Met 25	Pro	Asp	Val	Pro	Arg 30	Pro	Pro
Leu	Val	Gln 35	Leu	Gly	Leu	Leu	Gln 40	Arg	Lys	Asn	Cys	Thr 45	Gly	Arg	Arg
Gly	Gln 50	Trp	Glu	Asp	Pro	Gly 55	Ala	Trp	His	Thr	Cys 60	Arg	Ser	Gly	Gly
Pro 65	Ser	Trp	Val	Leu	Ala 70	Ser	Ser	Gln	Tyr	Ala 75	Ser	His	Met	Ala	Pro 80
Cys	Gly	Pro	His 85	Gly	Val	Cys	Ala	Arg 90	Ala	Pro	Pro	Ala	Gln 95	Thr	
Ser	Arg	Met	Arg 100	Ser	Val	Thr	Pro	Ser 105	His	Leu	Trp	Leu	Leu 110	Lys	Ser
Trp	Pro	Ala 115	Pro	Ser	Pro	Leu	Trp 120	Pro	Leu	Pro	Ser	Leu 125	Leu	Glu	Ser
Ser	Gly 130	Ser													

<210> 160

<211> 94
 <212> PRT
 <213> homo sapiens

<400> 160

Lys 1	Arg	Arg	Pro	Lys 5	Leu	Gly	Pro	Gly	Phe 10	Phe	Thr	Val	Arg	Ile 15	Thr
His	Gly	Ser	Leu 20	Trp	Pro	Pro	Gln	Arg 25	Gly	Val	Arg	Lys	Gly 30	Pro	Ala
Ser	Thr	Asp 35	Phe	Gln	Asn	Glu	Val 40	Arg	Asn	Ser	Phe	Ser 45	Ser	Leu	Ala
Ser	Glu 50	Val	Leu	Ala	Cys	Pro 55	Phe	Thr	Thr	Leu	Ala 60	Thr	Ala	Phe	Ser
Ser 65	Gly	Val	Phe	Gly	Val 70	Met	Arg	Ala	Leu	Ile 75	Ser	Gly	Arg	Leu	Gly 80
Ser	Ser	Met	Ser	Gly 85	Glu	Ala	Trp	Gly	Gln 90	Leu	Gly	Glu	Gly		

<210> 161
 <211> 136
 <212> PRT
 <213> homo sapiens

<400> 161

Leu 1	His	Gln	Leu	Ala 5	Ala	Gln	Arg	Leu	Tyr 10	Leu	Arg	Pro	Val	Arg 15	Val
Gly	Ala	Trp	Ala 20	Leu	Ser	Leu	Pro	Gly 25	Glu	Arg	Arg	Ala	Glu 30	Ile	Ser
Asn	Gln	Trp 35	Ser	Ala	Leu	Val	Thr 40	Trp	Ile	Pro	Glu	Gly 45	Arg	Glu	Gly
Ser	Thr 50	Val	Ser	Ser	Ala	Ala 55	Asp	Cys	Cys	Ser	Lys 60	Asn	Val	Phe	Ser
Thr 65	Ser	Phe	Glu	Ser	Pro 70	Ser	His	Gly	Asn	Pro 75	Ser	Thr	Pro	Thr	Arg 80
Asp	Pro	Thr	Pro	Ala 85	Val	Ser	Arg	Ile	Ser 90	Ser	Thr	Cys	Thr	Ser 95	Arg
Asp	Pro	Asn	Asp 100	Ser	Cys	Thr	Asn	Glu 105	His	Tyr	Gly	Ser	Cys 110	Ser	Asn
Cys	Leu	Ser 115	Thr	His	Cys	Val	Tyr 120	Gly	Trp	Lys	Ala	Phe 125	Gly	Arg	Lys
Lys	Gly 130	Ser	Ser	Arg	Leu	Lys 135	Gly								

<210> 162
 <211> 281
 <212> PRT
 <213> homo sapiens

<400> 162

Pro 1	Gly	Ser	Gln	Lys 5	Val	Ala	Lys	Ala	Val 10	Pro	Phe	Pro	Gln	Arg 15	Arg
Thr	Ala	Ala	Val 20	Arg	Met	Ser	Phe	Pro 25	Pro	His	Leu	Asn	Arg 30	Pro	Pro
Met	Gly	Ile 35	Pro	Ala	Leu	Pro	Pro 40	Gly	Ile	Pro	Pro	Pro 45	Gln	Phe	Pro
Gly	Phe 50	Pro	Pro	Pro	Val	Pro 55	Pro	Gly	Thr	Pro	Met	Ile	Pro	Val	Pro
Met 65	Ser	Ile	Met	Ala	Pro 70	Ala	Pro	Thr	Val	Leu 75	Val	Pro	Thr	Val	Ser 80
Met	Val	Gly	Lys	His 85	Leu	Gly	Ala	Arg	Lys 90	Asp	His	Pro	Gly	Leu 95	Lys
Ala	Lys	Glu	Asn 100	Asp	Glu	Asn	Cys	Gly 105	Pro	Thr	Thr	Thr	Val 110	Phe	Val
Gly	Asn	Ile 115	Ser	Glu	Lys	Ala	Ser 120	Asp	Met	Leu	Ile	Arg 125	Gln	Leu	Leu
Ala	Lys 130	Cys	Gly	Leu	Val	Leu 135	Ser	Trp	Lys	Arg	Val 140	Gln	Gly	Ala	Ser
Gly 145	Lys	Leu	Gln	Ala	Phe 150	Gly	Phe	Cys	Glu	Tyr 155	Lys	Glu	Pro	Glu	Ser 160
Thr	Leu	Arg	Ala	Leu 165	Arg	Leu	Leu	His	Asp 170	Leu	Gln	Ile	Gly	Glu 175	Lys
Lys	Leu	Leu	Val 180	Lys	Val	Asp	Ala	Lys 185	Thr	Lys	Ala	Gln	Leu 190	Asp	Glu
Trp	Lys	Ala 195	Lys	Lys	Lys	Ala	Ser 200	Asn	Gly	Asn	Ala	Arg 205	Pro	Glu	Thr
Val	Thr 210	Asn	Asp	Asp	Glu	Glu 215	Ala	Leu	Asp	Glu	Glu 220	Thr	Lys	Arg	Arg
Asp 225	Gln	Met	Ile	Lys	Gly 230	Ala	Ile	Glu	Val	Leu 235	Ile	Arg	Glu	Tyr	Ser 240
Ser	Glu	Leu	Asn	Ala 245	Pro	Ser	Gln	Glu	Ser 250	Asp	Ser	His	Pro	Gln 255	Glu
Glu	Glu	Glu	Gly 260	Lys	Glu	Gly	Gly	His 265	Phe	Pro	Gln	Ile	Ser 270	Ser	Gly
Pro	Thr	Asp 275	Pro	Leu	Ser	Thr	His 280	His							

<210> 163

<211> 103

<212> PRT

<213> homo sapiens

<400> 163

Cys 1	Ser	Leu	Val	Gln 5	Glu	Ser	Leu	Gly	Ser 10	Leu	Glu	Val	Gln	Val 15	Glu
Glu	Ile	Leu	Glu 20	Thr	Ala	Gly	Val	Gly 25	Ser	Leu	Val	Gly	Val 30	Leu	Gly
Phe	Pro	Trp 35	Glu	Gly	Asp	Ser	Asn 40	Glu	Val	Glu	Lys	Thr 45	Phe	Leu	Leu
Gln	Gln 50	Ser	Ala	Ala	Glu	Glu 55	Thr	Val	Leu	Pro	Ser 60	Arg	Pro	Ser	Gly
Ile 65	Gln	Val	Thr	Ser	Ala 70	Leu	His	Trp	Phe	Glu 75	Ile	Ser	Ala	Arg	Arg 80
Ser	Pro	Gly	Arg	Leu 85	Ser	Ala	Gln	Ala	Pro 90	Thr	Arg	Thr	Gly	Arg 95	Lys
Tyr	Ser	Arg	Cys 100	Ala	Ala	Ser									

<210> 164

<211> 127

<212> PRT

<213> homo sapiens

<400> 164

Asn 1	Ile	Ser	Leu	Leu 5	Asp	His	Pro	Gly	Leu 10	Gln	Ser	Cys	Leu	Tyr 15	Phe
Leu	Phe	Trp	Ile 20	Leu	Phe	Thr	Asn	Arg 25	Glu	Arg	Tyr	Ile	Ser 30	Ala	Trp
Lys	Trp	Pro 35	Asp	Val	Trp	Lys	Leu 40	Asp	Ile	Trp	His	Phe 45	Gly	Leu	His
Ser	His 50	Gly	Tyr	Tyr	Ser	His 55	Asn	Lys	Asp	Gly	Ser 60	Gly	Asn	Ser	Phe
Leu 65	Asp	Leu	Asp	Gln	Pro 70	Ser	Arg	Tyr	Leu	Gly 75	Ile	Tyr	Tyr	Ile	Leu 80
Phe	Cys	Ile	Phe	Leu 85	Val	Leu	Trp	Arg	Asp 90	Ser	Leu	Ala	Ile	Phe 95	Gly
Leu	Pro	Glu	Tyr 100	Val	Phe	Cys	Val	Tyr 105	Ser	Ala	Pro	Val	Lys 110	Trp	Phe
Cys	Leu	Val 115	Cys	His	Asn	Pro	His 120	Gly	Cys	Tyr	Met	Ser 125	Ile	Ser	

<210> 165

<211> 382

<212> PRT

<213> homo sapiens

<400> 165

His 1	Glu	Val	Leu	Cys 5	Cys	Arg	Met	Ala	Pro 10	Leu	Gln	Lys	Ala	Lys 15	Val
Ile	Arg	Leu	Ile	Lys	Ile	Ser	Pro	Glu	Lys	Pro	Ile	Thr	Leu	Ala	Val

20							25					30				
Gly	Asp	Gly 35	Ala	Asn	Asp	Val	Ser 40	Met	Ile	Gln	Glu	Ala 45	His	Val	Gly	
Ile	Gly 50	Ile	Met	Gly	Lys	Glu 55	Gly	Arg	Gln	Ala	Ala 60	Arg	Asn	Ser	Asp	
Tyr 65	Ala	Ile	Ala	Arg	Phe 70	Lys	Phe	Leu	Ser	Lys 75	Leu	Leu	Phe	Val	His 80	
Gly	His	Phe	Tyr	Tyr 85	Ile	Arg	Ile	Ala	Thr 90	Leu	Val	Gln	Tyr	Phe 95	Phe	
Tyr	Lys	Asn	Val 100	Cys	Phe	Ile	Thr	Pro 105	Gln	Phe	Leu	Tyr	Gln 110	Phe	Tyr	
Cys	Leu	Phe 115	Ser	Gln	Gln	Thr	Leu 120	Tyr	Asp	Ser	Val	Tyr 125	Leu	Thr	Leu	
Tyr	Asn 130	Ile	Cys	Phe	Thr	Ser 135	Leu	Pro	Ile	Leu	Ile 140	Tyr	Ser	Leu	Leu	
Glu 145	Gln	His	Val	Asp	Pro 150	His	Val	Leu	Gln	Asn 155	Lys	Pro	Thr	Leu	Tyr 160	
Arg	Asp	Ile	Ser	Lys 165	Asn	Arg	Leu	Leu	Ser 170	Ile	Lys	Thr	Phe	Leu 175	Tyr	
Trp	Thr	Ile	Leu 180	Gly	Phe	Ser	His	Ala 185	Phe	Ile	Phe	Phe	Phe 190	Gly	Ser	
Tyr	Leu	Leu 195	Ile	Gly	Lys	Asp	Thr 200	Ser	Leu	Leu	Gly	Asn 205	Gly	Gln	Met	
Phe	Gly 210	Asn	Trp	Thr	Phe	Gly 215	Thr	Leu	Val	Phe	Thr 220	Val	Met	Val	Ile	
Thr 225	Val	Thr	Ile	Lys	Met 230	Ala	Leu	Glu	Thr	His 235	Phe	Trp	Thr	Trp	Ile 240	
Asn	His	Leu	Val	Thr 245	Trp	Gly	Ser	Ile	Ile 250	Phe	Tyr	Phe	Val	Phe 255	Ser	
Leu	Phe	Tyr	Gly 260	Gly	Ile	Leu	Trp	Pro 265	Phe	Leu	Gly	Ser	Gln 270	Asn	Met	
Tyr	Phe	Val 275	Phe	Ile	Gln	Leu	Leu 280	Ser	Ser	Gly	Ser	Ala 285	Trp	Phe	Ala	
Ile	Ile 290	Leu	Met	Val	Val	Thr 295	Cys	Leu	Phe	Leu	Asp 300	Ile	Ile	Lys	Lys	
Val 305	Phe	Asp	Arg	His	Leu 310	His	Pro	Thr	Ser	Thr 315	Glu	Lys	Ala	Gln	Met 320	
Tyr	Ser	Asn	Thr	Val 325	Ala	Leu	Ser	Asp	Glu 330	Phe	Ile	Ala	Leu	Gln 335	Pro	
Leu	Ser	Arg	Ala 340	Arg	Asn	Gln	Leu	Ser 345	Lys	Leu	Ser	Leu	Leu 350	Lys	Gln	
Met	Gln	Val	Ser	Ser	Ala	Trp	Thr	Pro	Cys	Ala	Val	Ser	Arg	Lys	Glu	

Pro 145	Gly	Glu	Gln	Pro	Val 150	Asp	Leu	Asn	Leu	Pro 155	Leu	Glu	Ala	Pro	Pro 160
Ile	Ser	Lys	Val	Arg 165	Val	His	Ile	Gln	Gly 170	Ala	Gln	Val	Glu	Ser 175	Gln
Glu	Val	Thr	Ile 180	His	Ser	Ile	Val	Thr 185	Pro	Glu	Phe	Val	Asp 190	Leu	Ser
Val	Pro	Arg 195	Thr	Phe	Ser	Thr	Gln 200	Ile	Val	Arg	Glu	Ser 205	Glu	Ile	Pro
Thr	Ser 210	Glu	Ile	Gln	Thr	Pro 215	Ser	Tyr	Gly	Phe	Ser 220	Leu	Leu	Lys	Val
Lys 225	Ile	Pro	Glu	Pro	His 230	Thr	Gln	Ala	Arg	Val 235	Tyr	Thr	Thr	Met	Thr 240
Gln	His	Ser	Arg	Thr 245	Gln	Glu	Gly	Thr	Glu 250	Glu	Ala	Pro	Ile	Gln 255	Ala
Thr	Pro	Gly	Val 260	Asp	Ser	Ile	Ser	Gly 265	Asp	Leu	Gln	Pro	Asp 270	Thr	Gly
Glu	Pro	Phe 275	Glu	Met	Ile	Ser	Ser 280	Ser	Val	Asn	Val	Leu 285	Gly	Gln	Gln
Thr	Leu 290	Thr	Phe	Glu	Val	Pro 295	Ser	Gly	His	Gln	Leu 300	Ala	Asp	Ser	Cys
Ser 305	Asp	Glu	Glu	Pro	Ala 310	Glu	Ile	Leu	Glu	Phe 315	Pro	Pro	Asp	Asp	Ser 320
Gln	Glu	Ala	Thr	Thr 325	Pro	Leu	Ala	Asp	Glu 330	Gly	Arg	Ala	Pro	Lys 335	Asp
Lys	Pro	Glu	Ser 340	Lys	Lys	Ser	Gly	Leu 345	Leu	Trp	Phe	Trp	Leu 350	Pro	Asn
Ile	Gly	Phe 355	Ser	Ser	Ser	Val	Asp 360	Glu	Thr	Gly	Val	Asp 365	Ser	Lys	Asn
Asp	Val 370	Gln	Arg	Ser	Ala	Pro 375	Ile	Gln	Thr	Gln	Pro 380	Glu	Ala	Arg	Pro
Glu 385	Ala	Glu	Leu	Pro	Lys 390	Lys	Gln	Glu	Lys	Ala 395	Gly	Trp	Phe	Arg	Phe 400
Pro	Lys	Leu	Gly	Phe 405	Ser	Ser	Ser	Pro	Thr 410	Lys	Lys	Ser	Lys	Ser 415	Thr
Glu	Asp	Gly	Ala 420	Glu	Leu	Glu	Glu	Gln 425	Lys	Leu	Gln	Glu	Glu 430	Thr	Ile
Thr	Phe	Phe 435	Asp	Ala	Arg	Glu	Ser 440	Phe	Ser	Pro	Glu	Glu 445	Lys	Glu	Glu
Gly	Glu 450	Leu	Ile	Gly	Pro	Val 455	Gly	Thr	Gly	Leu	Asp 460	Ser	Arg	Val	Met
Val 465	Thr	Ser	Ala	Ala	Arg 470	Thr	Glu	Leu	Ile	Leu 475	Pro	Glu	Gln	Asp	Arg 480

Lys Ala Asp Asp Glu Ser Lys Gly Ser Gly Leu Gly Pro Asn Glu Gly
485 490 495

<210> 168
<211> 125
<212> PRT
<213> homo sapiens

<400> 168

Ser	Leu	Pro	Ala	Ser	Met	Tyr	Trp	Asp	Ser	Lys	His	Ser	His	Leu	Lys
1				5					10					15	
Phe	Leu	Leu	Ala	Thr	Ser	Leu	Gln	Thr	Ala	Val	Gln	Met	Arg	Ser	Gln
			20					25					30		
Gln	Lys	Phe	Leu	Ser	Phe	Pro	Leu	Met	Ile	Ala	Lys	Arg	Gln	Pro	His
		35					40					45			
His	Trp	Gln	Met	Lys	Ala	Gly	Leu	Gln	Lys	Thr	Asn	Gln	Lys	Val	Lys
	50					55					60				
Asn	Leu	Val	Cys	Ser	Gly	Phe	Gly	Phe	Gln	Thr	Leu	Gly	Phe	Pro	Leu
65					70					75					80
Leu	Leu	Met	Arg	Gln	Val	Leu	Ile	Pro	Lys	Met	Thr	Ser	Arg	Asp	Leu
				85					90					95	
Leu	Pro	Phe	Lys	His	Ser	Leu	Arg	His	Asp	Gln	Arg	Gln	Asn	Cys	Leu
			100					105					110		
Lys	Asn	Arg	Arg	Arg	Gln	Ala	Gly	Ser	Asp	Phe	Pro	Asn			
		115					120					125			

<210> 169
<211> 130
<212> PRT
<213> homo sapiens

<400> 169

Met	Gly	Ala	Asp	Leu	Trp	Thr	Ser	Phe	Leu	Glu	Ser	Thr	Pro	Val	Ser
1				5					10					15	
Ser	Thr	Glu	Glu	Glu	Asn	Pro	Met	Phe	Gly	Ser	Gln	Asn	Gln	Ser	Arg
			20					25					30		
Pro	Asp	Phe	Leu	Leu	Ser	Gly	Leu	Ser	Phe	Gly	Ala	Leu	Pro	Ser	Ser
		35					40					45			
Ala	Ser	Gly	Val	Val	Ala	Ser	Trp	Leu	Ser	Ser	Gly	Gly	Asn	Ser	Arg
	50					55					60				
Ile	Ser	Ala	Gly	Ser	Ser	Ser	Glu	Gln	Leu	Ser	Ala	Ser	Trp	Trp	Pro
65					70				75						80
Glu	Gly	Thr	Ser	Asn	Val	Ser	Val	Cys	Cys	Pro	Ser	Thr	Leu	Thr	Leu
				85					90					95	
Glu	Glu	Ile	Ile	Ser	Asn	Gly	Ser	Pro	Val	Ser	Gly	Trp	Arg	Ser	Pro
			100					105					110		

Glu	Met	Glu	Ser	Thr	Pro	Gly	Val	Ala	Cys	Met	Gly	Ala	Ser	Ser	Val
		115					120					125			

Pro	Ser
	130

<210> 170
 <211> 123
 <212> PRT
 <213> homo sapiens

<400> 170

Val	Val	Tyr	Arg	Gly	Val	Lys	Cys	Phe	Ile	Asp	Lys	Lys	Lys	Lys	Thr
1				5					10					15	
Ala	Leu	Glu	Pro	Thr	Tyr	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser
			20					25					30		
Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser
		35					40					45			
Ser	Ser	Ser	Ser	Phe	Phe	Phe	Leu	Leu	Phe	Ser	Ala	Leu	Thr	Thr	Pro
		50				55					60				
Phe	Phe	Ala	Ala	Ser	Gly	Phe	Pro	Leu	Ala	Arg	Tyr	Ala	Ala	Ile	Ser
65					70					75				80	
Phe	Ser	Tyr	Phe	Ser	Phe	Thr	Ser	Gln	Pro	Ser	Phe	His	Lys	Ala	Ala
				85					90					95	
Cys	His	Leu	Gln	Gln	Cys	Tyr	Ser	Thr	Ser	Leu	Pro	Val	Ser	Ser	Gln
			100					105					110		
His	His	Gln	Trp	Thr	Gly	Gln	Asp	Val	Leu	Leu					
		115					120								

<210> 171
 <211> 157
 <212> PRT
 <213> homo sapiens

<400> 171

Lys	Lys	Leu	Tyr	Leu	Leu	Arg	Ser	Ile	Gln	Asn	Val	Asn	Lys	Thr	Ala
1				5					10					15	
Ala	Ile	Phe	Phe	Leu	Gln	Leu	Gln	Ser	Gly	Ile	Gln	Leu	Thr	Glu	Gln
			20					25					30		
Gln	Leu	Ser	Ser	Tyr	Lys	Leu	His	Gln	Arg	Gln	Leu	Lys	Met	Lys	Lys
		35					40					45			
Ile	Lys	Pro	Lys	Lys	Lys	Thr	Lys	Arg	Lys	Lys	Lys	Lys	Lys	Gln	Lys
	50					55					60				
Thr	Lys	Leu	Pro	Ser	Pro	Tyr	Ile	Thr	Asn	Leu	Cys	Cys	Ala	Pro	Thr
65					70					75				80	
Arg	Thr	Cys	Phe	Lys	Phe	Pro	Cys	Gln	Phe	Thr	Thr	Pro	Ile	Leu	Tyr
				85					90					95	
Gln	Ala	Arg	Leu	Val	Ala	Ile	Glu	Asn	Thr	Thr	Arg	Thr	Gly	Leu	Ser

100							105					110				
Lys	Asp	Thr	Phe	Gly	Ser	Val	Leu	Thr	Ile	Gln	Lys	Lys	Thr	Leu	Tyr	
		115					120					125				
Ser	Leu	Lys	Thr	Asn	Leu	Thr	Gln	Pro	Tyr	Ile	Ser	Ile	Phe	Phe	Phe	
	130					135					140					
Lys	Arg	Ser	Glu	Leu	Cys	Thr	Gly	Gly	Leu	Asn	Ala	Leu				
145					150					155						

<210> 172
 <211> 152
 <212> PRT
 <213> homo sapiens

<400> 172

Leu	Asn	Met	Gly	Lys	Gly	Asp	Pro	Lys	Lys	Pro	Arg	Gly	Lys	Met	Ser
1				5					10					15	
Ser	Tyr	Ala	Phe	Val	Gln	Thr	Cys	Arg	Glu	Glu	His	Lys	Lys	Lys	
			20				25					30			
His	Pro	Asp	Ala	Ser	Val	Asn	Phe	Ser	Glu	Phe	Ser	Lys	Lys	Cys	Ser
		35					40					45			
Glu	Arg	Trp	Lys	Thr	Met	Ser	Ala	Lys	Glu	Lys	Gly	Lys	Phe	Glu	Asp
	50					55					60				
Met	Ala	Lys	Ala	Asp	Lys	Ala	Arg	Tyr	Glu	Arg	Glu	Met	Lys	Thr	Tyr
65					70					75					80
Ile	Pro	Pro	Lys	Gly	Glu	Thr	Lys	Lys	Lys	Phe	Lys	Asp	Pro	Asn	Ala
				85					90					95	
Pro	Lys	Arg	Pro	Pro	Ser	Ala	Phe	Phe	Leu	Phe	Cys	Ser	Glu	Tyr	Arg
			100					105					110		
Pro	Lys	Ile	Lys	Gly	Glu	His	Pro	Gly	Leu	Ser	Ile	Gly	Asp	Val	Ala
		115					120					125			
Lys	Lys	Leu	Gly	Glu	Met	Trp	Asn	Asn	Thr	Ala	Ala	Asp	Asp	Lys	Gln
	130					135					140				
Pro	Tyr	Glu	Lys	Lys	Ala	Ala	Lys								
145					150										

<210> 173
 <211> 281
 <212> PRT
 <213> homo sapiens

<400> 173

Ser	Gly	Ser	Ala	Gly	Pro	Gly	Pro	Arg	Gly	Pro	Arg	Ala	Thr	Glu	Ser
1				5					10					15	
Gly	Lys	Arg	Met	Asp	Cys	Pro	Ala	Leu	Pro	Pro	Gly	Trp	Lys	Lys	Glu
			20					25				30			
Glu	Val	Ile	Arg	Lys	Ser	Gly	Leu	Ser	Ala	Gly	Lys	Ser	Asp	Val	Tyr
		35					40					45			

Tyr	Phe 50	Ser	Pro	Ser	Gly	Lys 55	Lys	Phe	Arg	Ser	Lys 60	Pro	Gln	Leu	Ala
Arg 65	Tyr	Leu	Gly	Asn	Thr 70	Val	Asp	Leu	Ser	Ser 75	Phe	Asp	Phe	Arg	Thr 80
Gly	Lys	Met	Met	Pro 85	Ser	Lys	Leu	Gln	Lys 90	Asn	Lys	Gln	Arg	Leu 95	Arg
Asn	Asp	Pro	Leu 100	Asn	Gln	Asn	Lys	Gly 105	Lys	Pro	Asp	Leu	Asn 110	Thr	Thr
Leu	Pro	Ile 115	Arg	Gln	Thr	Ala	Ser 120	Ile	Phe	Lys	Gln	Pro 125	Val	Thr	Lys
Val	Thr 130	Asn	His	Pro	Ser	Asn 135	Lys	Val	Lys	Ser	Asp 140	Pro	Gln	Arg	Met
Asn 145	Glu	Gln	Pro	Arg	Gln 150	Leu	Phe	Trp	Glu	Lys 155	Arg	Leu	Gln	Gly	Leu 160
Ser	Ala	Ser	Asp	Val 165	Thr	Glu	Gln	Ile	Ile 170	Lys	Thr	Met	Glu	Leu 175	Pro
Lys	Gly	Leu	Gln 180	Gly	Val	Gly	Pro	Gly 185	Ser	Asn	Asp	Glu	Thr 190	Leu	Leu
Ser	Ala	Val 195	Ala	Ser	Ala	Leu	His 200	Thr	Ser	Ser	Ala	Pro 205	Ile	Thr	Gly
Gln	Val 210	Ser	Ala	Ala	Val	Glu 215	Lys	Asn	Pro	Ala	Val 220	Trp	Leu	Asn	Thr
Ser 225	Gln	Pro	Leu	Cys 230	Lys	Ala	Phe	Ile	Val	Thr 235	Asp	Glu	Asp	Ile	Arg 240
Lys	Gln	Glu	Glu	Arg 245	Val	Gln	Gln	Val	Arg 250	Lys	Lys	Leu	Glu	Glu 255	Ala
Leu	Met	Ala	Asp 260	Ile	Leu	Ser	Arg	Ala 265	Ala	Asp	Thr	Glu	Glu 270	Met	Asp
Ile	Glu	Met 275	Asp	Ser	Gly	Asp	Glu 280	Ala							

<210> 174

<211> 102

<212> PRT

<213> homo sapiens

<400> 174

Ile 1	Ile	Asp	Ile	Tyr 5	Ile	Lys	Asn	Thr	Ser 10	Lys	Lys	Ala	Leu	Val 15	Ser
Ala	Ile	Lys	Lys 20	Leu	Tyr	Val	Leu	Gly 25	Tyr	Ile	Phe	Phe	Leu 30	Thr	Gly
Lys	Ser	Gln 35	Trp	Lys	His	Phe	Cys 40	Ser	Ile	Ser	Arg	Asn 45	Phe	Leu	Leu
Gly	Lys	Val	Gly	Arg	Lys	Leu	Pro	Asp	His	Ile	Leu	Arg	Leu	His	Leu

	50					55					60					
His	Cys	Pro	Phe	Gln	Tyr	Pro	Ser	Leu	Leu	Tyr	Gln	Gln	Leu	Ala	Thr	
65					70					75					80	
Arg	Cys	Leu	Pro	Ser	Val	Leu	Leu	Pro	Ile	Ser	Cys	Val	Leu	Ala	Val	
				85					90					95		
Leu	Ala	Leu	Pro	Val	Ser											
			100													

<210> 175
 <211> 147
 <212> PRT
 <213> homo sapiens

Ile	Tyr	Thr	Ser	Lys	Ile	His	Leu	Lys	Arg	His	Trp	Leu	Val	Leu	Leu	
1				5					10					15		
Lys	Ser	Ser	Met	Cys	Ser	Gly	Thr	Phe	Phe	Phe	Leu	Gln	Ala	Lys	Ala	
			20					25					30			
Ser	Gly	Asn	Ile	Phe	Val	Gln	Phe	Leu	Gly	Ile	Phe	Ser	Trp	Gly	Lys	
		35					40					45				
Ser	Val	Glu	Ser	Tyr	Leu	Ile	Ile	Phe	Leu	Gly	Phe	Ile	Ser	Thr	Val	
		50				55					60					
His	Phe	Asn	Ile	His	Leu	Phe	Cys	Ile	Ser	Ser	Ser	Arg	Gln	Asp	Val	
65					70					75					80	
Cys	His	Gln	Cys	Phe	Phe	Gln	Phe	Leu	Ala	Tyr	Leu	Leu	Tyr	Ser	Leu	
				85					90					95		
Phe	Leu	Phe	Pro	Asp	Val	Phe	Ile	Cys	Asp	Asn	Lys	Ser	Phe	Ala	Glu	
			100					105					110			
Gly	Leu	Arg	Cys	Val	Lys	Pro	Asn	Ser	Arg	Val	Leu	Phe	His	Ser	Ser	
		115					120					125				
Gly	Asp	Leu	Pro	Cys	Asp	Trp	Arg	Arg	Ala	Cys	Val	Gln	Ser	Thr	Gly	
	130					135					140					
Asn	Ser	Arg														
145																

<210> 176
 <211> 85
 <212> PRT
 <213> homo sapiens

Glu	Cys	Pro	Leu	Gly	Ala	Arg	Gly	Pro	Trp	Glu	Pro	Arg	His	Pro	Phe	
1				5					10					15		
Pro	Leu	Gly	Arg	Gly	Ala	Arg	Ser	Arg	His	Pro	Cys	Thr	His	Gly	Arg	
			20					25					30			
Leu	Ala	Pro	Pro	Gln	Ser	Pro	Pro	His	Ser	Gln	Gln	Pro	Phe	His	Ser	
		35					40					45				

His	Cys	Pro	Ser	Arg	Ser	Pro	Gln	Pro	Ser	Leu	Arg	Pro	His	Pro	His
	50					55					60				
Pro	Leu	Arg	Ala	Gln	Gly	Cys	Asn	Pro	Ser	Leu	Ser	Thr	Thr	His	Arg
65					70					75					80
Trp	Tyr	Ser	Trp	Gly											
				85											

<210> 177
 <211> 128
 <212> PRT
 <213> homo sapiens

<400> 177

Asn	Ala	Leu	Trp	Gly	Pro	Gly	Ala	Pro	Gly	Ser	Pro	Ala	Thr	Leu	Ser
1				5					10					15	
His	Leu	Ala	Gly	Val	Pro	Ala	Ala	Ala	Thr	Pro	Ala	Arg	Met	Ala	Gly
			20					25					30		
Trp	His	Pro	Pro	Arg	Ala	Leu	Pro	Thr	Ala	Ser	Ser	Leu	Ser	Thr	Val
		35					40					45			
Thr	Ala	Leu	Pro	Ala	Val	Pro	Ser	Leu	Pro	Tyr	Gly	Leu	Thr	Arg	Thr
	50					55					60				
Pro	Ser	Glu	Pro	Arg	Ala	Ala	Thr	Pro	His	Tyr	Pro	Pro	Arg	Thr	Asp
65					70					75					80
Gly	Thr	Ala	Gly	Ala	Glu	Gln	Pro	His	Val	Glu	Pro	Glu	Arg	Val	Pro
				85					90					95	
Gly	Ala	Arg	Gly	Gln	Asp	Ala	Gly	Gly	Arg	Met	Thr	Ala	Cys	Pro	Cys
			100					105					110		
Leu	Thr	Ser	Trp	Gly	Thr	Thr	Leu	Asp	Arg	Gly	Ile	Gly	Gln	Asp	Pro
		115					120					125			

<210> 178
 <211> 106
 <212> PRT
 <213> homo sapiens

<400> 178

Met	Pro	Phe	Gly	Gly	Gln	Gly	Pro	Leu	Gly	Ala	Pro	Pro	Pro	Phe	Pro
1				5					10					15	
Thr	Trp	Pro	Gly	Cys	Pro	Gln	Pro	Pro	Pro	Leu	His	Ala	Trp	Gln	Ala
			20					25					30		
Gly	Thr	Pro	Pro	Glu	Pro	Ser	Pro	Gln	Pro	Ala	Ala	Phe	Pro	Gln	Ser
		35					40					45			
Leu	Pro	Phe	Pro	Gln	Ser	Pro	Ala	Phe	Pro	Thr	Ala	Ser	Pro	Ala	Pro
	50					55					60				
Pro	Gln	Ser	Pro	Gly	Leu	Gln	Pro	Leu	Ile	Ile	His	His	Ala	Gln	Met
65					70					75					80

Val	Gln	Leu	Gly	Leu 85	Asn	Asn	His	Met	Trp 90	Asn	Gln	Arg	Gly	Ser 95	Gln
Ala	Pro	Glu	Asp 100	Lys	Thr	Gln	Glu	Ala 105	Glu						

<210> 179
 <211> 77
 <212> PRT
 <213> homo sapiens

<400> 179

Gly 1	Asn	Pro	Glu	Leu 5	Pro	Trp	Arg	Lys	Phe 10	Gln	Cys	Gln	His	Ser 15	Cys
Ser	Leu	Trp	Pro 20	Ser	Pro	Thr	Leu	Trp 25	Pro	Glu	Ile	Pro	Gln 30	Ser	Asn
Leu	Glu	Pro 35	Lys	Arg	Thr	Gln	Arg 40	Thr	Leu	Asp	Pro	Asn 45	Cys	Pro	Arg
Pro	Ser 50	Pro	Glu	Val	Gly	Val 55	Thr	Asn	Ser	Ser	Gly 60	Leu	Arg	His	Met
Lys 65	Lys	Leu	Tyr	Ile	Asn 70	Pro	Arg	Gln	Ala	Thr 75	Asn	Pro			

<210> 180
 <211> 64
 <212> PRT
 <213> homo sapiens

<400> 180

Pro 1	Pro	Thr	His	Thr 5	Arg	Gln	Val	Gly	Glu 10	Glu	Ile	Gln	Ser	Cys 15	His
Gly	Glu	Asn	Ser 20	Ser	Val	Ser	Ile	Leu 25	Ala	Pro	Cys	Gly	Pro 30	Leu	Leu
His	Ser	Gly 35	Gln	Arg	Tyr	His	Ser 40	Gln	Thr	Trp	Ser	Gln 45	Lys	Gly	His
Lys	Gly 50	Leu	Ser	Thr	Gln	Thr 55	Ala	Pro	Asp	Pro	Leu 60	Gln	Arg	Leu	Gly

<210> 181
 <211> 206
 <212> PRT
 <213> homo sapiens

<400> 181

Arg 1	Leu	Ser	Cys	Ala 5	Gly	Thr	Leu	Ser	Gly 10	Ser	Gly	Pro	His	Pro 15	Ser
Arg	Arg	Leu	Thr 20	Gln	Gly	Arg	Trp	Val 25	Arg	Lys	Ser	Arg	Val 30	Ala	Met
Glu	Lys	Ile 35	Pro	Val	Ser	Ala	Phe 40	Leu	Leu	Leu	Val	Ala 45	Leu	Ser	Tyr

Thr	Leu 50	Ala	Arg	Asp	Thr	Thr 55	Val	Lys	Pro	Gly	Ala 60	Lys	Lys	Asp	Thr
Lys 65	Asp	Ser	Arg	Pro	Lys 70	Leu	Pro	Gln	Thr	Leu 75	Ser	Arg	Gly	Trp	Gly 80
Asp	Gln	Leu	Ile	Trp 85	Thr	Gln	Thr	Tyr	Glu 90	Glu	Ala	Leu	Tyr	Lys 95	Ser
Lys	Thr	Ser	Asn 100	Lys	Pro	Leu	Met	Ile 105	Ile	His	His	Leu	Asp 110	Glu	Cys
Pro	His	Ser 115	Gln	Ala	Leu	Lys	Lys 120	Val	Phe	Ala	Glu	Asn 125	Lys	Glu	Ile
Gln	Lys 130	Leu	Ala	Glu	Gln	Phe 135	Val	Leu	Leu	Asn	Leu 140	Val	Tyr	Glu	Thr
Thr 145	Asp	Lys	His	Leu	Ser 150	Pro	Asp	Gly	Gln	Tyr 155	Val	Pro	Arg	Ile	Met 160
Phe	Val	Asp	Pro	Ser 165	Leu	Thr	Val	Arg	Ala 170	Asp	Ile	Thr	Gly	Arg 175	Tyr
Ser	Asn	Arg	Leu 180	Tyr	Ala	Tyr	Glu	Pro 185	Ala	Asp	Thr	Ala	Leu 190	Leu	Leu
Asp	Asn	Met 195	Lys	Lys	Ala	Leu	Lys 200	Leu	Leu	Lys	Thr	Glu 205	Leu		

<210> 182

<211> 206

<212> PRT

<213> homo sapiens

<400> 182

Arg 1	Val	Phe	Gln	Glu 5	Glu	Glu	Leu	Val	Arg 10	Arg	Gln	Arg	Asn	Gly 15	Ala
Ser	Gly	Pro	Arg 20	Pro	Gly	Leu	Arg	Arg 25	Leu	Arg	Gly	Gly	Arg 30	Arg	Ala
Val	Arg	Arg 35	Lys	Glu	Arg	Leu	Leu 40	His	Arg	Gln	Leu	Pro 45	Ala	Val	His
Lys	Arg 50	Gly	Ala	Arg	Val	Lys 55	Leu	Ser	Ser	Pro	Glu 60	Arg	Asp	Val	Glu
Arg 65	Asp	Val	Phe	Leu	Tyr 70	Arg	Ala	Tyr	Leu	Ala 75	Gln	Arg	Lys	Phe	Gly 80
Val	Val	Leu	Asp	Glu 85	Ile	Lys	Pro	Ser	Ser 90	Ala	Pro	Glu	Leu	Gln 95	Ala
Val	Arg	Met	Phe 100	Ala	Asp	Tyr	Leu	Ala 105	His	Glu	Ser	Arg	Arg 110	Asp	Ser
Ile	Val	Ala 115	Glu	Leu	Asp	Arg	Glu 120	Met	Ser	Arg	Ser	Val 125	Asp	Val	Thr
Asn	Thr 130	Thr	Phe	Leu	Leu	Met 135	Ala	Ala	Ser	Ile	Tyr 140	Leu	His	Asp	Gln

Asn 145	Pro	Asp	Ala	Ala	Leu 150	Arg	Ala	Leu	His	Gln 155	Gly	Asp	Ser	Leu	Glu 160
Cys	Thr	Ala	Met	Thr 165	Val	Gln	Ile	Leu	Leu 170	Lys	Leu	Asp	Arg	Leu 175	Asp
Leu	Ala	Arg	Lys 180	Glu	Leu	Lys	Arg	Met 185	Gln	Asp	Leu	Asp	Glu 190	Asp	Ala
Thr	Leu	Thr 195	Gln	Leu	Lys	Val	Leu 200	Val	Ser	Leu	Gln	Arg 205	Val		

<210> 183
 <211> 111
 <212> PRT
 <213> homo sapiens

<400> 183

Leu 1	Pro	Arg	Pro	Arg 5	Glu	Ser	Glu	Gly	Gln 10	His	Arg	Gly	Arg	Ala 15	Gly
Pro	Arg	Asp	Glu 20	Gln	Glu	Arg	Gly	Arg 25	Asp	Gln	His	His	Leu 30	Pro	Ala
His	Gly	Arg 35	Leu	His	Leu	Ser	Pro 40	Arg	Pro	Glu	Pro	Gly 45	Cys	Arg	Pro
Ala	Cys 50	Ala	Ala	Pro	Gly	Gly 55	Gln	Pro	Gly	Val	His 60	Ser	His	Asp	Ser
Ala 65	Asp	Pro	Ala	Glu	Ala 70	Gly	Pro	Pro	Gly	Pro 75	Arg	Pro	Glu	Gly	Ala 80
Glu	Glu	Asn	Ala	Gly 85	Pro	Gly	Arg	Gly	Cys 90	His	Pro	His	Pro	Ala 95	Gln
Gly	Leu	Gly	Lys 100	Leu	Ala	Thr	Gly	Val 105	Lys	Ala	Gln	Gly	Ser 110	Phe	

<210> 184
 <211> 165
 <212> PRT
 <213> homo sapiens

<400> 184

Gly 1	Thr	Ile	Leu	Pro 5	Ile	Pro	Glu	Ile	Arg 10	Arg	Ile	Leu	Glu	Leu 15	Leu
His	Pro	Leu	Gln 20	Ala	Tyr	Gln	Asp	Leu 25	Glu	Leu	Gly	Glu	Gly 30	Gly	Ile
Leu	Val	Gln 35	Val	Leu	His	Ser	Leu 40	Gln	Leu	Leu	Pro	Gly 45	Glu	Val	Gln
Ala	Val 50	Gln	Leu	Gln	Gln	Asp 55	Leu	His	Cys	His	Gly 60	Cys	Ala	Leu	Gln
Ala 65	Val	Pro	Leu	Val	Gln 70	Arg	Thr	Gln	Gly	Gly 75	Ile	Arg	Val	Leu	Val 80

Val	Glu	Ile	Asp	Gly 85	Gly	Gly	His	Glu	Gln 90	Glu	Gly	Gly	Val	Gly 95	His
Val	His	Ala	Pro 100	Ala	His	Leu	Ser	Val 105	Gln	Leu	Gly	His	Asp 110	Ala	Val
Pro	Pro	Thr 115	Leu	Val	Gly	Glu	Val 120	Val	Ser	Lys	His	Ala 125	His	Gly	Leu
Glu	Leu 130	Arg	Gly	Arg	Gly	Gly 135	Leu	Asp	Leu	Ile	Gln 140	Asp	His	Thr	Glu
Leu 145	Pro	Leu	Arg	Gln	Val 150	Arg	Ser	Ile	Gln	Glu 155	Asp	Val	Pro	Leu	His 160
Val	Ser	Leu	Trp	Ala 165											

<210> 185
 <211> 75
 <212> PRT
 <213> homo sapiens

<400> 185

Leu 1	Leu	Ser	Met	Arg 5	Met	Ile	Leu	Lys	Pro 10	Gln	Ser	Phe	Met	Ile 15	Leu
Met	Met	Leu	Arg 20	Ser	Ser	Asn	Arg	Val 25	Thr	Trp	Lys	Leu	Leu 30	Leu	Ile
Gly	Leu	Asp 35	Tyr	Ile	Arg	Tyr	Gln 40	Met	Glu	Asn	Gln	Lys 45	Thr	Ser	Leu
Leu	Leu 50	Met	Glu	Asn	Ser	Lys 55	Thr	Arg	Leu	Leu	Leu 60	Leu	Lys	Leu	Leu
Asn 65	Pro	Leu	Ile	Asn	Val 70	Gly	Lys	His	Cys	Leu 75					

<210> 186
 <211> 340
 <212> PRT
 <213> homo sapiens

<400> 186

Arg 1	Thr	Val	Ile	Asp 5	Ala	Met	Ser	Ala	Leu 10	Leu	Arg	Leu	Leu	Arg 15	Thr
Gly	Ala	Pro	Ala 20	Ala	Ala	Cys	Leu	Arg 25	Leu	Gly	Thr	Ser	Ala 30	Gly	Thr
Gly	Ser	Arg 35	Arg	Ala	Met	Ala	Leu 40	Tyr	His	Thr	Glu	Glu 45	Arg	Gly	Gln
Pro	Cys 50	Ser	Gln	Asn	Tyr	Arg 55	Leu	Phe	Phe	Lys	Asn 60	Val	Thr	Gly	His
Tyr 65	Ile	Ser	Pro	Phe	His 70	Asp	Ile	Pro	Leu	Lys 75	Val	Asn	Ser	Lys	Glu 80
Glu	Asn	Gly	Ile	Pro	Met	Lys	Lys	Ala	Arg	Asn	Asp	Glu	Tyr	Glu	Asn

85								90					95				
Leu	Phe	Asn	Met 100	Ile	Val	Glu	Ile	Pro 105	Arg	Trp	Thr	Asn	Ala 110	Lys	Met		
Glu	Ile	Ala 115	Thr	Lys	Glu	Pro	Met 120	Asn	Pro	Ile	Lys	Gln 125	Tyr	Val	Lys		
Asp	Gly 130	Lys	Leu	Arg	Tyr	Val 135	Ala	Asn	Ile	Phe	Pro 140	Tyr	Lys	Gly	Tyr		
Ile 145	Trp	Asn	Tyr	Gly	Thr 150	Leu	Pro	Gln	Thr	Trp 155	Glu	Asp	Pro	His	Glu 160		
Lys	Asp	Lys	Ser	Thr 165	Asn	Cys	Phe	Gly	Asp 170	Asn	Asp	Pro	Ile	Asp 175	Val		
Cys	Glu	Ile	Gly 180	Ser	Lys	Ile	Leu	Ser 185	Cys	Gly	Glu	Val	Ile 190	His	Val		
Lys	Ile	Leu 195	Gly	Ile	Leu	Ala	Leu 200	Ile	Asp	Glu	Gly	Glu 205	Thr	Asp	Trp		
Lys	Leu 210	Ile	Ala	Ile	Asn	Ala 215	Asn	Asp	Pro	Glu	Ala 220	Ser	Lys	Phe	His		
Asp 225	Ile	Asp	Asp	Val	Lys 230	Lys	Phe	Lys	Pro	Gly 235	Tyr	Leu	Glu	Ala	Thr 240		
Leu	Asn	Trp	Phe	Arg 245	Leu	Tyr	Lys	Val	Pro 250	Asp	Gly	Lys	Pro	Glu 255	Asn		
Gln	Phe	Ala	Phe 260	Asn	Gly	Glu	Phe	Lys 265	Asn	Lys	Ala	Phe	Ala 270	Leu	Glu		
Val	Ile	Lys 275	Ser	Thr	His	Gln	Cys 280	Trp	Lys	Ala	Leu	Leu 285	Met	Lys	Lys		
Cys	Asn 290	Gly	Gly	Ala	Ile	Asn 295	Cys	Thr	Asn	Val	Gln 300	Ile	Ser	Asp	Ser		
Pro 305	Phe	Arg	Cys	Thr	Gln 310	Glu	Glu	Ala	Arg	Ser 315	Leu	Val	Glu	Ser	Val 320		
Ser	Ser	Ser	Pro	Asn 325	Lys	Glu	Ser	Asn	Glu 330	Glu	Glu	Gln	Val	Trp 335	His		
Phe	Leu	Gly	Lys 340														

<210> 187

<211> 131

<212> PRT

<213> homo sapiens

<400> 187

Leu 1	Ser	Ile	Leu	Tyr 5	Ile	Leu	Phe	Asn	Gly 10	Ile	His	Trp	Leu	Leu 15	Gly
Gly	Asn	Leu	His 20	Phe	Ser	Ile	Cys	Pro 25	Pro	Arg	Tyr	Phe	Tyr 30	Asn	His

Ile	Lys	Gln 35	Ile	Leu	Ile	Phe	Ile 40	Ile	Ser	Cys	Phe	Leu 45	His	Arg	Asn	
Ala	Ile 50	Phe	Leu	Phe	Arg	Val 55	His	Leu	Gln	Arg	Asn 60	Ile	Met	Lys	Gly	
Gly 65	Asn	Val	Val	Thr	Ser 70	Tyr	Ile	Leu	Lys	Glu 75	Glu	Ala	Val	Ile	Leu 80	
Arg	Ala	Gly	Leu	Ala 85	Ala	Leu	Leu	Ser	Val 90	Val	Gln	Gly	His	Ser 95	Thr	
Ala	Arg	Pro	Gly 100	Pro	Cys	Thr	Gly	Pro 105	Gln	Pro	Gln	Ala	Arg 110	Ser	Gly	
Trp	Gly	Thr 115	Arg	Ala	Gln	Gln	Pro 120	Gln	Gln	Arg	Ala	His 125	Gly	Val	Asn	
Asp	Gly 130	Pro														
<210> 188																
<211> 436																
<212> PRT																
<213> homo sapiens																
<400> 188																
Gly 1	Arg	Gly	Met	Gly 5	Arg	Val	Gln	Leu	Phe 10	Glu	Ile	Ser	Leu	Ser 15	His	
Gly	Arg	Val	Val 20	Tyr	Ser	Pro	Gly	Glu 25	Pro	Leu	Ala	Gly	Thr 30	Val	Arg	
Val	Arg	Leu 35	Gly	Ala	Pro	Leu	Pro 40	Phe	Arg	Ala	Ile	Arg 45	Val	Thr	Cys	
Ile	Gly 50	Ser	Cys	Gly	Val	Ser 55	Asn	Lys	Ala	Asn	Asp 60	Thr	Ala	Trp	Val	
Val 65	Glu	Glu	Gly	Tyr	Phe 70	Asn	Ser	Ser	Leu	Ser 75	Leu	Ala	Asp	Lys	Gly 80	
Ser	Leu	Pro	Ala	Gly 85	Glu	His	Ser	Phe	Pro 90	Phe	Gln	Phe	Leu	Leu 95	Pro	
Ala	Thr	Ala	Pro 100	Thr	Ser	Phe	Glu	Gly 105	Pro	Phe	Gly	Lys	Ile 110	Val	His	
Gln	Val	Arg 115	Ala	Ala	Ile	His	Thr 120	Pro	Arg	Phe	Ser	Lys 125	Asp	His	Lys	
Cys	Ser 130	Leu	Val	Phe	Tyr	Ile 135	Leu	Ser	Pro	Leu	Asn 140	Leu	Asn	Ser	Ile	
Pro 145	Asp	Ile	Glu	Gln	Pro 150	Asn	Val	Ala	Ser	Ala 155	Thr	Lys	Lys	Phe	Ser 160	
Tyr	Lys	Leu	Val	Lys 165	Thr	Gly	Ser	Val	Val 170	Leu	Thr	Ala	Ser	Thr 175	Asp	
Leu	Arg	Gly	Tyr 180	Val	Val	Gly	Gln	Ala 185	Leu	Gln	Leu	His	Ala 190	Asp	Val	

Glu	Asn	Gln	Ser	Gly	Lys	Asp	Thr	Ser	Pro	Val	Val	Ala	Ser	Leu	Leu
		195					200					205			
Gln	Lys	Val	Ser	Tyr	Lys	Ala	Lys	Arg	Trp	Ile	His	Asp	Val	Arg	Thr
	210					215					220				
Ile	Ala	Glu	Val	Glu	Gly	Ala	Gly	Val	Lys	Ala	Trp	Arg	Arg	Ala	Gln
225					230					235					240
Trp	His	Glu	Gln	Ile	Leu	Val	Pro	Ala	Leu	Pro	Gln	Ser	Ala	Leu	Pro
				245					250					255	
Gly	Cys	Ser	Leu	Ile	His	Ile	Asp	Tyr	Tyr	Leu	Gln	Val	Ser	Leu	Lys
			260					265					270		
Ala	Pro	Glu	Ala	Thr	Val	Thr	Leu	Pro	Val	Phe	Ile	Gly	Asn	Ile	Ala
		275					280					285			
Val	Asn	His	Ala	Pro	Val	Ser	Pro	Arg	Pro	Gly	Leu	Gly	Leu	Pro	Pro
	290					295					300				
Gly	Ala	Pro	Pro	Leu	Val	Val	Pro	Ser	Ala	Pro	Pro	Gln	Glu	Glu	Ala
305					310					315					320
Glu	Ala	Glu	Ala	Ala	Ala	Gly	Gly	Pro	His	Phe	Leu	Asp	Pro	Val	Phe
			325						330					335	
Leu	Ser	Thr	Lys	Ser	His	Ser	Gln	Arg	Gln	Pro	Leu	Leu	Ala	Thr	Leu
			340					345					350		
Ser	Ser	Val	Pro	Gly	Ala	Pro	Glu	Pro	Cys	Pro	Gln	Asp	Gly	Ser	Pro
		355					360					365			
Ala	Ser	His	Pro	Leu	His	Pro	Pro	Leu	Cys	Ile	Ser	Thr	Gly	Ala	Thr
	370					375					380				
Val	Pro	Tyr	Phe	Ala	Glu	Gly	Ser	Gly	Gly	Pro	Val	Pro	Thr	Thr	Ser
385					390					395					400
Thr	Leu	Ile	Leu	Pro	Pro	Glu	Tyr	Ser	Ser	Trp	Gly	Tyr	Pro	Tyr	Glu
				405					410					415	
Ala	Pro	Pro	Ser	Tyr	Glu	Gln	Ser	Cys	Gly	Gly	Val	Glu	Pro	Ser	Leu
			420					425					430		
Thr	Pro	Glu	Ser												
		435													

<210> 189
 <211> 127
 <212> PRT
 <213> homo sapiens

<400> 189

Ser	Val	Leu	Phe	Thr	Gly	Val	Val	Ser	Pro	Gly	Pro	Ser	Ser	Leu	Pro
1				5					10					15	
Pro	Pro	Pro	Gln	Pro	Gln	Gly	Glu	Glu	Gly	Gly	Cys	Arg	Gly	Ala	Gly
			20					25					30		
Arg	Gly	Trp	Ala	Gly	Pro	Glu	Trp	Ala	Arg	Leu	Gly	Gln	Glu	Arg	Arg

		35					40					45					
His	Glu	Ala	Leu	Gly	Ala	Pro	Val	Pro	Gly	Gln	Arg	Pro	Gly	Leu	Pro		
	50					55					60						
Gly	Glu	Gly	Ser	Thr	Gly	Ser	Ala	Leu	Arg	Gly	Gln	Ala	Gly	Phe	His		
65					70					75					80		
Ala	Ala	Ala	Ala	Leu	Leu	Ile	Arg	Arg	Trp	Gly	Leu	Ile	Gly	Val	Ala		
				85					90					95			
Pro	Arg	Thr	Val	Leu	Trp	Arg	Lys	Asn	Gln	Gly	Ala	Gly	Ser	Gly	His		
			100					105					110				
Trp	Pro	Pro	Gly	Ala	Leu	Cys	Lys	Val	Gly	Asp	Ser	Gly	Thr	Cys			
		115					120					125					

<210> 190

<211> 213

<212> PRT

<213> homo sapiens

<400> 190

Leu	Val	Leu	Asn	Val	Gly	Met	Gln	Leu	Gln	Cys	Leu	Pro	His	His	Ile		
1				5					10					15			
Ala	Ala	Glu	Ile	Ser	Ala	Gly	Cys	Glu	Asp	His	Ala	Ala	Arg	Leu	His		
			20					25					30				
Gln	Leu	Val	Gly	Glu	Leu	Leu	Gly	Gly	Arg	Gly	His	Val	Gly	Leu	Leu		
		35					40					45					
Asn	Val	Trp	Asp	Ala	Val	Gln	Val	Gln	Gly	Ala	Gln	Asp	Ile	Glu	His		
	50					55					60						
Glu	Ala	Ala	Leu	Val	Ile	Leu	Gly	Lys	Pro	Trp	Arg	Val	Asp	Gly	Gly		
65					70					75				80			
Pro	His	Leu	Val	His	Asp	Leu	Pro	Glu	Arg	Thr	Leu	Lys	Gly	Arg	Gly		
				85					90					95			
Cys	Ser	Gly	Arg	Lys	Gln	Glu	Leu	Glu	Gly	Glu	Ala	Val	Leu	Ser	Ser		
			100					105					110				
Gly	Gln	Ala	Pro	Leu	Val	Cys	Gln	Arg	Gln	Gly	Thr	Val	Glu	Val	Thr		
		115					120					125					
Leu	Leu	His	Tyr	Pro	Arg	Cys	Val	Ile	Ser	Leu	Val	Gly	Asp	Pro	Ala		
	130					135					140						
Gly	Thr	Tyr	Ala	Gly	His	Pro	Asp	Gly	Ser	Glu	Arg	Gln	Arg	Cys	Pro		
145					150					155					160		
Gln	Ala	His	Ala	His	Gly	Pro	Ser	Gln	Arg	Leu	Pro	Gly	Ala	Val	Asp		
				165					170					175			
Asp	Ala	Ala	Val	Ala	Gln	Ala	Asp	Leu	Glu	Glu	Leu	His	Ser	Pro	His		
			180					185					190				
Ala	Ala	Ala	Ser	Pro	Ala	Ser	Arg	Ala	Ala	Thr	Pro	Pro	Pro	Ala	Ala		
		195					200					205					

Arg Glu Ser Arg Leu
210

<210> 191

<211> 635

<212> PRT

<213> homo sapiens

<400> 191

Gly 1	Gly	Val	Ser	Pro 5	Trp	Arg	Ala	Cys	Val 10	Gln	Gln	Arg	Met	Glu 15	Glu
Ser	Glu	Pro	Glu 20	Arg	Lys	Arg	Ala	Arg 25	Thr	Asp	Glu	Val	Pro 30	Ala	Gly
Gly	Ser	Arg 35	Ser	Glu	Ala	Glu	Asp 40	Glu	Asp	Asp	Glu	Asp 45	Tyr	Val	Pro
Tyr	Val 50	Pro	Leu	Arg	Gln	Arg 55	Arg	Gln	Leu	Leu	Leu 60	Gln	Lys	Leu	Leu
Gln 65	Arg	Arg	Arg	Lys	Gly 70	Ala	Ala	Glu	Glu	Glu 75	Gln	Gln	Asp	Ser	Gly 80
Ser	Glu	Pro	Arg	Gly 85	Asp	Glu	Asp	Asp	Ile 90	Pro	Leu	Gly	Pro	Gln 95	Ser
Asn	Val	Ser	Leu 100	Leu	Asp	Gln	His	Gln 105	His	Leu	Lys	Glu	Lys 110	Ala	Glu
Ala	Arg	Lys 115	Glu	Ser	Ala	Lys	Glu 120	Lys	Gln	Leu	Lys	Glu 125	Glu	Glu	Lys
Ile	Leu 130	Glu	Ser	Val	Ala	Glu 135	Gly	Arg	Ala	Leu	Met 140	Ser	Val	Lys	Glu
Met 145	Ala	Lys	Gly	Ile	Thr 150	Tyr	Asp	Asp	Pro	Ile 155	Lys	Thr	Ser	Trp	Thr 160
Pro	Pro	Arg	Tyr	Val 165	Leu	Ser	Met	Ser	Glu 170	Glu	Arg	His	Glu	Arg 175	Val
Arg	Lys	Lys	Tyr 180	His	Ile	Leu	Val	Glu 185	Gly	Asp	Gly	Ile	Pro 190	Pro	Pro
Ile	Lys	Ser 195	Phe	Lys	Glu	Met	Lys 200	Phe	Pro	Ala	Ala	Ile 205	Leu	Arg	Gly
Leu	Lys 210	Lys	Lys	Gly	Ile	His 215	His	Pro	Thr	Pro	Ile 220	Gln	Ile	Gln	Gly
Ile 225	Pro	Thr	Ile	Leu	Ser 230	Gly	Arg	Asp	Met	Ile 235	Gly	Ile	Ala	Phe	Thr 240
Gly	Ser	Gly	Lys	Thr 245	Leu	Val	Phe	Thr	Leu 250	Pro	Val	Ile	Met	Phe 255	Cys
Leu	Glu	Gln	Glu 260	Lys	Arg	Leu	Pro	Phe 265	Ser	Lys	Arg	Glu	Gly 270	Pro	Tyr
Gly	Leu	Ile 275	Ile	Cys	Pro	Ser	Arg 280	Glu	Leu	Ala	Arg	Gln 285	Thr	His	Gly

Ile	Leu	Glu	Tyr	Tyr	Cys	Arg	Leu	Leu	Gln	Glu	Asp	Ser	Ser	Pro	Leu
	290					295					300				
Leu	Arg	Cys	Ala	Leu	Cys	Ile	Gly	Gly	Met	Ser	Val	Lys	Glu	Gln	Met
305					310					315					320
Glu	Thr	Ile	Arg	His	Gly	Val	His	Met	Met	Val	Ala	Thr	Pro	Gly	Arg
				325					330					335	
Leu	Met	Asp	Leu	Leu	Gln	Lys	Lys	Met	Val	Ser	Leu	Asp	Ile	Cys	Arg
			340					345					350		
Tyr	Leu	Ala	Leu	Asp	Glu	Ala	Asp	Arg	Met	Ile	Asp	Met	Gly	Phe	Glu
		355					360					365			
Gly	Asp	Ile	Arg	Thr	Ile	Phe	Ser	Tyr	Phe	Lys	Gly	Gln	Arg	Gln	Thr
	370					375					380				
Leu	Leu	Phe	Ser	Ala	Thr	Met	Pro	Lys	Lys	Ile	Gln	Asn	Phe	Ala	Lys
385					390					395					400
Ser	Ala	Leu	Val	Lys	Pro	Val	Thr	Ile	Asn	Val	Gly	Arg	Ala	Gly	Ala
				405					410					415	
Ala	Ser	Leu	Asp	Val	Ile	Gln	Glu	Val	Glu	Tyr	Val	Lys	Glu	Glu	Ala
			420					425					430		
Lys	Met	Val	Tyr	Leu	Leu	Glu	Cys	Leu	Gln	Lys	Thr	Pro	Pro	Pro	Val
		435					440					445			
Leu	Ile	Phe	Ala	Glu	Lys	Lys	Ala	Asp	Val	Asp	Ala	Ile	His	Glu	Tyr
	450					455					460				
Leu	Leu	Leu	Lys	Gly	Val	Glu	Ala	Val	Ala	Ile	His	Gly	Gly	Lys	Asp
465					470					475					480
Gln	Glu	Glu	Arg	Thr	Lys	Ala	Ile	Glu	Ala	Phe	Arg	Glu	Gly	Lys	Lys
				485					490					495	
Asp	Val	Leu	Val	Ala	Thr	Asp	Val	Ala	Ser	Lys	Gly	Leu	Asp	Phe	Pro
			500					505					510		
Ala	Ile	Gln	His	Val	Ile	Asn	Tyr	Asp	Met	Pro	Glu	Glu	Ile	Glu	Asn
		515					520					525			
Tyr	Val	His	Arg	Ile	Gly	Arg	Thr	Gly	Arg	Ser	Gly	Asn	Thr	Gly	Ile
	530					535					540				
Ala	Thr	Thr	Phe	Ile	Asn	Lys	Ala	Cys	Asp	Glu	Ser	Val	Leu	Met	Asp
545					550					555					560
Leu	Lys	Ala	Leu	Leu	Leu	Glu	Ala	Lys	Gln	Lys	Val	Pro	Pro	Val	Leu
				565					570					575	
Gln	Val	Leu	His	Cys	Gly	Asp	Glu	Ser	Met	Leu	Asp	Ile	Gly	Gly	Glu
			580					585					590		
Arg	Gly	Cys	Ala	Phe	Cys	Gly	Gly	Leu	Gly	His	Arg	Ile	Thr	Asp	Cys
		595					600					605			
Pro	Lys	Leu	Glu	Ala	Met	Gln	Thr	Lys	Gln	Val	Ser	Asn	Ile	Gly	Arg
	610					615					620				

Lys Asp Tyr Leu Ala His Ser Ser Met Asp Phe
625 630 635

<210> 192
<211> 147
<212> PRT
<213> homo sapiens

<400> 192

Lys 1	Pro	Ser	Arg	Arg 5	Cys	Arg	Pro	Cys	Cys 10	Arg	Cys	Cys	Ile	Ala 15	Gly
Met	Ser	Pro	Cys 20	Trp	Thr	Leu	Glu	Glu 25	Ser	Ala	Ala	Val	Pro 30	Ser	Ala
Gly	Ala	Trp 35	Val	Ile	Gly	Ser	Leu 40	Thr	Ala	Pro	Asn	Ser 45	Arg	Leu	Cys
Arg	Pro 50	Ser	Arg	Ser	Ala	Thr 55	Ser	Val	Ala	Arg	Thr 60	Thr	Trp	Pro	Thr
Ala 65	Pro	Trp	Thr	Ser	Glu 70	Pro	Thr	Val	Phe	Pro 75	Ser	Leu	Gln	Glu	Ala 80
Ser	Val	Pro	Lys	Thr 85	Ala	Thr	Ser	Leu	His 90	Ile	Gln	Gln	Pro	Pro 95	Gly
Gln	Asn	Gln	His 100	Phe	Ser	Ser	Ala	Gly 105	Leu	Glu	Trp	Ala	Arg 110	Leu	Val
Leu	Ala	Ala 115	Cys	Ser	Leu	Cys	Ser 120	Ser	Glu	Leu	Leu	Phe 125	Leu	Phe	Pro
Phe	Thr 130	Pro	Ala	Ala	Ile	Lys 135	Ala	Gln	Thr	Ser	Ser 140	Pro	Lys	Lys	Lys
Lys 145	Lys	Lys													

<210> 193
<211> 150
<212> PRT
<213> homo sapiens

<400> 193

Asp 1	Ile	Leu	Leu	Ala 5	Leu	Pro	Glu	Cys	Leu 10	Asp	Gly	Leu	Ser	Pro 15	Phe
Leu	Leu	Val	Phe 20	Ala	Pro	Met	Asp	Gly 25	Tyr	Gly	Leu	Asn	Pro 30	Leu	Glu
Gln	Gln	Val 35	Leu	Val	Asp	Gly	Val 40	His	Val	Cys	Leu	Leu 45	Leu	Cys	Lys
Asp	Glu 50	Tyr	Arg	Arg	Gly	Cys 55	Leu	Leu	Gln	Ala	Leu 60	Glu	Gln	Val	His
His 65	Leu	Gly	Leu	Leu	Leu 70	His	Ile	Phe	Tyr	Leu 75	Leu	Asp	Asp	Ile	Gln 80

Ala	Gly	Ser	Pro	Ser 85	Ala	Pro	His	Ile	Asp 90	Gly	His	Arg	Leu	Tyr 95	Lys	
Gly	Thr	Leu	Ser 100	Lys	Val	Leu	Asn	Leu 105	Leu	Arg	His	Gly	Gly 110	Thr	Glu	
Glu	Gln	Gly 115	Leu	Ser	Leu	Ala	Leu 120	Glu	Val	Gly	Glu	Asp 125	Gly	Thr	Asp	
Val	Thr 130	Leu	Glu	Ala	His	Val 135	Asp	His	Ala	Val	Ser 140	Leu	Val	Gln	Gly	
Gln 145	Val	Ala	Thr	Asp	Val 150											

<210> 194

<211> 310

<212> PRT

<213> homo sapiens

<400> 194

Glu 1	Ala	Pro	Ala	Ala 5	Ala	Arg	Thr	Gln	Ser 10	Pro	Ala	Ala	Ala	Ala 15	Gln	
Arg	Gly	Asp	Asn 20	Val	Tyr	Val	Val	Thr 25	Glu	Val	Leu	Gln	Thr 30	Gln	Lys	
Glu	Val	Glu 35	Val	Thr	Arg	Thr	His 40	Lys	Arg	Glu	Gly	Ser 45	Gly	Arg	Phe	
Ser 50	Leu	Pro	Gly	Ala	Thr	Cys 55	Leu	Gln	Gly	Glu	Gly 60	Gln	Gly	His	Leu	
Ser 65	Gln	Lys	Lys	Thr	Val 70	Thr	Ile	Pro	Ser	Gly 75	Ser	Thr	Leu	Ala	Phe 80	
Arg	Val	Ala	Gln	Leu 85	Val	Ile	Asp	Ser	Asp 90	Leu	Asp	Val	Leu	Leu 95	Phe	
Pro	Asp	Lys	Lys 100	Gln	Arg	Thr	Phe	Gln 105	Pro	Pro	Ala	Thr	Gly 110	His	Lys	
Arg	Ser	Thr 115	Ser	Glu	Gly	Ala	Trp 120	Pro	Gln	Leu	Pro	Ser 125	Gly	Leu	Ser	
Met 130	Met	Arg	Cys	Leu	His	Asn 135	Phe	Leu	Thr	Asp	Gly 140	Val	Pro	Ala	Glu	
Gly 145	Ala	Phe	Thr	Glu	Asp 150	Phe	Gln	Gly	Leu	Arg 155	Ala	Glu	Val	Glu	Thr 160	
Ile	Ser	Lys	Glu	Leu 165	Glu	Leu	Leu	Asp	Arg 170	Glu	Leu	Cys	Gln	Leu 175	Leu	
Leu	Glu	Gly	Leu 180	Glu	Gly	Val	Leu	Arg 185	Asp	Gln	Leu	Ala	Leu 190	Arg	Ala	
Leu	Glu	Glu 195	Ala	Leu	Glu	Gln	Gly 200	Gln	Ser	Leu	Gly	Pro 205	Val	Glu	Pro	
Leu 210	Asp	Gly	Pro	Ala	Gly	Ala 215	Val	Leu	Glu	Cys	Leu 220	Val	Leu	Ser	Ser	

Gly 225	Met	Leu	Val	Pro	Glu 230	Leu	Ala	Ile	Pro	Val 235	Val	Tyr	Leu	Leu	Gly 240
Ala	Leu	Thr	Met	Leu 245	Ser	Glu	Thr	Gln	His 250	Lys	Leu	Leu	Ala	Glu 255	Ala
Leu	Glu	Ser	Gln 260	Thr	Leu	Leu	Gly	Pro 265	Leu	Glu	Leu	Val	Gly 270	Ser	Leu
Leu	Glu	Gln 275	Ser	Ala	Pro	Trp	Gln 280	Glu	Arg	Arg	Pro	Cys 285	Pro	Cys	Pro
Pro	Gly 290	Ser	Trp	Gly	Thr	Ala 295	Gly	Ala	Lys	Glu	His 300	Arg	Pro	Gly	Ser
Cys 305	Trp	Thr	Ser	Val	Ala 310										

<210> 195

<211> 244

<212> PRT

<213> homo sapiens

<400> 195

Thr 1	Thr	Gly	Ile	Ala 5	Ser	Ser	Gly	Thr	Ser 10	Ile	Pro	Glu	Asp	Asn 15	Thr
Arg	His	Ser	Arg 20	Thr	Ala	Pro	Ala	Gly 25	Pro	Ser	Arg	Gly	Ser 30	Thr	Gly
Pro	Arg	Leu 35	Trp	Pro	Cys	Ser	Ser 40	Ala	Ser	Ser	Lys	Ala 45	Arg	Arg	Ala
Ser 50	Trp	Ser	Arg	Ser	Thr	Pro 55	Ser	Arg	Pro	Ser	Ser 60	Ser	Ser	Trp	His
Ser 65	Ser	Leu	Ser	Lys	Ser 70	Ser	Ser	Ser	Leu	Glu 75	Met	Val	Ser	Thr	Ser 80
Ala	Arg	Arg	Pro 85	Lys	Ser	Ser	Val	Asn 90	Ala	Pro	Ser	Ala	Gly 95	Thr	
Pro	Ser	Val	Arg 100	Lys	Leu	Trp	Arg	His 105	Leu	Ile	Met	Glu	Arg 110	Pro	Glu
Gly	Ser	Cys 115	Gly	Gln	Ala	Pro	Ser 120	Leu	Val	Glu	Arg	Leu 125	Trp	Pro	Val
Ala	Gly 130	Gly	Trp	Lys	Val	Leu 135	Cys	Phe	Leu	Ser	Gly 140	Lys	Arg	Arg	Thr
Ser 145	Lys	Ser	Glu	Ser	Ile 150	Thr	Ser	Trp	Ala	Thr 155	Arg	Asn	Ala	Arg	Val 160
Leu	Pro	Glu	Gly	Met 165	Val	Thr	Val	Phe	Phe 170	Trp	Leu	Arg	Trp	Pro 175	Trp
Pro	Ser	Pro	Cys 180	Lys	His	Val	Ala	Pro 185	Gly	Arg	Glu	Asn	Arg 190	Pro	Glu
Pro	Ser	Arg	Leu	Trp	Val	Arg	Val	Thr	Ser	Thr	Ser	Phe	Cys	Val	Cys

			195					200					205						
Ser	Thr	Ser	Val	Thr	Thr	Tyr	Thr	Leu	Ser	Pro	Arg	Cys	Ala	Ala	Ala				
	210					215					220								
Ala	Gly	Leu	Cys	Val	Leu	Ala	Ala	Ala	Gly	Ala	Ser	His	Gly	Ala	Glu				
225					230					235					240				
Ser	Ala	Arg	Cys																

<210> 196
 <211> 229
 <212> PRT
 <213> homo sapiens

Thr	Gly	His	Met	Ala	Thr	Gly	Leu	Leu	Ala	Phe	Leu	Gly	Leu	Ala	Ala			
1				5					10					15				
Gly	Gly	Gln	Thr	Leu	Cys	Pro	Ala	Gly	Glu	Leu	Pro	Gly	His	Ala	Arg			
			20					25					30					
Ala	Gln	Ala	Ser	Gly	Ala	Pro	Gly	Ser	Val	Leu	Ile	Ala	Val	Pro	Gly			
		35					40					45						
Arg	Arg	Arg	Val	His	Thr	Cys	Gly	Pro	Gly	Pro	Ala	Ala	Pro	Ser	Thr			
	50					55					60							
Arg	Gly	Glu	Cys	Pro	Pro	Pro	Ala	Leu	Gly	His	Thr	Arg	Pro	Ala	Arg			
65					70					75					80			
Pro	Arg	Pro	Val	Leu	Leu	Arg	Pro	Ser	Cys	Ser	Pro	Gly	Ala	Arg	Gly			
				85					90					95				
Ala	Gly	Thr	Trp	Ser	Ala	Leu	Leu	Pro	Arg	Gly	Thr	Leu	Leu	Gln	Glu			
			100					105					110					
Ala	Ala	His	Gln	Leu	Glu	Arg	Pro	Gln	Gln	Gly	Leu	Arg	Leu	Gln	Arg			
		115					120					125						
Leu	Arg	Gln	Gln	Leu	Val	Leu	Arg	Phe	Thr	Gln	His	Gly	Gln	Cys	Pro			
	130					135					140							
Gln	Gln	Val	Asp	Asn	Arg	Asp	Ser	Glu	Phe	Arg	His	Gln	His	Ser	Gly			
145					150					155					160			
Gly	Gln	His	Gln	Ala	Leu	Gln	Asp	Ser	Thr	Cys	Trp	Thr	Val	Gln	Gly			
				165					170					175				
Leu	His	Arg	Pro	Lys	Ala	Leu	Ala	Leu	Leu	Gln	Arg	Leu	Leu	Gln	Gly			
			180					185					190					
Ser	Gln	Gly	Gln	Leu	Val	Pro	Gln	His	Pro	Leu	Gln	Ala	Leu	Gln	Gln			
		195					200					205						
Gln	Leu	Ala	Gln	Leu	Ser	Val	Gln	Lys	Leu	Gln	Phe	Leu	Gly	Asp	Gly			
	210					215					220							
Leu	His	Leu	Cys	Pro														
225																		

<210> 197

<211> 95
 <212> PRT
 <213> homo sapiens

<400> 197

Thr	Glu	Ile	Leu	Pro	Val	Phe	Val	Arg	Leu	Ala	Gly	Val	Pro	Ile	Cys
1				5					10					15	
Ser	Thr	Gly	Asn	Ala	Ser	Ala	Met	Leu	Gln	Pro	Gln	Lys	Pro	Gly	Leu
			20					25					30		
Ser	Leu	Gln	Gln	Ala	Glu	Pro	Cys	Leu	Trp	Ser	Gly	Ala	Val	His	
		35				40					45				
Ser	Ser	Val	Cys	Leu	Val	Leu	Gly	Leu	Glu	Leu	Asp	Arg	Gly	Gly	Val
	50					55					60				
Ser	Ser	Pro	Ser	Leu	Asn	Ser	Glu	Gln	Thr	Leu	Cys	Leu	Ala	Pro	Val
	65				70					75					80
Cys	Pro	Gly	Asn	Ser	Pro	Gly	Pro	His	Trp	Glu	Pro	Leu	Val	Phe	
				85					90					95	

<210> 198
 <211> 101
 <212> PRT
 <213> homo sapiens

<400> 198

Ala	Val	Pro	Arg	Gly	Ser	Leu	Arg	Glu	Asp	Gly	Lys	Val	Arg	Cys	Met
1				5					10					15	
Ser	Asn	Leu	Leu	Met	Ala	Gly	Ser	Pro	Leu	Cys	Pro	Leu	Ser	Leu	Ala
			20					25					30		
Leu	Val	Ile	Ala	Glu	Leu	Cys	Ala	Gln	Cys	Cys	Gly	Leu	Ala	Val	Ala
		35					40					45			
Arg	Leu	Phe	Leu	Trp	Gly	Ala	Arg	Ala	Gly	Cys	Gly	Asn	Gln	Ser	Ser
	50					55					60				
Gln	Thr	Asp	Val	Ser	Gln	Ala	Glu	Asp	Ser	Phe	Leu	Ala	Glu	Val	Ser
	65				70					75					80
Pro	His	Leu	Gln	Val	Ser	Gly	Trp	Gly	Gly	Ala	Arg	Arg	Gly	Arg	His
				85					90					95	
Thr	Pro	Cys	Leu	Thr											
			100												

<210> 199
 <211> 155
 <212> PRT
 <213> homo sapiens

<400> 199

Val	Arg	His	Thr	Ser	His	Leu	Ala	Val	Leu	Thr	Gln	Gly	Ala	Pro	Gly
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His	Cys	Ser	Cys	Ala	Ala	Trp	Ala	Leu	Leu	Leu	Arg	Thr	Pro	Arg	Ala

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Pro	Asn	Glu 35	Gly	Leu	Gly	Asn	Cys 40	Leu	Gly	Thr	Leu	Gly 45	Pro	Gly	Thr				
Gly	Ser 50	Val	Leu	Asn	Ser	Gly 55	Lys	Val	Lys	Arg	Pro 60	His	Leu	Tyr	Pro				
Ala 65	Gln	Ala	Gln	Glu	Gln 70	Gly	Arg	Gln	Ser	Cys 75	Gly	Gln	His	Pro	Thr 80				
Thr	Asp	Thr	Val	Leu 85	Pro	Ala	Ala	Gly	Val 90	Arg	Gly	Leu	Val	Ser 95	Glu				
Ala	Ala	Ala	Trp 100	His	Trp	His	Cys	Leu 105	Cys	Tyr	Arg	Trp	Gly 110	Leu	Leu				
Arg	Val	Ser 115	Gln	Ile	Gln	Gly	Glu 120	Phe	Gln	Phe	Thr	Gln 125	Pro	Lys	Gly				
Pro	Val 130	Cys	Arg	Ala	Ala	Leu 135	Thr	Arg	Ala	Gln	Gln 140	His	Ser	Thr	Glu				
Leu 145	Gly	Lys	Gly	Arg	Gly 150	Glu	Arg	Val	Lys	Asp 155									

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 <212> PRT
 <213> homo sapiens
 <400> 200

Arg 1	Met	Lys	Cys	Ser 5	Gln	Pro	Pro	Arg	Cys 10	His	Phe	Gln	Ser	Asp 15	Phe				
Gln	Lys	Cys	Ala 20	Pro	Cys	Pro	Arg	Ala 25	Gln	Thr	His	Trp	Leu 30	Glu	Pro				
Pro	Gly	Arg 35	Val	Gln	Thr	Ile	Ser 40	Ser	Met	Arg	Asn	Ala 45	Gln	Lys	Gly				
Phe	Ala 50	Asp	Ser	Ile	Arg	Leu 55	Trp	Arg	Leu	Pro	Ala 60	Ser	Gly	Val	Gly				
Trp 65	Val	Val	Ser	Pro	Pro 70	Ile	Gln	Thr	Gln	Glu 75	Val	Ala	Pro	Glu	Gly 80				
Met	Tyr	Leu	Val	Gly 85	Ser	Ser	Ser	Gly	Thr 90	Leu	Gly	Gly	Cys	Arg 95	Ala				
Leu	Thr	Gln	Val 100	Phe	Leu	Ser	Leu	Ser 105	Ser	Leu	Gly	Cys	Val 110	Cys	Ala				
Cys	Ala	Cys 115	Ala	Cys	Leu	Cys	Phe 120	Ser	Leu	Trp	Ala	His 125	Gln	Asp	Ala				
Pro	Arg 130	Arg	Ala	Cys	Ala	Arg 135	Val	Pro	Thr										

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<213> homo sapiens

<400> 201

[illegible]

<210> 202

<211> 131

<212> PRT

<213> homo sapiens

<400> 202

[illegible]

<210> 203
 <211> 76
 <212> PRT
 <213> homo sapiens

<400> 203

Leu	Ala	Ala	Ile	Lys	Asp	Gln	Leu	Glu	Gly	Val	Gln	Gln	Ala	Leu	Ser
1				5					10					15	
Gln	Ala	Ala	Pro	Ile	Pro	Glu	Glu	Asp	Thr	Asp	Thr	Glu	Glu	Gly	Asp
			20					25					30		
Asp	Phe	Glu	Leu	Leu	Asp	Gln	Ser	Glu	Leu	Asp	Gln	Ile	Glu	Ser	Glu
		35					40					45			
Leu	Gly	Leu	Thr	Gln	Asp	Gln	Glu	Ala	Glu	Ala	Gln	Gln	Asn	Lys	Lys
	50					55					60				
Ser	Ser	Gly	Phe	Leu	Ser	Asn	Leu	Leu	Gly	Gly	His				
65					70					75					

<210> 204
 <211> 102
 <212> PRT
 <213> homo sapiens

<400> 204

Arg	Val	Cys	Ser	Lys	His	Phe	Leu	Arg	Leu	Pro	Pro	Ser	Gln	Lys	Arg
1				5					10					15	
Thr	Gln	Thr	Leu	Lys	Lys	Val	Met	Thr	Leu	Asn	Tyr	Leu	Thr	Ser	Gln
			20					25					30		
Ser	Trp	Ile	Lys	Leu	Arg	Val	Asn	Trp	Asp	Leu	His	Lys	Thr	Arg	Lys
		35					40					45			
Gln	Lys	His	Ser	Lys	Ile	Arg	Ser	Leu	Gln	Val	Ser	Phe	Gln	Ile	Cys
	50					55					60				
Trp	Glu	Ala	Ile	Asn	Leu	Gly	Ile	Ser	Leu	Gln	Gln	Ser	Thr	Lys	Asn
65					70					75				80	
Thr	Lys	Lys	Ile	Ser	Asn	Lys	Lys	Lys	Lys	Lys	Lys	Arg	Lys	Arg	Lys
				85					90					95	
Lys	Leu	Asn	Cys	Lys	Leu										
			100												

<210> 205
 <211> 80
 <212> PRT
 <213> homo sapiens

<400> 205

Ile	Cys	Leu	His	His	Asn	His	Cys	Leu	Cys	Asp	Thr	Gln	Leu	Leu	Ala
1				5					10					15	
Phe	Tyr	Gly	Leu	Ile	Pro	Pro	Thr	Ala	Arg	Leu	Glu	Met	Ala	Val	Asn

20										25					30				
Gly	Ala	Cys	Phe	Phe	Thr	Asn	Lys	Pro	Lys	Ser	Thr	Thr	Ala	Glu	Ile				
		35					40					45							
Thr	Trp	Lys	Arg	Phe	Ser	Leu	Ser	Arg	Val	Leu	Lys	Tyr	Thr	Phe	Lys				
	50					55					60								
Phe	Phe	Pro	Lys	Lys	Leu	Ile	Leu	Ile	Val	Phe	Pro	Lys	Ser	Phe	Asn				
65					70					75					80				

<210> 206
 <211> 76
 <212> PRT
 <213> homo sapiens

Gly	Lys	Pro	Ala	Ala	Leu	Glu	Ala	His	Gln	Gly	Ser	Arg	Leu	Gln	Gly			
1				5					10					15				
Arg	Ser	Arg	Glu	Gln	Ala	Ala	Ile	Pro	Pro	Leu	Leu	Ser	Ser	Arg	Thr			
			20					25					30					
Gln	Leu	Cys	Gly	Leu	Gly	Phe	Leu	Phe	Ala	Gly	Leu	Ala	Pro	Cys	Arg			
		35					40					45						
Thr	Leu	Val	Leu	Glu	Leu	Glu	Gly	Pro	Ile	Leu	Pro	Arg	Gly	Asp	Ser			
	50					55					60							
Gln	Gly	Cys	Arg	Gly	Ile	Gly	Trp	Arg	Arg	Val	Leu							
65					70					75								

<210> 207
 <211> 72
 <212> PRT
 <213> homo sapiens

Asn	Leu	Arg	Val	Ser	Gln	Leu	Pro	Trp	Lys	Pro	Thr	Arg	Ala	Pro	Asp			
1				5					10					15				
Cys	Arg	Glu	Glu	Ala	Gly	Ser	Arg	Gln	Pro	Tyr	Leu	His	Ser	Cys	Pro			
			20					25					30					
Gln	Gly	Leu	Ser	Cys	Val	Ala	Leu	Asp	Phe	Phe	Leu	Arg	Asp	Leu	Arg			
		35					40					45						
Pro	Ala	Gly	His	Trp	Cys	Trp	Ser	Trp	Arg	Val	Leu	Ser	Cys	Pro	Gly			
	50					55					60							
Val	Thr	Pro	Arg	Val	Ala	Gly	Gly											
65					70													

<210> 208
 <211> 73
 <212> PRT
 <213> homo sapiens

<400> 208
 Pro Gly Met Ser Ser Leu Gln Asp Arg His Gly Arg Thr Ile Trp Phe

1				5					10					15		
Gln	Val	Gly	Pro 20	Tyr	Cys	Ser	His	Arg 25	Gln	Arg	Pro	Gln	Glu 30	Ala	Asp	
Gly	Trp	Lys 35	Arg	Gly	Val	Thr	Ile 40	Thr	Gly	Val	Val	Met 45	Leu	Arg	Val	
Cys	Leu 50	Asp	Pro	Pro	Arg	Thr 55	Thr	Leu	Phe	Leu	Arg 60	Val	Thr	Pro	Leu	
Pro 65	Ser	His	Ala	Ser	Gln 70	Gly	Cys	Ser								

<210> 209

<211> 182

<212> PRT

<213> homo sapiens

<400> 209

Gln 1	Arg	Trp	Leu	Trp 5	Thr	Ser	Ser	Thr	Ser 10	Pro	Cys	Trp	Ile	Arg 15	Ala	
Phe	Leu	Pro	Pro 20	Ala	Gly	Gln	Val	Trp 25	Pro	Cys	Ser	Leu	Gly 30	Arg	Ala	
Pro	Ala	Pro 35	Leu	Thr	Thr	Leu	Gln 40	Leu	Thr	Met	Gln	Leu 45	Met	Pro	Lys	
Leu	Trp 50	Cys	Pro	Val	Cys	Ser 55	Ser	Pro	Gly	Ser	His 60	Cys	His	Leu	Gln	
Arg 65	Gly	Ser	Leu	Leu	Arg 70	Pro	Thr	Leu	Leu	His 75	Leu	Ala	Pro	Pro	Trp 80	
Leu	Leu	Ala	Trp	Pro 85	Asn	Leu	Ala	Phe	Cys 90	Ala	Met	Leu	Glu	Leu 95	Glu	
Leu	Leu	Leu	Phe 100	Phe	Arg	Gly	Gly	Asn 105	Arg	Val	Glu	Ser	Gly 110	Lys	Gly	
Leu	Ala	Pro 115	Lys	Cys	Cys	Cys	Cys	Gly 120	Phe	Phe	Ala	Phe 125	Ser	Lys	Asp	
Ala	Leu 130	Pro	Gly	Pro	Lys	Leu 135	Gln	Thr	Ala	Val	Leu 140	Ser	Lys	Gln	Val	
Arg 145	Ser	Leu	Gly	Phe	Gly 150	Ala	His	Leu	Leu	Ser 155	Gly	Ser	Ile	Ser	Ile 160	
Leu	Leu	Leu	Ala	Thr 165	Ser	Gly	Gln	Arg	Pro 170	Pro	Gln	Pro	His	Ile 175	Ala	
Arg	Cys	Trp	Gln 180	Lys	Gly											

<210> 210

<211> 130

<212> PRT

<213> homo sapiens

<400> 210

Val 1	Gly	Pro	Gly	Lys 5	Gln	Pro	Trp	Trp	Gly 10	Gln	Val	Lys	Gln	Cys 15	Gly
Ser	Gln	Gln	Gly 20	Thr	Pro	Leu	Lys	Val 25	Ala	Val	Ala	Pro	Arg 30	Ala	Ala
Ala	His	Trp 35	Thr	Pro	Gln	Leu	Trp 40	His	Gln	Leu	His	Gly 45	Glu	Leu	Gln
Ser	Gly 50	Gln	Arg	Gly	Trp	Gly 55	Pro	Ala	Lys	Arg	Ala 60	Arg	Pro	Asp	Leu
Pro 65	Ser	Gly	Arg	Gln	Glu 70	Gly	Pro	Asp	Pro	Ala 75	Arg	Arg	Ser	Arg	Gly 80
Ser	Pro	Gln	Pro	Pro 85	Leu	Leu	Leu	Ile	Ala 90	Thr	Gly	Thr	Ser	Gly 95	Asp
Arg	Leu	Cys	Ser 100	Trp	Glu	Ser	Arg	Ser 105	Pro	Gly	Phe	Val	Gly 110	Leu	Pro
Ala	Gly	Asp 115	Arg	His	Val	Ser	His 120	Arg	Glu	Arg	Pro	Gly 125	Ser	Arg	Pro
Gln	Leu 130														

<210> 211
 <211> 111
 <212> PRT
 <213> homo sapiens

<400> 211

Val 1	Thr	Gly	Lys	Gly 5	Arg	Asp	Pro	Gly	Leu 10	Ser	Cys	Ser	Ser	Ser 15	Trp
Lys	Arg	Trp	Ser 20	Arg	Thr	Val	Thr	Ile 25	His	Ala	Asp	Thr	Glu 30	Gln	Gln
Tyr	Glu	Thr 35	Glu	Gln	Leu	Arg	Ala 40	Val	Ser	Ser	Ser	Ala 45	Glu	Ala	Ala
Trp	Ala 50	Ala	Thr	Pro	Pro	Phe 55	Cys	Asn	His	Pro	Met 60	Met	Ser	Pro	Pro
His 65	Leu	Thr	Ser	Arg	Trp 70	Gly	Trp	Met	Ala	Glu 75	Gln	Met	Lys	Pro	Ala 80
Leu	Trp	Arg	Gly	Ser 85	Leu	Thr	Glu	Met	His 90	Thr	Phe	Met	Gly	Glu 95	Val
Asp	Gly	His	Leu 100	Thr	Ser	Leu	Met	Phe 105	His	Thr	Val	Asp	Cys 110	Thr	

<210> 212
 <211> 243
 <212> PRT
 <213> homo sapiens

<400> 212

Asp 1	Val	Gln	Val	Ala 5	Gly	Pro	Glu	Pro	Asp 10	Cys	Arg	Val	His	Ser 15	His	
Val	Leu	Pro	Gly 20	Gln	Ala	His	Arg	Leu 25	Ala	Pro	Gly	Pro	Tyr 30	Ser	Val	
Gly	Glu	Ser 35	Leu	Gln	Pro	Arg	Glu 40	Gly	Cys	Glu	Asp	Cys 45	Asp	Arg	Gln	
Lys	Ala 50	Asn	Leu	Arg	Ile	Arg 55	Phe	Lys	Pro	Ser	Leu 60	Phe	Gln	His	Val	
Gly 65	Thr	His	Ser	Ser	Leu 70	Ala	Gly	Lys	Ile	Gln 75	Lys	Leu	Lys	Asp	Lys 80	
Asp	Phe	Gly	Lys	Gln 85	Ala	Leu	Arg	Lys	Glu 90	His	Val	Asn	Pro	Pro 95	Ala	
Glu	Val	Ser	Thr 100	Ser	Leu	Lys	Thr	Tyr 105	Gln	His	Phe	Thr	Leu 110	Glu	Lys	
Ala	Tyr	Leu 115	Arg	Glu	Asp	Phe	Phe 120	Trp	Ala	Phe	Thr	Pro 125	Ala	Ala	Gly	
Asp	Phe 130	Ile	Arg	Phe	Arg	Phe 135	Phe	Gln	Pro	Leu	Arg 140	Leu	Glu	Arg	Phe	
Phe 145	Phe	Arg	Ser	Gly	Asn 150	Ile	Glu	His	Pro	Glu 155	Asp	Lys	Leu	Phe	Asn 160	
Thr	Ser	Val	Glu	Val 165	Leu	Pro	Phe	Asp	Asn 170	Pro	Gln	Ser	Asp	Lys 175	Glu	
Ala	Leu	Gln	Glu 180	Gly	Arg	Thr	Ala	Thr 185	Leu	Arg	Tyr	Pro	Arg 190	Ser	Pro	
Asp	Gly	Tyr 195	Leu	Gln	Ile	Gly	Ser 200	Phe	Tyr	Lys	Gly	Val 205	Ala	Glu	Gly	
Glu	Val 210	Asp	Pro	Ala	Phe	Gly 215	Pro	Leu	Glu	Ala	Leu 220	Arg	Leu	Ser	Ile	
Gln 225	Thr	Asp	Ser	Pro	Val 230	Trp	Val	Ile	Leu	Ser 235	Glu	Ile	Phe	Leu	Lys 240	
Lys	Ala	Asp														

<210> 213
 <211> 244
 <212> PRT
 <213> homo sapiens

<400> 213

Gly 1	Arg	Thr	Gly	Val 5	Ser	Val	Val	Met	Gly 10	Ile	Pro	Ser	Val	Arg 15	Arg	
Glu	Val	His	Ser 20	Tyr	Leu	Thr	Asp	Thr 25	Leu	His	Ser	Leu	Ile 30	Ser	Glu	
Leu	Ser	Pro 35	Gln	Glu	Lys	Glu	Asp 40	Ser	Val	Ile	Val	Val 45	Leu	Ile	Ala	

Glu	Thr	Asp	Ser	Gln	Tyr	Thr	Ser	Ala	Val	Thr	Glu	Asn	Ile	Lys	Ala
	50					55					60				
Leu	Phe	Pro	Thr	Glu	Ile	His	Ser	Gly	Leu	Leu	Glu	Val	Ile	Ser	Pro
65					70					75					80
Ser	Pro	His	Phe	Tyr	Pro	Asp	Phe	Ser	Arg	Leu	Arg	Glu	Ser	Phe	Gly
				85					90					95	
Asp	Pro	Lys	Glu	Arg	Val	Arg	Trp	Arg	Thr	Lys	Gln	Asn	Leu	Asp	Tyr
			100					105					110		
Cys	Phe	Leu	Met	Met	Tyr	Ala	Gln	Ser	Lys	Gly	Ile	Tyr	Tyr	Val	Gln
		115					120					125			
Leu	Glu	Asp	Asp	Ile	Val	Ala	Lys	Pro	Asn	Tyr	Leu	Ser	Thr	Met	Lys
	130					135					140				
Asn	Phe	Ala	Leu	Gln	Gln	Pro	Ser	Glu	Asp	Trp	Met	Ile	Leu	Glu	Phe
145					150					155					160
Ser	Gln	Leu	Gly	Phe	Ile	Gly	Lys	Met	Phe	Lys	Ser	Leu	Asp	Leu	Ser
				165					170					175	
Leu	Ile	Val	Glu	Phe	Ile	Leu	Met	Phe	Tyr	Arg	Asp	Lys	Pro	Ile	Asp
			180					185					190		
Trp	Leu	Leu	Asp	His	Ile	Leu	Trp	Val	Lys	Val	Cys	Asn	Pro	Glu	Lys
		195					200					205			
Asp	Ala	Lys	Thr	Val	Thr	Gly	Arg	Lys	Pro	Thr	Cys	Gly	Ser	Ala	Ser
	210					215					220				
Asn	Arg	Pro	Ser	Ser	Ser	Thr	Trp	Ala	Leu	Thr	Pro	Arg	Trp	Leu	Ala
225					230					235					240
Arg	Ser	Arg	Asn												

<210> 214
 <211> 210
 <212> PRT
 <213> homo sapiens

<400> 214

Pro	Ala	Glu	Ser	Gln	Pro	Ala	Asp	Pro	Leu	Gln	Thr	Val	Pro	Leu	Pro
1				5					10					15	
Ala	Arg	Gly	His	Ser	Leu	Leu	Ala	Gly	Trp	Gln	Asp	Pro	Glu	Thr	Glu
			20					25					30		
Gly	Gln	Arg	Leu	Trp	Lys	Ala	Gly	Ala	Ala	Glu	Gly	Ala	Cys	Glu	Pro
		35					40					45			
Ala	Ser	Arg	Gly	Glu	His	Glu	Pro	Glu	Asp	Ile	Pro	Ala	Leu	His	Pro
	50					55					60				
Gly	Glu	Ser	Leu	Pro	Ala	Arg	Gly	Leu	Leu	Leu	Gly	Leu	His	Pro	Cys
65					70					75					80
Arg	Gly	Gly	Leu	His	Pro	Leu	Pro	Leu	Leu	Pro	Thr	Ser	Lys	Thr	Gly
				85					90					95	

Ala	Val	Leu	Leu	Pro	Gln	Trp	Glu	His	Arg	Ala	Pro	Gly	Gly	Gln	Ala
		100						105					110		
Leu	Gln	His	Val	Cys	Gly	Gly	Ala	Ala	Leu	Arg	Gln	Pro	Ser	Val	Arg
		115					120					125			
Gln	Gly	Gly	Pro	Ala	Gly	Gly	Pro	His	Arg	His	Pro	Pro	Val	Pro	Ser
	130					135					140				
Glu	Pro	Arg	Arg	Leu	Pro	Pro	Asp	Arg	Leu	Leu	Leu	Gln	Gly	Ser	Gly
145					150					155					160
Arg	Gly	Arg	Gly	Gly	Pro	Ser	Leu	Arg	Pro	Ser	Gly	Ser	Thr	Ala	Pro
				165					170					175	
Leu	Asp	Pro	Asp	Gly	Leu	Pro	Cys	Val	Gly	Asp	Ser	Glu	Arg	Asp	Leu
			180					185					190		
Pro	Glu	Lys	Gly	Arg	Leu	Ser	Cys	Gly	Leu	Leu	Arg	Val	Pro	Cys	Gly
		195					200					205			
Gln	Pro														
	210														

<210> 215
 <211> 128
 <212> PRT
 <213> homo sapiens

<400> 215

Gly	Gly	Ala	Gly	Leu	Val	His	Gly	Ser	Ala	Asp	Trp	Pro	Cys	Leu	Ala
1				5					10					15	
Pro	Trp	Arg	Val	Ser	Ser	Cys	Phe	Leu	Pro	Gly	Thr	Glu	Leu	Arg	Gly
			20					25					30		
Leu	Gly	Ala	Pro	Gly	Ala	Lys	Ser	Arg	Leu	Trp	Cys	Arg	Gly	Gly	Gly
		35					40					45			
Leu	Ser	Leu	Asn	Arg	His	Pro	Glu	Val	Leu	Leu	Arg	Cys	Trp	Val	His
	50					55					60				
Pro	Glu	Trp	His	Gly	Glu	Gln	Leu	Trp	Pro	Val	Leu	Leu	Pro	Arg	Pro
65					70					75					80
Val	Leu	Gly	Lys	Leu	Ser	Ser	Gly	Pro	Ser	Leu	Gln	Arg	Pro	Arg	Met
				85					90					95	
Gly	Trp	Val	Trp	Gly	Thr	His	Gly	Glu	Trp	Pro	Glu	Glu	Leu	Arg	Val
		100						105					110		
Lys	Arg	Ala	Pro	Val	Cys	Trp	Leu	Gln	Arg	Pro	Gly	Ala	Pro	Leu	Ser
		115					120					125			

<210> 216
 <211> 124
 <212> PRT
 <213> homo sapiens

<400> 216

Phe Pro Gln Asp Trp Pro Arg Lys Glu His Arg Pro Gln Leu Leu Pro

1				5				10				15			
Val	Pro	Leu	Arg 20	Val	Asp	Pro	Ala	Ser 25	Gln	Glu	His	Leu	Arg 30	Val	Ser
Val	Lys	Arg 35	Gln	Ala	Ser	Thr	Pro 40	Ala	Pro	Glu	Pro	Ala 45	Leu	Ser	Ser
Arg	Cys 50	Pro	Gln	Thr	Pro	Gln 55	Leu	Cys	Ala	Arg	Gln 60	Glu	Ala	Ala	Arg
His 65	Thr	Pro	Gly	Arg	Gln 70	Ala	Arg	Pro	Val	Arg 75	Gly	Pro	Met	Asp	Lys 80
Pro	Ser	Pro	Ala	Ser 85	Gly	Lys	Thr	Gly	Pro 90	Phe	Pro	Thr	Gly	His 95	Ala
Pro	Glu	Leu	Trp 100	Gln	Ile	Ala	Gly	Ala 105	Ile	Val	Trp	Gly	Glu 110	Phe	Asn
Lys	Ser	Pro 115	Phe	Glu	Asn	Glu	Lys 120	Lys	Lys	Lys	Lys	Lys			

<210> 217
 <211> 142
 <212> PRT
 <213> homo sapiens

<400> 217

Val 1	Pro	His	Thr	His 5	Pro	Ile	Leu	Gly	Leu 10	Cys	Lys	Glu	Gly	Pro 15	Glu
Leu	Ser	Phe	Pro 20	Arg	Thr	Gly	Leu	Gly 25	Arg	Ser	Thr	Gly	His 30	Ser	Cys
Ser	Pro	Cys 35	His	Ser	Gly	Trp	Thr 40	Gln	His	Leu	Arg	Ser 45	Thr	Ser	Gly
Cys 50	Arg	Leu	Arg	Asp	Arg	Pro 55	Pro	Pro	Leu	His	Gln 60	Ser	Leu	Leu	Leu
Ala 65	Pro	Gly	Ala	Pro	Arg 70	Pro	Arg	Ser	Ser	Val 75	Pro	Gly	Lys	Lys	Gln 80
Leu	Asp	Thr	Arg	Gln 85	Gly	Ala	Lys	His	Gly 90	Gln	Ser	Ala	Asp	Pro 95	Trp
Thr	Ser	Pro	Ala 100	Pro	Pro	Gln	Gly	Lys 105	Gln	Gly	Leu	Ser	Leu 110	Gln	Asp
Thr	Pro	Gln 115	Ser	Cys	Gly	Arg	Leu 120	Gln	Glu	Pro	Ser	Cys 125	Gly	Glu	Asn
Leu	Ile 130	Lys	Ala	Leu	Leu	Lys 135	Met	Lys	Lys	Lys	Lys 140	Lys	Lys		

<210> 218
 <211> 379
 <212> PRT
 <213> homo sapiens

<400> 218

Arg 1	Arg	Gly	Leu	Glu 5	Gly	Phe	Asn	Gly	Gly 10	Trp	Thr	Glu	Met	Pro 15	Gly
Ile	Leu	Trp	Met 20	Glu	Pro	Thr	Gln	Pro 25	Pro	Asp	Phe	Ala	Leu 30	Ala	Tyr
Arg	Pro	Ser 35	Phe	Pro	Glu	Asp	Arg 40	Glu	Pro	Gln	Ile	Pro 45	Tyr	Pro	Glu
Pro	Thr 50	Trp	Pro	Pro	Pro	Leu 55	Ser	Ala	Pro	Arg	Val 60	Pro	Tyr	His	Ser
Ser 65	Val	Leu	Ser	Val	Thr 70	Arg	Pro	Val	Val	Val 75	Ser	Ala	Thr	His	Pro 80
Thr	Leu	Pro	Ser	Ala 85	His	Gln	Pro	Pro	Val 90	Ile	Pro	Ala	Thr	His 95	Pro
Ala	Leu	Ser	Arg 100	Asp	His	Gln	Ile	Pro 105	Val	Ile	Ala	Ala	Asn 110	Tyr	Pro
Asp	Leu	Pro 115	Ser	Ala	Tyr	Gln	Pro 120	Gly	Ile	Leu	Ser	Val 125	Ser	His	Ser
Ala	Gln 130	Pro	Pro	Ala	His	Gln 135	Pro	Pro	Met	Ile	Ser 140	Thr	Lys	Tyr	Pro
Glu 145	Leu	Phe	Pro	Ala	His 150	Gln	Ser	Pro	Met	Phe 155	Pro	Asp	Thr	Arg	Val 160
Ala	Gly	Thr	Gln	Thr 165	Thr	Thr	His	Leu	Pro 170	Gly	Ile	Pro	Pro	Asn 175	His
Ala	Pro	Leu	Val 180	Thr	Thr	Leu	Gly	Ala 185	Gln	Arg	Pro	Pro	Gln 190	Ala	Pro
Asp	Ala	Leu 195	Val	Leu	Arg	Thr	Gln 200	Ala	Thr	Gln	Leu	Pro 205	Ile	Ile	Pro
Thr	Ala 210	Gln	Pro	Ser	Leu	Thr 215	Thr	Thr	Ser	Arg	Ser 220	Pro	Val	Ser	Pro
Ala 225	His	Gln	Ile	Ser	Val 230	Pro	Ala	Ala	Thr	Gln 235	Pro	Ala	Ala	Leu	Pro 240
Thr	Leu	Leu	Pro	Ser 245	Gln	Ser	Pro	Thr	Asn 250	Gln	Thr	Ser	Pro	Ile 255	Ser
Pro	Thr	His	Pro 260	His	Ser	Lys	Ala	Pro 265	Gln	Ile	Pro	Arg	Glu 270	Asp	Gly
Pro	Ser	Pro 275	Lys	Leu	Ala	Leu	Trp 280	Leu	Pro	Ser	Pro	Ala 285	Pro	Thr	Ala
Ala	Pro 290	Thr	Ala	Leu	Gly	Glu 295	Ala	Gly	Leu	Ala	Glu 300	His	Ser	Gln	Arg
Asp 305	Asp	Arg	Trp	Leu	Leu 310	Val	Ala	Leu	Leu	Val 315	Pro	Thr	Cys	Val	Phe 320
Leu	Val	Val	Leu	Leu 325	Ala	Leu	Gly	Ile	Val 330	Tyr	Cys	Thr	Arg	Cys 335	Gly

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Pro	His	Ala	Pro	Asn	Lys	Arg	Ile	Thr	Asp	Cys	Tyr	Arg	Trp	Val	Ile
			340					345					350		
His	Ala	Gly	Ser	Lys	Ser	Pro	Thr	Glu	Pro	Met	Pro	Pro	Arg	Gly	Ser
		355					360					365			
Leu	Thr	Gly	Val	Gln	Thr	Cys	Arg	Thr	Ser	Val					
	370					375									

<210> 219
 <211> 157
 <212> PRT
 <213> homo sapiens

Val	Asp	Thr	Asp	Glu	Cys	Gln	Ile	Ala	Gly	Val	Cys	Gln	Gln	Met	Cys
1				5					10					15	
Val	Asn	Tyr	Val	Gly	Gly	Phe	Glu	Cys	Tyr	Cys	Ser	Glu	Gly	His	Glu
			20					25					30		
Leu	Glu	Ala	Asp	Gly	Ile	Ser	Cys	Ser	Pro	Ala	Gly	Ala	Met	Gly	Ala
		35					40					45			
Gln	Gly	Ser	Gln	Asp	Leu	Gly	Asp	Glu	Leu	Leu	Asp	Gly	Glu	Asp	
	50					55					60				
Glu	Glu	Asp	Glu	Asp	Glu	Ala	Trp	Lys	Ala	Ser	Thr	Val	Ala	Gly	Arg
	65				70					75					80
Arg	Cys	Leu	Gly	Ser	Cys	Gly	Trp	Ser	Leu	Arg	Ser	Arg	Leu	Thr	Leu
				85					90					95	
Pro	Trp	Pro	Ile	Asp	Arg	Ala	Ser	Gln	Arg	Thr	Glu	Ser	His	Arg	Tyr
			100					105					110		
Pro	Thr	Arg	Ser	Pro	Pro	Gly	His	Pro	Arg	Ser	Val	Pro	Pro	Gly	Ser
		115					120					125			
Pro	Thr	Thr	Pro	Gln	Cys	Ser	Pro	Ser	Pro	Gly	Leu	Trp	Trp	Ser	Leu
	130					135					140				
Pro	Arg	Ile	Pro	His	Cys	Leu	Leu	Pro	Thr	Ser	Leu	Leu			
	145				150					155					

<210> 220
 <211> 211
 <212> PRT
 <213> homo sapiens

Pro	Pro	Pro	Pro	Gly	Pro	Leu	Cys	Leu	Leu	Pro	Ile	Lys	Ser	Leu	Cys
1				5					10					15	
Leu	Leu	Pro	Pro	Ser	Pro	Gln	Pro	Ser	Pro	Pro	Ser	Cys	Pro	Leu	Arg
			20					25					30		
Ala	Pro	Leu	Thr	Arg	Pro	His	Pro	Ser	Ala	Leu	His	Ile	Pro	Ile	Pro
		35					40					45			

<210> 222
 <211> 198
 <212> PRT
 <213> homo sapiens

<400> 222

Asn 1	Lys	Glu	Leu	Ser 5	Ser	Leu	Lys	Ser	Ser 10	Asp	Val	Val	Met	Thr 15	His
Thr	Glu	Ser	Cys 20	Ile	Thr	Val	Ala	Ser 25	Arg	Ala	Thr	His	Leu 30	Phe	Gly
Leu	Ser	Asp 35	Gly	His	Ser	Phe	Thr 40	Thr	Gln	Gln	Gln	Thr 45	Pro	His	Thr
Gly	Thr 50	Arg	Met	Ser	Ala	Ser 55	Thr	Trp	Glu	Ala	Val 60	Ala	Glu	Pro	Gly
Arg 65	Trp	Pro	Gly	Pro	Asp 70	His	Gly	Leu	Ser	Gly 75	Ala	Gly	His	Gln	Gly 80
Val	Arg	Val	Pro	Met 85	Leu	Pro	Gln	Gly	Val 90	Gly	Met	Thr	Gly	Arg 95	Ser
Leu	Val	Thr	Arg 100	Gln	Trp	Thr	Ser	Leu 105	Gly	Glu	Gly	Trp	Arg 110	Glu	Arg
Ala	Gly	Gln 115	Ala	Pro	Ala	Ala	His 120	Arg	Leu	Ala	His	Ala 125	Asn	Thr	Leu
Lys	Ala 130	Leu	Leu	Gly	Gly	Phe 135	Ser	Glu	Asn	Gln	Gly 140	Glu	Ala	Leu	Val
Ser 145	Phe	Pro	Arg	Lys	Val 150	Pro	Ile	Leu	Pro	Pro 155	Ala	Pro	Leu	Ser	Pro 160
Glu	Pro	Arg	Asp	Pro 165	Gln	Gly	Val	Leu	Ala 170	Gly	Gly	Ala	Lys	Gln 175	Arg
Cys	Leu	Arg	Pro 180	Pro	Glu	Pro	Ser	Leu 185	Pro	Met	Ile	Pro	Arg 190	His	Ala
Arg	Gln	Gly 195	Val	Gly	Leu										

<210> 223
 <211> 98
 <212> PRT
 <213> homo sapiens

<400> 223

Ser 1	His	Gly	Met	Pro 5	Gly	Arg	Gly	Trp	Ala 10	Cys	Glu	Val	Asp	Trp 15	His
Ser	Cys	Pro	His 20	Thr	Leu	Pro	Gly	Trp 25	Ala	Pro	Glu	Ile	Trp 30	Gly	Ser
Pro	Ser	Gln 35	His	Gly	Val	Leu	Gly 40	Ala	Cys	Pro	Gly	Pro 45	Phe	Thr	Arg

Thr	Glu	Ala	Pro	His	Pro	Leu	Ser	His	Phe	Ser	Arg	Trp	Lys	Thr	Gln
	50					55					60				
Arg	Arg	Lys	Arg	Pro	Trp	Gly	Gly	Val	Pro	Ser	Cys	Leu	Gln	Leu	Ala
65					70					75					80
Pro	Trp	Val	Pro	Leu	Cys	Gly	Gly	Ser	Pro	Asp	Ser	Ile	Ser	Ser	Ala
				85					90					95	
Ser	Glu														

<210> 224
 <211> 298
 <212> PRT
 <213> homo sapiens

<400> 224

Ala	Thr	Arg	Arg	Arg	Ala	Ala	Glu	Ala	Gly	Met	Ala	Ala	Val	Leu	Gln
1				5					10					15	
Arg	Val	Glu	Arg	Leu	Ser	Asn	Arg	Val	Val	Arg	Val	Leu	Gly	Cys	Asn
			20					25					30		
Pro	Gly	Pro	Met	Thr	Leu	Gln	Gly	Thr	Asn	Thr	Tyr	Leu	Val	Gly	Thr
		35					40					45			
Gly	Pro	Arg	Arg	Ile	Leu	Ile	Asp	Thr	Gly	Glu	Pro	Ala	Ile	Pro	Glu
	50					55					60				
Tyr	Ile	Ser	Cys	Leu	Lys	Gln	Ala	Leu	Thr	Glu	Phe	Asn	Thr	Ala	Ile
65					70					75					80
Gln	Glu	Ile	Val	Val	Thr	His	Trp	His	Arg	Asp	His	Ser	Gly	Gly	Ile
				85					90					95	
Gly	Asp	Ile	Cys	Lys	Ser	Ile	Asn	Asn	Asp	Thr	Thr	Tyr	Cys	Ile	Lys
			100					105					110		
Lys	Leu	Pro	Arg	Asn	Pro	Gln	Arg	Glu	Glu	Ile	Ile	Gly	Asn	Gly	Glu
		115					120					125			
Gln	Gln	Tyr	Val	Tyr	Leu	Lys	Asp	Gly	Asp	Val	Ile	Lys	Thr	Glu	Gly
	130					135					140				
Ala	Thr	Leu	Arg	Val	Leu	Tyr	Thr	Pro	Gly	His	Thr	Asp	Asp	His	Met
145					150					155					160
Ala	Leu	Leu	Leu	Glu	Glu	Asn	Ala	Ile	Phe	Ser	Gly	Asp	Cys	Ile	
				165				170					175		
Leu	Gly	Glu	Gly	Thr	Thr	Val	Phe	Glu	Asp	Leu	Tyr	Asp	Tyr	Met	Asn
			180					185					190		
Ser	Leu	Lys	Glu	Leu	Leu	Lys	Ile	Lys	Ala	Asp	Ile	Ile	Tyr	Pro	Gly
		195					200					205			
His	Gly	Pro	Val	Ile	His	Asn	Ala	Glu	Ala	Lys	Ile	Gln	Gln	Tyr	Ile
	210					215					220				
Ser	His	Arg	Asn	Ile	Arg	Glu	Gln	Gln	Ile	Leu	Thr	Leu	Phe	Arg	Glu
225					230					235					240

Asn	Phe	Glu	Lys	Ser 245	Phe	Thr	Val	Met	Glu 250	Leu	Val	Lys	Ile	Ile 255	Tyr
Lys	Asn	Thr	Pro 260	Glu	Asn	Leu	His	Glu 265	Met	Ala	Lys	His	Asn 270	Leu	Leu
Leu	His	Leu 275	Lys	Lys	Leu	Glu	Lys 280	Glu	Gly	Lys	Ile	Phe 285	Ser	Asn	Thr
Asp	Pro 290	Asp	Lys	Lys	Trp	Lys 295	Ala	His	Leu						

<210> 225
 <211> 58
 <212> PRT
 <213> homo sapiens

<400> 225															
Gly 1	Phe	Ser	Trp	Gly 5	Arg	Ser	Pro	Leu	Gly 10	Arg	Cys	Trp	Cys	Leu 15	Gly
Gly	Ser	Trp	Asp 20	Pro	Gly	Tyr	Ser	Pro 25	Thr	His	Ala	Arg	Leu 30	Asp	Trp
Thr	Ala	Ala 35	Arg	Arg	Ala	Ala	Val 40	Gln	Gln	Pro	Phe	Pro 45	Pro	Gln	Pro
Pro	Ala 50	Gly	Val	Ser	Pro	Ile 55	Trp	Ile	Leu						

<210> 226
 <211> 73
 <212> PRT
 <213> homo sapiens

<400> 226															
Ser 1	Gly	Ser	Leu	Ser 5	Leu	Asn	His	Ile	Ser 10	Ile	Phe	Gln	Ile	Asn 15	Ile
Leu	Leu	Leu	Ser 20	Ile	Ser	Tyr	Asn	Phe 25	Phe	Ser	Leu	Arg	Ile 30	Pro	Trp
Glu	Phe	Phe 35	Asn	Ala	Ile	Gly	Ser 40	Val	Ile	Ile	Asp	Ala 45	Phe	Thr	Asn
Ile	Ser 50	Tyr	Ala	Ser	Arg	Met 55	Ile	Ser	Val	Pro	Val 60	Ser	His	Tyr	Asn
Phe 65	Leu	Asp	Cys	Cys	Val 70	Lys	Phe	Ser							

<210> 227
 <211> 141
 <212> PRT
 <213> homo sapiens

<400> 227															
Ala 1	Phe	Leu	Leu	Arg 5	Pro	Ser	Val	Thr	Ala 10	Ser	Thr	Arg	Leu	Leu 15	Pro

Val	Cys	Ala	Ser 20	Pro	Arg	Ser	Ser	Pro 25	Gly	Pro	Ser	Pro	Ala 30	Gln	Gln
Gln	Gln	Ala 35	Trp	Gln	Gln	Ala	Trp 40	Ser	Ser	Ala	Arg	Ala 45	Pro	Ser	Arg
Cys	Arg 50	Ala	Arg	Pro	Ser	Ser 55	Ser	Glu	Arg	Pro	Cys 60	Pro	Ala	Val	Gly
Arg 65	Leu	Ala	Ser	Leu	Tyr 70	Cys	Cys	Cys	Met	Val 75	Phe	Ala	Ser	Pro	Pro 80
Arg	Pro	Gly	Arg	Thr 85	Trp	Val	His	Cys	Thr 90	Gly	Trp	Pro	Arg	Leu 95	Ala
Thr	Gly	Leu	Trp 100	Pro	Leu	Thr	Cys	Gln 105	Val	Trp	Gly	Thr	Pro 110	Arg	Lys
Gln	Gln	Pro 115	Leu	Pro	Leu	Leu	Gly 120	Ser	Trp	Pro	Leu	Ala 125	Ala	Ser	Trp
Arg	Leu 130	Trp	Trp	Met	Pro	Trp 135	Ser	Trp	Ala	Pro	Arg 140	Leu			

<210> 228
 <211> 244
 <212> PRT
 <213> homo sapiens

<400> 228

Val 1	Pro	Pro	Pro	Ala 5	Leu	Gly	His	Arg	Gln 10	His	Ala	Pro	Ala	Ser 15	Arg
Leu	Arg	Glu	Ser 20	Thr	Gln	Leu	Pro	Arg 25	Pro	Phe	Thr	Ser	Thr 30	Ala	Ala
Ala	Gly	Met 35	Ala	Ala	Ser	Val	Glu 40	Gln	Arg	Glu	Gly	Thr 45	Ile	Gln	Val
Gln	Gly 50	Gln	Ala	Leu	Phe	Phe 55	Arg	Glu	Ala	Leu	Pro 60	Gly	Ser	Gly	Gln
Ala 65	Arg	Phe	Ser	Val	Leu 70	Leu	Leu	His	Gly	Ile 75	Arg	Phe	Ser	Ser	Glu 80
Thr	Trp	Gln	Asn 85	Gly	Thr	Leu	His	Arg 90	Leu	Ala	Gln	Ala	Gly 95	Tyr	
Arg	Ala	Val	Ala 100	Ile	Asp	Leu	Pro	Gly 105	Leu	Gly	His	Ser	Lys 110	Glu	Ala
Ala	Ala	Pro 115	Ala	Pro	Ile	Gly	Glu 120	Leu	Ala	Pro	Gly	Ser 125	Phe	Leu	Ala
Ala	Val 130	Val	Asp	Ala	Leu	Glu 135	Leu	Gly	Pro	Pro	Val 140	Val	Ile	Ser	Pro
Ser 145	Leu	Ser	Gly	Met	Tyr 150	Ser	Leu	Pro	Phe	Leu 155	Thr	Ala	Pro	Gly	Ser 160
Gln	Leu	Pro	Gly	Phe 165	Val	Pro	Val	Ala	Pro 170	Ile	Cys	Thr	Asp	Lys 175	Ile

Asn	Ala	Ala	Asn 180	Tyr	Ala	Ser	Val	Lys 185	Thr	Pro	Ala	Leu	Ile 190	Val	Tyr
Gly	Asp	Gln 195	Asp	Pro	Met	Gly	Gln 200	Thr	Ser	Phe	Glu	His 205	Leu	Lys	Gln
Leu	Pro 210	Asn	His	Arg	Val	Leu 215	Ile	Met	Lys	Gly	Ala 220	Gly	His	Pro	Cys
Tyr 225	Leu	Asp	Lys	Pro	Glu 230	Glu	Trp	His	Thr	Gly 235	Leu	Leu	Asp	Phe	Leu 240
Gln	Gly	Leu	Gln												

<210> 229
 <211> 144
 <212> PRT
 <213> homo sapiens

<400> 229

Trp 1	Thr	Asp	His	Asn 5	Arg	Gly	Ala	Gln	Leu 10	Gln	Gly	Ile	His	His 15	Ser
Arg	Gln	Glu	Ala 20	Ala	Arg	Gly	Gln	Leu 25	Pro	Asn	Arg	Gly	Arg 30	Gly	Cys
Cys	Phe	Leu 35	Gly	Val	Pro	Gln	Thr 40	Trp	Gln	Val	Asn	Gly 45	His	Ser	Pro
Val	Ala 50	Ser	Leu	Gly	Gln	Pro 55	Val	Gln	Cys	Thr	Gln 60	Val	Leu	Pro	Gly
Leu 65	Gly	Gly	Glu	Ala	Asn 70	Thr	Met	Gln	Gln	Gln 75	Tyr	Arg	Glu	Ala	Ser 80
Leu	Pro	Thr	Ala	Gly 85	Gln	Gly	Leu	Ser	Glu 90	Glu	Glu	Gly	Leu	Ala 95	Leu
His	Leu	Asp	Gly 100	Ala	Leu	Ala	Leu	Leu 105	His	Ala	Cys	Cys	His 110	Ala	Cys
Cys	Cys	Cys 115	Ala	Gly	Glu	Gly	Pro 120	Gly	Glu	Leu	Arg	Gly 125	Leu	Ala	Gln
Thr	Gly 130	Ser	Arg	Arg	Val	Leu 135	Ala	Val	Thr	Glu	Gly 140	Arg	Arg	Arg	Asn

<210> 230
 <211> 135
 <212> PRT
 <213> homo sapiens

<400> 230

Leu 1	Glu	Phe	Phe	Ile 5	Pro	Cys	Leu	Gly	Ser 10	Val	Asn	Glu	Ala	Cys 15	Leu
Phe	Pro	Gly	Val 20	Ser	Phe	His	Gly	Leu 25	Tyr	Phe	Ser	Ser	Ser 30	Ser	Gly
Ser	Phe	Ala	Gly	Ser	Ser	Leu	Trp	Lys	Leu	His	Glu	Arg	Trp	Leu	Gly

			35				40				45						
Leu	Gly 50	Phe	Ala	Gly	Val	Tyr 55	Ser	Arg	Val	Lys	Ala 60	Glu	Trp	Asp	Leu		
Arg 65	Pro	Arg	Leu	Gly	Thr 70	Thr	Gln	Ala	Glu	Lys 75	Gly	Arg	Phe	His	His 80		
Ser	Gln	Cys	Pro	Pro 85	His	Ser	Thr	Thr	Ser 90	Ala	Arg	Ala	Pro	Pro 95	Ser		
Leu	Leu	Pro	His 100	Pro	Ala	Ile	Val	Arg 105	Gly	Ala	Thr	Val	Gly 110	Arg	Arg		
Val	Pro	Arg 115	Arg	Gly	Leu	Phe	Leu 120	Leu	Pro	Val	Pro	Glu 125	Lys	Ala	Phe		
Pro	Leu 130	Leu	Lys	Phe	Lys	His 135											
<210> 231																	
<211> 96																	
<212> PRT																	
<213> homo sapiens																	
<400> 231																	
Gly 1	Gly	Pro	Val	Cys 5	Trp	Glu	Pro	Gln	Val 10	Thr	Pro	Phe	Ser	Ser 15	Tyr		
Ser	Val	Pro	Gly 20	Ala	Ser	Cys	Pro	Pro 25	Leu	Gln	Ile	Leu	Gly 30	Lys	Glu		
Asn	Val	Tyr 35	Val	Ala	Gly	Tyr	Cys 40	Met	Val	Thr	Ser	Glu 45	Gly	Arg	Pro		
Leu	Gly 50	Thr	His	Leu	Pro	Thr 55	Ala	Ala	Gln	Ala	Arg 60	Ala	Gln	Ala	His		
Leu 65	Leu	Val	Leu	Arg	Pro 70	Gln	Ile	Lys	Pro	Ser 75	Pro	His	His	Met	Ala 80		
Ser	Asp	Arg	Phe	Leu 85	Pro	Ser	Arg	Lys	Phe 90	Cys	Gly	Cys	Ala	Val 95	Leu		
<210> 232																	
<211> 83																	
<212> PRT																	
<213> homo sapiens																	
<400> 232																	
Cys 1	Cys	Gly	Glu	Gly 5	Thr	Val	Asn	Asp	Gly 10	Asn	Val	Pro	Ser	Gln 15	Pro		
Gly	Ser	Cys	Leu 20	Thr	Trp	Val	Ser	Asn 25	Pro	Thr	Leu	Pro	Ser 30	Pro	Trp		
Ser	Thr	Leu 35	Gln	Arg	Ser	Arg	Gly 40	Pro	Ala	Asn	Ala	Arg 45	Glu	Val	Ser		
Thr	Glu 50	Lys	Ser	Leu	Gln	Asn 55	Ser	His	Trp	Lys	Arg 60	Arg	Asn	Lys	Gly		

His Gly Lys Lys Pro Gln Gly Arg Asp Arg Pro Arg Ser Gln Thr Leu
65 70 75 80

Gly Arg Glu

<210> 233

<211> 52

<212> PRT

<213> homo sapiens

<400> 233

Ala Ser Pro Ala Ser Leu Ala Gln Ala Thr Ser Arg Gln Pro Ala Pro
1 5 15

Ser Pro Arg Ala Arg Ser His Leu Ala Thr Ser Thr Ser Trp Thr Ser
20 25 30

Ser Ala Arg Ser Asp Ala Gly Cys Gly Glu Cys Arg Arg Asp Pro Gly
35 40 45

Ala Pro Pro Arg
50

<210> 234

<211> 94

<212> PRT

<213> homo sapiens

<400> 234

Leu Gly Ser Ala Trp Gln Gln Leu Arg Arg Pro Glu Ala Ser Glu Thr
1 5 15

Leu Arg Leu Val Gly Thr His Arg Pro Arg Gln Arg Ala Leu Pro Arg
20 25 30

Gln Arg Val Ala Ser Pro Pro Pro Arg Arg Gly Leu Gly Leu Thr Ser
35 40 45

Pro Pro Val Arg Leu Gly Gln Val Val Pro Gly Leu Met Pro Gly Val
50 55 60

Val Ser Ala Ala Gly Thr Gln Val Arg Arg Leu Asp Glu Val Pro Ala
65 70 75 80

Ser Leu Arg Leu Gln His His Leu Gln Leu Arg Glu Gly Leu
85 90

<210> 235

<211> 95

<212> PRT

<213> homo sapiens

<400> 235

Ala Arg Pro Ser Arg Ser Trp Arg Trp Cys Cys Ser Arg Ser Asp Ala
1 5 15

Gly Thr Ser Ser Arg Arg Arg Thr Trp Val Pro Ala Ala Leu Thr Thr
20 25 30

Pro	Gly	Ile	Arg	Pro	Gly	Thr	Thr	Cys	Pro	Arg	Arg	Thr	Gly	Gly	Glu
		35					40					45			
Val	Arg	Pro	Ser	Pro	Arg	Arg	Gly	Gly	Gly	Leu	Ala	Thr	Arg	Cys	Leu
	50					55					60				
Gly	Lys	Ala	Arg	Trp	Arg	Gly	Leu	Cys	Val	Pro	Thr	Ser	Arg	Arg	Val
	65				70					75					80
Ser	Asp	Ala	Ser	Gly	Arg	Arg	Ser	Cys	Cys	Gln	Ala	Glu	Pro	Arg	
				85					90					95	

<210> 236

<211> 174

<212> PRT

<213> homo sapiens

<400> 236

Ala	Pro	Thr	Asn	Thr	Arg	Ser	Ser	Ser	Lys	Phe	Ala	Thr	Ser	Gly	Ser
1				5					10					15	
Pro	Gly	Tyr	Pro	Ile	Ala	Ser	Ser	Gly	Ala	Ser	Pro	Glu	Val	Arg	Gln
			20					25					30		
Arg	Arg	Thr	Thr	Phe	Phe	Arg	Phe	Arg	Pro	Gly	Glu	Ser	Leu	Cys	Gly
		35					40					45			
Asp	Met	Lys	Leu	Leu	Thr	His	Asn	Leu	Leu	Ser	Ser	His	Val	Arg	Gly
	50					55					60				
Val	Gly	Ser	Arg	Gly	Phe	Pro	Leu	Arg	Leu	Gln	Ala	Thr	Glu	Val	Arg
	65				70					75					80
Ile	Cys	Pro	Val	Glu	Phe	Asn	Pro	Asn	Phe	Val	Ala	Arg	Met	Ile	Pro
				85					90					95	
Lys	Val	Glu	Trp	Ser	Ala	Phe	Leu	Glu	Ala	Ala	Asp	Asn	Leu	Arg	Leu
			100					105					110		
Ile	Gln	Val	Pro	Lys	Gly	Pro	Val	Glu	Gly	Tyr	Glu	Glu	Asn	Glu	Glu
		115					120					125			
Phe	Leu	Arg	Thr	Met	His	His	Leu	Leu	Leu	Glu	Val	Glu	Val	Ile	Glu
	130					135					140				
Gly	Thr	Leu	Gln	Cys	Pro	Glu	Ser	Gly	Arg	Met	Phe	Pro	Ile	Ser	Arg
	145				150					155					160
Gly	Ile	Pro	Asn	Met	Leu	Leu	Ser	Glu	Glu	Glu	Thr	Glu	Ser		
				165					170						

<210> 237

<211> 225

<212> PRT

<213> homo sapiens

<400> 237

Tyr	Arg	Ala	Gln	Lys	His	Cys	Val	Trp	Cys	His	Trp	Val	Lys	Gly	Trp
1				5					10					15	
Gly	Tyr	Thr	Arg	Gln	Asn	Ser	Glu	Thr	Gly	Tyr	Arg	Ser	Thr	Lys	Ile

20						25						30					
His	Ser	His	Asn	Lys	Lys	Asn	Trp	Arg	Leu	Ala	Gln	Ser	Thr	Leu	Ser		
		35					40					45					
Phe	Leu	Phe	Thr	Gln	Gln	His	Val	Gly	Asp	Pro	Ala	Ala	Asp	Gly	Glu		
	50					55					60						
His	Thr	Ser	Arg	Phe	Arg	Ala	Leu	Gln	Gly	Ala	Leu	Tyr	His	Phe	His		
	65				70					75					80		
Leu	Gln	Gln	Gln	Val	Val	His	Gly	Pro	Gln	Lys	Leu	Leu	Ile	Leu	Leu		
				85					90					95			
Ile	Ser	Leu	Asn	Arg	Pro	Phe	Arg	His	Leu	Asp	Gln	Thr	Gln	Val	Ile		
			100					105					110				
Gly	Arg	Leu	Gln	Glu	Arg	Arg	Pro	Leu	His	Phe	Arg	Tyr	His	Thr	Arg		
		115					120					125					
His	Glu	Val	Gly	Val	Glu	Phe	His	Arg	Ala	Asp	Thr	Asp	Leu	Gly	Gly		
	130					135					140						
Leu	Glu	Ala	Gln	Gly	Glu	Ala	Thr	Gly	Pro	His	Pro	Pro	His	Met	Arg		
	145				150					155				160			
Ala	Gln	Gln	Ile	Val	Gly	Lys	Gln	Phe	His	Val	Ala	Ala	Gln	Thr	Leu		
				165					170					175			
Ala	Arg	Pro	Glu	Pro	Glu	Lys	Gly	Arg	Pro	Pro	Leu	Pro	His	Phe	Arg		
			180					185					190				
Gly	Cys	Ser	Thr	Arg	Cys	Tyr	Trp	Ile	Ala	Arg	Arg	Thr	Gly	Ser	Gly		
		195					200					205					
Glu	Leu	Ala	Gly	Thr	Ser	Arg	Val	Cys	Gly	Ser	Ser	Phe	Leu	Tyr	Ala		
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<210> 238
 <211> 209
 <212> PRT
 <213> homo sapiens

<400> 238

Thr	Phe	Asn	Glu	Lys	Lys	Ile	Tyr	Asn	Thr	Glu	Leu	Lys	Asn	Thr	Val
1				5					10					15	
Phe	Gly	Val	Ile	Gly	Ser	Arg	Val	Gly	Asp	Thr	His	Gly	Arg	Ile	Arg
			20					25					30		
Lys	Gln	Gly	Ile	Asp	Gln	Gln	Lys	Tyr	Thr	Val	Ile	Thr	Arg	Lys	Thr
		35					40					45			
Gly	Ala	Trp	His	Asn	Gln	Leu	Ser	Val	Ser	Ser	Ser	Leu	Ser	Ser	Met
	50					55					60				
Leu	Gly	Ile	Pro	Arg	Leu	Met	Gly	Asn	Ile	Arg	Pro	Asp	Ser	Gly	His
	65				70					75					80

<210> 240
 <211> 134
 <212> PRT
 <213> homo sapiens

<400> 240

Ser	Arg	Thr	Phe	Ser	Phe	Leu	Ser	Phe	Leu	His	Cys	Ala	Asn	Ile	Leu
1				5					10					15	
Thr	Leu	Phe	Val	Ser	Phe	Gln	Glu	Pro	His	Arg	His	Ile	Gln	Val	Lys
			20					25					30		
Arg	Ser	Leu	Asn	Lys	Cys	Leu	Gln	Pro	Ser	Gln	Cys	Lys	Asn	Lys	Tyr
		35					40					45			
Gln	Ser	Ser	Arg	Arg	Ser	Ser	Ser	Arg	Ala	Ala	Pro	Lys	Val	Pro	Thr
	50					55					60				
Ala	Thr	Pro	Asn	Asn	Tyr	Lys	Ser	Val	Gln	Arg	Glu	Cys	Trp	Arg	Glu
	65				70					75					80
Cys	Glu	Trp	Val	Cys	Ala	Gly	Gly	His	Gly	Gly	Ala	Val	Cys	Lys	Ile
				85					90					95	
Gly	Val	Ala	Asn	His	Arg	Thr	Arg	Ala	Trp	Ser	Gly	Tyr	Pro	Pro	Pro
			100					105					110		
Thr	Gln	Arg	Gly	Arg	Ala	Ser	Pro	His	Thr	Leu	Thr	Ala	Glu	Phe	Ala
		115					120					125			
Leu	Gly	Arg	Val	Lys	Lys										
	130														

<210> 241
 <211> 147
 <212> PRT
 <213> homo sapiens

<400> 241

Pro	Ala	Arg	Thr	Arg	Asp	Arg	Pro	Leu	Leu	Ala	Arg	Phe	Gly	Leu	Pro
1				5					10					15	
Pro	Arg	Cys	Glu	Pro	Val	Gly	Ala	Pro	Leu	Ala	Ala	Leu	Ala	Leu	Ala
			20					25					30		
Arg	Glu	Arg	Arg	Glu	Arg	Gly	Arg	Phe	Pro	Arg	Pro	Cys	Lys	Cys	Leu
		35					40					45			
Phe	Phe	Asn	Ser	Ser	Gln	Cys	Glu	Leu	Cys	Cys	Glu	Cys	Val	Arg	Gly
	50					55					60				
Gly	Ala	Pro	Ala	Leu	Ser	Arg	Arg	Arg	Val	Ala	Thr	Pro	Cys	Pro	Cys
					70					75					80
Pro	Met	Val	Cys	Asn	Ser	Asp	Phe	Ala	His	Arg	Ser	Thr	Val	Pro	Pro
				85					90					95	
Ser	Ala	His	Pro	Phe	Thr	Leu	Thr	Pro	Thr	Leu	Ser	Leu	Asn	Thr	Phe
			100					105					110		
Ile	Ile	Val	Arg	Arg	Gly	Arg	Trp	Asp	Phe	Gly	Arg	Ser	Ala	Ala	Ala

Trp	Arg	Val	Asp	Ile	Lys	Thr	Ser	Ser	Asp	Ser	Ile	Ser	Arg	Met	Ala
	130					135					140				
Val	Ala	Pro	Pro	Gly	Leu	Val	Pro	Asp	Gly	Arg	Phe	Gln	Gly	Gly	Ser
145					150					155					160
Gln	Ala	Met	Gly												

<210> 244
 <211> 87
 <212> PRT
 <213> homo sapiens

<400> 244

Phe	Ala	Trp	Ala	Ser	Val	Leu	Gln	Val	Asp	Thr	Cys	Ser	Arg	Met	Ile
1				5					10					15	
Phe	Val	Ser	Arg	Phe	Leu	Arg	Phe	Trp	Trp	Lys	Phe	Ser	Gly	Lys	Arg
			20					25					30		
Ala	Arg	Ile	Ala	Ser	Ala	Glu	Asp	Arg	Ser	Arg	Asn	Ala	Thr	Ser	Leu
		35					40					45			
Val	Arg	Arg	Cys	Arg	Ala	Trp	Ser	Ser	Ser	Ser	Ala	Ser	Ser	Trp	Val
	50					55					60				
Thr	Asp	Lys	Leu	Glu	His	Val	Thr	Ser	Lys	Ser	Phe	Phe	Lys	Pro	Arg
65					70					75					80
Ala	Glu	Leu	Glu	Lys	Leu	Ser									
				85											

<210> 245
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 <212> PRT
 <213> homo sapiens

<400> 245

Asp	Gly	Pro	Gly	Gly	Pro	Thr	Ala	His	Pro	His	Arg	Cys	Ala	His	Pro
1				5					10					15	
Pro	Gly	Val	Cys	Pro	Gly	Gln	Ala	Pro	Ala	His	Leu	Leu	Leu	Cys	Ala
			20					25					30		
Ala	Ala	Pro	Gly	His	Pro	Gly	Gln	Gly	Gln	Gln	Pro	Ala	Ala	Gly	Gly
		35					40					45			
Leu	Val	Gly	Asp	Ala	Asp	Arg	Ala	Gly	Asp	Leu	Glu	Cys	Ser	Pro	Arg
	50					55					60				
Arg	Ile	Phe	Leu	His	Pro	Arg	Leu	His	Pro	Pro	Arg	His	Leu	Gly	Ser
65					70					75					80
Cys	His	Leu	Asp	Arg	Gly	Cys	Gly	Cys	Ala	Gly	Trp	Ser	Cys	Cys	Leu
				85					90					95	
His	Leu	Arg	Glu	Thr	Gly	Trp	Tyr	Ile	Leu	Gly	Pro	Ala	Glu	Asp	Ser
			100					105					110		
Ala	Ser	Ala	Gly	Ser	Phe	Leu	His	Ser	His	Arg	Cys	Pro	Gln	Thr	Leu

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<210> 246
 <211> 268
 <212> PRT
 <213> homo sapiens

<400> 246

Ala 1	Ser	Pro	Ser	Asn 5	Ser	Gln	Pro	Thr	Ser 10	Pro	Ala	Ser	Ala	Pro 15	Ala
Leu	Pro	Pro	Pro 20	Ala	Arg	Arg	Ser	Arg 25	Gly	Ala	Gln	Thr	Val 30	Ser	Leu
Thr	Met	Gly 35	Thr	Ala	Asp	Ser	Asp 40	Glu	Met	Ala	Pro	Glu 45	Ala	Pro	Gln
His 50	Thr	His	Ile	Asp	Val	His 55	Ile	His	Gln	Glu	Ser 60	Ala	Leu	Ala	Lys
Leu 65	Leu	Leu	Thr	Cys	Cys 70	Ser	Ala	Leu	Arg	Pro 75	Arg	Ala	Thr	Gln	Ala 80
Arg	Gly	Ser	Ser	Arg 85	Leu	Leu	Val	Ala	Ser 90	Trp	Val	Met	Gln	Ile 95	Val
Leu	Gly	Ile	Leu 100	Ser	Ala	Val	Leu	Gly 105	Gly	Phe	Phe	Tyr	Ile 110	Arg	Asp
Tyr	Thr	Leu 115	Leu	Val	Thr	Ser	Gly 120	Ala	Ala	Ile	Trp	Thr 125	Gly	Ala	Val
Ala 130	Val	Leu	Ala	Gly	Ala	Ala 135	Phe	Ile	Tyr	Glu 140	Lys	Arg	Gly	Gly	
Thr 145	Tyr	Trp	Ala	Leu	Leu 150	Arg	Thr	Leu	Leu	Ala 155	Leu	Ala	Ala	Phe	Ser 160
Thr	Ala	Ile	Ala	Ala 165	Leu	Lys	Leu	Trp	Asn 170	Glu	Asp	Phe	Arg	Tyr 175	Gly
Tyr	Ser	Tyr	Tyr 180	Asn	Ser	Ala	Cys	Arg 185	Ile	Ser	Ser	Ser	Ser 190	Asp	Trp
Asn	Thr	Pro 195	Ala	Pro	Thr	Gln	Ser 200	Pro	Glu	Glu	Val	Arg 205	Arg	Leu	His
Leu	Cys 210	Thr	Ser	Phe	Met	Asp 215	Met	Leu	Lys	Ala	Leu 220	Phe	Arg	Thr	Leu
Gln 225	Ala	Met	Leu	Leu	Gly 230	Val	Trp	Ile	Leu	Leu 235	Leu	Leu	Ala	Ser	Leu 240
Ala	Pro	Leu	Trp	Leu 245	Tyr	Cys	Trp	Arg	Met 250	Phe	Pro	Thr	Lys	Gly 255	Lys
Arg	Asp	Gln	Lys 260	Glu	Met	Leu	Glu	Val 265	Ser	Gly	Ile				

<210> 247

<211> 103
 <212> PRT
 <213> homo sapiens

<400> 247

Asp 1	Cys	Thr	Gln	Asp 5	Pro	Gln	His	Asp	Leu 10	His	His	Pro	Arg	Gly 15	His
Gln	Gln	Pro	Ala 20	Ala	Ala	Pro	Gly	Leu 25	Gly	Gly	Pro	Gly	Pro 30	Gln	Arg
Arg	Ala	Ala 35	Gly	Glu	Gln	Glu	Leu 40	Gly	Gln	Gly	Arg	Leu 45	Leu	Val	Asp
Val	His 50	Ile	Asp	Val	Gly	Val 55	Leu	Trp	Gly	Leu	Arg 60	Gly	His	Leu	Ile
Thr 65	Val	Gly	Cys	Ser	His 70	Cys	Gln	Gly	His	Ser 75	Leu	Arg	Ser	Ser	Gly 80
Pro	Ala	Ser	Gly	Arg 85	Arg	Glu	Gly	Trp	Gly 90	Ala	Gly	Trp	Arg	Ser 95	Gly
Leu	Arg	Val	Gly 100	Gly	Gly	Gly									

<210> 248
 <211> 86
 <212> PRT
 <213> homo sapiens

<400> 248

Gly 1	Ser	Arg	Arg	Arg 5	Asp	Gly	Gly	Gly	Ala 10	Gly	Ala	Ala	Pro	Val 15	Ala
Pro	Arg	Ala	Leu 20	Gly	Arg	Arg	Ala	Arg 25	Ala	Gly	Arg	Cys	Ser 30	Glu	Asp
Glu	Gly	Gly 35	Gly	Gly	Ala	Gln	Arg 40	Val	Trp	Gly	Glu	Gln 45	Pro	Val	Leu
Ala	Ser 50	Gly	Gln	Ser	Pro	Pro 55	Gly	Gln	Glu	Gly	Ser 60	Phe	Thr	Arg	Val
Trp 65	Thr	Arg	Ala	Ser	Leu 70	Pro	Thr	Leu	Gly	Gln 75	Val	Leu	Gln	Pro	Gly 80
Gly	Val	His	Val	Gln 85	Val										

<210> 249
 <211> 154
 <212> PRT
 <213> homo sapiens

<400> 249

Ala 1	Arg	Gly	Gly	Ala 5	Met	Ala	Ala	Gly	Leu 10	Ala	Arg	Leu	Leu	Leu 15	Leu
Leu	Gly	Leu	Ser	Ala	Gly	Gly	Pro	Ala	Pro	Ala	Gly	Ala	Ala	Lys	Met

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Lys	Val	Val	Glu	Glu	Pro	Asn	Ala	Phe	Gly	Val	Asn	Asn	Pro	Phe	Leu														
		35					40					45																	
Pro	Gln	Ala	Ser	Arg	Leu	Gln	Ala	Lys	Arg	Asp	Pro	Ser	Pro	Val	Ser														
	50					55					60																		
Gly	Pro	Val	His	Leu	Phe	Arg	Leu	Ser	Gly	Lys	Cys	Phe	Ser	Leu	Val	80													
	65				70					75																			
Glu	Ser	Thr	Tyr	Lys	Tyr	Glu	Phe	Cys	Pro	Phe	His	Asn	Val	Thr	Gln														
				85					90					95															
His	Glu	Gln	Thr	Phe	Arg	Trp	Asn	Ala	Tyr	Ser	Gly	Ile	Leu	Gly	Ile														
			100					105					110																
Trp	His	Glu	Trp	Glu	Ile	Ala	Asn	Asn	Thr	Phe	Thr	Gly	Met	Trp	Met														
		115					120					125																	
Arg	Asp	Gly	Asp	Asp	Cys	Arg	Ser	Arg	Ser	Arg	Gln	Ser	Lys	Val	Glu														
	130					135					140																		
Leu	Ala	Cys	Ala	Ser	Pro	Ser	Asn	Cys	Val																				
	145				150																								
<210> 250																													
<211> 95																													
<212> PRT																													
<213> homo sapiens																													
<400> 250																													
Pro	Leu	Asp	Ala	Val	Ala	Arg	Ala	Arg	Thr	Arg	Gln	Leu	His	Leu	Ala														
	1			5					10					15															
Leu	Pro	Ala	Pro	Gly	Thr	Ala	Val	Val	Thr	Val	Pro	His	Pro	His	Ala														
			20					25					30																
Arg	Glu	Gly	Val	Val	Gly	Asp	Leu	Pro	Leu	Val	Pro	Asp	Ala	Glu	Asp														
		35					40					45																	
Pro	Thr	Val	Gly	Val	Pro	Ala	Glu	Gly	Leu	Leu	Val	Leu	Gly	His	Val														
	50					55				60																			
Val	Glu	Arg	Ala	Glu	Leu	Ile	Leu	Val	Arg	Gly	Leu	His	Gln	Ala	Glu	80													
	65				70					75																			
Ala	Leu	Ala	Arg	Glu	Ser	Glu	Glu	Met	His	Gly	Ser	Arg	His	Gly															
				85					90					95															
<210> 251																													
<211> 240																													
<212> PRT																													
<213> homo sapiens																													
<400> 251																													
Lys	Val	Thr	Asp	Gly	His	Thr	Arg	Thr	Pro	Arg	Ser	Gly	Val	Pro	Arg														
	1			5					10					15															
Gln	His	Glu	Ala	Gly	Ser	Pro	Gly	Leu	Thr	Ala	Ser	His	Ala	Met	Ser														
			20					25					30																

Ile	His	Leu	Ala	Gly	Ser	Leu	Thr	Ala	Met	Asp	Ser	Ile	Cys	Ala	Ser
		35					40					45			
Glu	Arg	Ser	Gln	Gly	Val	Trp	Arg	Ala	Pro	Thr	Pro	Gly	Cys	Gln	Gly
	50					55					60				
Leu	Ser	Pro	Gly	Pro	Arg	Pro	Gly	Glu	Leu	Pro	Gly	Gly	Ser	Ser	Pro
	65				70					75					80
Glu	Glu	Arg	Leu	Gly	Arg	Leu	Ala	Val	Ala	Gly	Pro	Pro	Arg	Gly	Ala
				85					90					95	
Gln	Asn	Val	Ser	Gln	Ala	Gly	Pro	Glu	Ala	Glu	Ala	Pro	Pro	Leu	Arg
			100					105					110		
Phe	Gly	His	Ala	Trp	Gly	Ala	Gln	Thr	Pro	Arg	Leu	Gly	Ala	Pro	Gly
		115					120					125			
Pro	Trp	Thr	Pro	Leu	Pro	Thr	Leu	Pro	Ser	His	Ile	Pro	Pro	Phe	Trp
	130					135					140				
Ser	Gln	Thr	Pro	Ala	Gln	Arg	Lys	Glu	Gly	Phe	Thr	Glu	Glu	Gly	Gln
	145				150					155				160	
Gly	Arg	Ala	Trp	Pro	Gln	Gly	Gly	Asp	Glu	Asp	Ile	Ser	Gly	Pro	Gly
				165					170					175	
Ser	Cys	Arg	Leu	Leu	Trp	Glu	Glu	Glu	Pro	Cys	Val	Cys	Lys	Leu	Leu
			180					185					190		
Gly	Leu	Ala	Ala	Arg	Pro	Thr	Ala	Gly	Pro	Ser	Leu	Asp	Pro	Cys	Thr
		195					200					205			
Trp	Pro	Ser	Ser	Cys	Pro	Leu	Ala	Ala	Pro	Gly	Leu	Gly	Thr	Gly	Ile
	210					215					220				
Glu	Pro	Arg	Gly	Leu	Gly	Trp	Leu	Gly	Gln	Gly	Asp	Arg	Arg	Glu	Gly
	225				230					235					240

<210> 252
 <211> 216
 <212> PRT
 <213> homo sapiens

<400> 252

Gly	Leu	Val	Met	Pro	Gly	Glu	Leu	Arg	Arg	Pro	Gly	Leu	Gly	Pro	Gln
	1			5					10					15	
Ala	His	Gly	Leu	Pro	Ser	Pro	Leu	Cys	Pro	Pro	Ile	Phe	Pro	Leu	Phe
			20					25					30		
Gly	Pro	Arg	His	Gln	His	Lys	Glu	Arg	Arg	Gly	Ser	Gln	Arg	Lys	Ala
		35					40					45			
Arg	Ala	Glu	Pro	Gly	Pro	Arg	Glu	Gly	Met	Arg	Thr	Phe	Pro	Val	Gln
	50					55				60					
Val	Ala	Ala	Gly	Cys	Ser	Gly	Arg	Lys	Ser	His	Ala	Ser	Val	Asn	Cys
	65				70					75					80
Trp	Gly	Trp	Arg	Pro	Ala	Pro	Leu	Gln	Gly	Pro	Ala	Leu	Thr	Pro	Ala

Val 1	Leu	Arg	Arg	Leu 5	Tyr	Ile	Tyr	Ile	Leu 10	Tyr	Ile	Thr	Asn	Met 15	Lys
Trp	Phe	Ser	Thr 20	Gln	Pro	Leu	Trp	Leu 25	Asn	Thr	Lys	Gln	Arg 30	Ser	His
Arg	Arg	Gly 35	Pro	Gly	Pro	Pro	Pro 40	Ala	Pro	Leu	Ser	Gly 45	Val	Leu	Gly
Ser	Arg 50	Gly	Leu	Pro	His	His 55	Pro	Ser	Gln	Gly	Trp 60	Gly	Arg	Ala	Gly
Pro 65	Arg	Ala	Gly	Ala	Asn 70	Val	Ala	Trp	Asn	Ser 75	Asn	Cys	Ile	Val	Arg 80
Trp	Val	Gly	Gly	Gln 85	Trp	Ala	Arg	Gly	Cys 90	Ser	Gln	Pro	Gly	Pro 95	Phe
Thr	Thr	Asn	Leu 100	Ala	Met	Thr	Cys	Gly 105	Gly	Pro	Trp	Gly	Ser 110	Gly	Cys
Leu	Leu	Gly 115	Ser	Thr	Leu	Ser	Glu 120	Val	Ser	Pro	Trp	Ala 125	Pro	Pro	Ser
Cys	Pro 130	Gln	Gly	His	Pro	Val 135	Leu	Pro	Thr	Arg	Leu 140	Trp	Ala	Trp	Gly
Leu 145	Gln	Asp	Pro	Leu	Cys 150	Arg	Val	Arg	Val	Gly 155	Ala	Gly	His	Gly	Ser 160

Arg	His	Gln	Pro	Asp 165	Ala	Pro	Val	Gly	Val 170	Ala	Arg	Ser	Trp	Asp 175	Gly
Val	Val	Arg	Asn 180	Thr	Ala	Pro	Lys	Thr 185	Gln	Asn	Lys	Asn	Thr 190	Thr	Asn
Gly	Arg	Arg 195	Ser	Pro	Pro	Pro	Thr 200	Glu	Val	Gly	Phe	Glu 205	Pro	Leu	Leu
Ile	Phe 210	Pro	Val	Ser	Phe	Leu 215	Gln	Pro	Trp						

<210> 254
 <211> 79
 <212> PRT
 <213> homo sapiens

<400> 254

Arg 1	Asp	Gly	Gly	Gly 5	Ala	Gly	Ala	Ala	Pro 10	Val	Ala	Pro	Arg	Ala 15	Leu
Gly	Arg	Arg	Ala 20	Arg	Ala	Gly	Arg	Cys 25	Ser	Glu	Asp	Glu	Gly 30	Gly	Gly
Gly	Ala	Gln 35	Arg	Val	Trp	Val	Ser 40	Ser	Leu	Ala	Gly	Trp 45	Arg	Leu	Glu
Arg	Gly 50	Thr	Ala	Arg	Ala	Arg 55	Ser	Pro	Leu	Thr	Leu 60	Pro	Leu	Pro	Val
Gly 65	Gly	Thr	Thr	Arg	Ser 70	Cys	Leu	Arg	Pro	Val 75	Ala	Ser	Arg	Pro	

<210> 255
 <211> 79
 <212> PRT
 <213> homo sapiens

<400> 255

Leu 1	Gly	Leu	Glu	Ala 5	Thr	Gly	Leu	Arg	Gln 10	Glu	Arg	Val	Val	Pro 15	Pro
Thr	Gly	Ser	Gly 20	Lys	Val	Ser	Gly	Glu 25	Arg	Ala	Arg	Ala	Val 30	Pro	Arg
Ser	Ser	Arg 35	Gln	Pro	Ala	Arg	Leu 40	Leu	Thr	Gln	Thr	Arg 45	Trp	Ala	Pro
Pro	Pro 50	Pro	Ser	Ser	Ser	Leu 55	His	Leu	Pro	Ala	Arg 60	Ala	Arg	Arg	Pro
Arg 65	Ala	Arg	Gly	Ala	Thr 70	Gly	Ala	Ala	Pro	Ala 75	Pro	Pro	Pro	Ser	

<210> 256
 <211> 79
 <212> PRT
 <213> homo sapiens

<400> 256

Trp 1	Pro	Gly	Gly	Asp 5	Trp	Pro	Glu	Ala	Arg 10	Thr	Gly	Cys	Ser	Thr 15	Tyr
Gly	Lys	Arg	Gln 20	Gly	Gln	Arg	Gly	Thr 25	Gly	Pro	Gly	Arg	Pro 30	Pro	Leu
Glu	Pro	Pro 35	Ala	Arg	Glu	Ala	Ala 40	His	Pro	Asn	Ala	Leu 45	Gly	Ser	Ser
Thr	Thr 50	Phe	Ile	Phe	Ala	Ala 55	Pro	Ala	Gly	Ala	Gly 60	Pro	Pro	Ala	Glu
Ser 65	Pro	Arg	Ser	Asn	Arg 70	Ser	Arg	Ala	Ser	Pro 75	Ala	Ala	Ile	Ala	

<210> 257
 <211> 51
 <212> PRT
 <213> homo sapiens

<400> 257

Gly 1	His	Leu	Gly	Gly 5	Pro	Thr	Gly	Ser	Val 10	Cys	Ser	Arg	Ile	Leu 15	Leu
Ala	Ser	Ser	Pro 20	Phe	Tyr	Met	Asn	Cys 25	Cys	Ile	Asn	Lys	His 30	Arg	Val
Pro	Glu	Thr 35	Thr	Glu	Val	Ile	Ile 40	Leu	Pro	Thr	Glu	Cys 45	Trp	Pro	Gly
Gln	Ala 50	Trp													

<210> 258
 <211> 49
 <212> PRT
 <213> homo sapiens

<400> 258

Gly 1	Gly	Gly	Phe	Leu 5	Gly	Gln	Ile	Asp	Lys 10	Ser	Lys	Asp	Asn	Ile 15	Ser
Leu	Val	Thr	Val 20	Ile	Gln	Leu	His	Ser 25	Tyr	Thr	Val	Ala	Leu 30	Phe	Gly
Leu	Ser	His 35	Glu	Glu	Val	Leu	Val 40	Thr	Asn	Tyr	Val	Phe 45	Val	Gly	Cys
Phe															

<210> 259
 <211> 48
 <212> PRT
 <213> homo sapiens

<400> 259

Ala 1	Phe	Thr	Arg	Asn 5	Thr	Thr	Asn	Lys	Val 10	Ser	Asp	Met	Leu	Ala 15	Asn
Gln	Ala	Arg	Leu	Arg	Ser	Leu	Arg	Arg	Pro	Asn	Trp	Leu	Cys	Leu	Leu

				20					25					30			
Lys	Asp	Ser	Ser	Gly	Leu	Val	Ser	Ile	Leu	His	Glu	Leu	Leu	His	Lys		
	35						40					45					

<210> 260
 <211> 179
 <212> PRT
 <213> homo sapiens

<400> 260

Pro	Gly	Ile	Ser	Val	Ser	Val	Asp	Lys	Met	Glu	Ser	Ser	Pro	Phe	Asn		
1				5					10					15			
Arg	Arg	Gln	Trp	Thr	Ser	Leu	Ser	Leu	Arg	Val	Thr	Ala	Lys	Glu	Leu		
			20					25					30				
Ser	Leu	Val	Asn	Lys	Asn	Lys	Ser	Ser	Ala	Ile	Val	Glu	Ile	Phe	Ser		
		35					40					45					
Lys	Tyr	Gln	Lys	Ala	Ala	Glu	Glu	Thr	Asn	Met	Glu	Lys	Lys	Arg	Ser		
	50					55					60						
Asn	Thr	Glu	Asn	Leu	Ser	Gln	His	Phe	Arg	Lys	Gly	Thr	Leu	Thr	Val		
65					70					75					80		
Leu	Lys	Lys	Lys	Trp	Glu	Asn	Pro	Gly	Leu	Gly	Ala	Glu	Ser	His	Thr		
				85					90					95			
Asp	Ser	Leu	Arg	Asn	Ser	Ser	Thr	Glu	Ile	Arg	His	Arg	Ala	Asp	His		
			100					105					110				
Pro	Pro	Ala	Glu	Val	Thr	Ser	His	Ala	Ala	Ser	Gly	Ala	Lys	Ala	Asp		
		115					120					125					
Gln	Glu	Glu	Gln	Ile	His	Pro	Arg	Ser	Arg	Leu	Arg	Ser	Pro	Pro	Glu		
	130					135					140						
Ala	Leu	Val	Gln	Gly	Arg	Tyr	Pro	His	Ile	Lys	Asp	Gly	Glu	Asp	Leu		
145				150						155					160		
Lys	Asp	His	Ser	Thr	Glu	Ser	Lys	Lys	Met	Glu	Asn	Cys	Leu	Gly	Glu		
				165					170					175			
Ser	Arg	His															

<210> 261
 <211> 56
 <212> PRT
 <213> homo sapiens

<400> 261

Gln	Ala	Thr	Leu	Leu	Leu	Glu	Pro	Lys	Leu	Thr	Lys	Lys	Asn	Lys	Ser		
1				5					10					15			
Thr	Pro	Asp	Leu	Asp	Ser	Gly	His	Leu	Leu	Lys	Pro	Ser	Phe	Arg	Val		
			20					25					30				
Asp	Ile	Pro	Thr	Ser	Arg	Thr	Val	Arg	Ile	Leu	Lys	Thr	Thr	Gln	Gln		
		35					40					45					

Lys Val Lys Lys Trp Lys Ile Val
50 55

<210> 262
<211> 94
<212> PRT
<213> homo sapiens

<400> 262

Asp 1	Ser	Ala	Pro	Ser 5	Pro	Gly	Phe	Ser	His 10	Phe	Phe	Phe	Asn	Thr 15	Val
Arg	Val	Pro	Phe 20	Leu	Lys	Cys	Trp	Glu 25	Arg	Phe	Ser	Val	Leu 30	Leu	Leu
Phe	Phe	Ser 35	Met	Phe	Val	Ser	Ser 40	Ala	Ala	Phe	Trp	Tyr 45	Leu	Glu	Asn
Ile	Ser 50	Thr	Ile	Ala	Asp	Asp 55	Leu	Phe	Leu	Leu	Thr 60	Arg	Glu	Ser	Ser
Leu 65	Ala	Val	Thr	Leu	Asn 70	Asp	Ser	Glu	Val	His 75	Cys	Arg	Leu	Leu	Asn 80
Gly	Asp	Asp	Ser	Ile 85	Leu	Ser	Thr	Asp	Thr 90	Glu	Ile	Pro	Gly		

<210> 263
<211> 75
<212> PRT
<213> homo sapiens

<400> 263

Val 1	Met	Ser	Asp	Pro 5	Ala	Asp	Lys	Ala	Ala 10	Arg	Ala	Asp	Ser	Ala 15	Arg
Ala	Ala	Arg	Gly 20	Lys	Arg	Lys	Lys	Asn 25	Val	Glu	Glu	Asn	Met 30	Ala	Tyr
Ser	Ala	Leu 35	Met	Glu	Val	Ala	Gly 40	Tyr	Cys	Leu	Ile	Glu 45	Arg	Met	Leu
Trp	Asn 50	Pro	Met	Leu	Lys	Ile 55	Lys	Ser	Val	Trp	Leu 60	Cys	Ser	Tyr	Ala
Val 65	Met	Val	Ile	Pro	Arg 70	Gln	Leu	Ala	Lys	Val 75					

<210> 264
<211> 74
<212> PRT
<213> homo sapiens

<400> 264

Ala 1	Met	Phe	Ser	Ser 5	Thr	Phe	Phe	Phe	Leu 10	Leu	Pro	Arg	Ala	Ala 15	Arg
Ala	Glu	Ser	Ala 20	Arg	Ala	Ala	Leu	Ser 25	Ala	Gly	Ser	Leu	Ile 30	Thr	Tyr

Ala	Phe	Tyr	Lys	Arg	Leu	Pro	Lys	Lys	Lys	Leu	Leu	Thr	Arg	Asn	Val
		35					40					45			
Asp	Lys	Pro	Leu	Lys	Ala	Asn	Lys	Gln	Gln	Thr	Val	Val	Phe	Ala	Phe
	50					55					60				
Ser	Tyr	Ser	Trp	Gln	Ala	Glu	Val	Arg	Ala						
	65				70										

<210> 265
 <211> 63
 <212> PRT
 <213> homo sapiens

<400> 265

Asp	Ser	Lys	Ala	Phe	Ser	Leu	Leu	Ser	Ser	10	Asn	Gln	Pro	Leu	Pro	Ser
1				5											15	
Lys	Leu	Ser	Arg	Pro	Cys	Phe	Pro	Pro	25	His	Phe	Phe	Phe	Phe	30	Tyr
			20													Leu
Glu	Pro	Leu	Glu	Pro	Asn	Arg	Leu	Glu	Pro	Pro	Cys	Leu	Leu	Asp	His	
		35					40					45				
Ser	Ser	Pro	Thr	His	Phe	Ile	Lys	Gly	Tyr	Pro	Lys	Arg	Asn	Cys		
	50					55					60					

<210> 266
 <211> 94
 <212> PRT
 <213> homo sapiens

<400> 266

Arg	Arg	Gly	Ser	Gly	Ser	Arg	Ser	Ser	Met	Ala	Pro	Val	Leu	Ala	Ser
1				5					10					15	
Met	Leu	Trp	Met	Ser	Thr	Arg	Gly	Thr	Ala	Met	Thr	Ser	Thr	Ser	Leu
			20					25					30		
Cys	Thr	Ser	Arg	Ala	Arg	Ser	Arg	Pro	Met	Pro	Ser	Ser	Ser	Ser	Pro
		35					40					45			
Thr	Pro	Thr	Ala	Trp	Arg	Cys	Cys	Cys	Ala	Thr	Arg	Thr	Arg	Val	Ser
	50					55					60				
Thr	Ser	Thr	Arg	Thr	Gly	Ala	Ser	Leu	Arg	Met	Trp	Cys	Cys	Ser	Gly
	65				70				75						80
Gly	Arg	Cys	Leu	Leu	Leu	Trp	Pro	Thr	Ser	Ala	Pro	Thr	Arg		
				85					90						

<210> 267
 <211> 254
 <212> PRT
 <213> homo sapiens

<400> 267

Gly	Asp	Arg	Lys	Pro	Leu	Tyr	His	Tyr	Gly	Arg	Gly	Met	Asn	Pro	Ala
1				5					10					15	

Asp	Lys	Pro	Ala 20	Trp	Ala	Arg	Glu	Val 25	Lys	Glu	Arg	Thr	Arg 30	Met	Asn	
Lys	Gln	Gln 35	Asn	Ser	Pro	Leu	Ala 40	Lys	Ser	Lys	Pro	Gly 45	Ser	Thr	Gly	
Pro	Glu 50	Pro	Pro	Ser	Pro	Gln 55	Ala	Ser	Pro	Gly	Pro 60	Pro	Gly	Leu	Pro	
Trp 65	Ala	Pro	Lys	Pro	Tyr 70	His	Lys	Phe	Met	Ala 75	Phe	Lys	Ser	Phe	Ala 80	
Asp	Leu	Pro	His 85	Pro	Leu	Leu	Val	Asp 90	Leu	Thr	Val	Glu	Glu 95	Gly		
Gln	Arg	Leu	Lys 100	Val	Ile	Tyr	Gly	Ser 105	Ser	Ala	Gly	Phe	His 110	Ala	Val	
Asp	Val	Asp 115	Ser	Gly	Asn	Ser	Tyr 120	Asp	Ile	Tyr	Ile	Pro 125	Val	His	Ile	
Gln	Ser 130	Gln	Ile	Thr	Pro	His 135	Ala	Ile	Ile	Phe	Leu 140	Pro	Asn	Thr	Asp	
Gly 145	Met	Glu	Met	Leu	Leu 150	Cys	Tyr	Glu	Asp	Glu 155	Gly	Val	Tyr	Val	Asn 160	
Thr	Tyr	Gly	Arg	Ile 165	Ile	Lys	Asp	Val	Val 170	Leu	Gln	Trp	Gly	Glu 175	Met	
Pro	Thr	Ser	Val 180	Ala	Tyr	Ile	Cys	Ser 185	Asn	Gln	Ile	Met	Gly 190	Trp	Gly	
Glu	Lys	Ala 195	Ile	Glu	Ile	Arg	Ser 200	Val	Glu	Thr	Gly	His 205	Leu	Asp	Gly	
Val	Phe 210	Met	His	Lys	Arg	Ala 215	Gln	Arg	Leu	Lys	Phe 220	Leu	Cys	Glu	Arg	
Asn 225	Asp	Lys	Val	Phe	Phe 230	Ala	Ser	Val	Arg	Ser 235	Gly	Gly	Ser	Ser	Gln 240	
Val	Tyr	Phe	Met	Thr 245	Leu	Asn	Arg	Asn	Cys 250	Ile	Met	Asn	Trp			

<210> 268

<211> 231

<212> PRT

<213> homo sapiens

<400> 268

Gly 1	Lys	Lys	His	Leu 5	Val	Ile	Pro	Leu	Thr 10	Gln	Glu	Leu	Glu	Pro 15	Leu	
Ser	Ser	Phe	Val 20	His	Glu	Asp	Pro	Val 25	Glu	Val	Ala	Arg	Leu 30	His	Arg	
Ala	Asp	Leu 35	Asn	Gly	Phe	Leu	Thr 40	Pro	Ala	His	Tyr	Leu 45	Val	Gly	Ala	
Asp	Val 50	Gly	His	Arg	Ser	Arg 55	His	Leu	Pro	Pro	Leu 60	Gln	His	His	Ile	

Leu 65	Asn	Asp	Ala	Pro	Val 70	Arg	Val	Asp	Val	Asp 75	Thr	Leu	Val	Leu	Val 80
Ala	Gln	Gln	His	Leu 85	His	Ala	Val	Gly	Val 90	Gly	Glu	Glu	Asp	Asp 95	Gly
Met	Gly	Arg	Asp 100	Leu	Ala	Leu	Asp	Val 105	His	Arg	Asp	Val	Asp 110	Val	Ile
Ala	Val	Pro 115	Arg	Val	Asp	Ile	His 120	Ser	Met	Glu	Ala	Ser 125	Thr	Gly	Ala
Ile	Asp 130	Asp	Leu	Glu	Pro	Leu 135	Pro	Leu	Leu	Tyr	Cys 140	Gln	Val	Asp	Gln
Gln 145	Arg	Ala	Val	Gly	Glu 150	Val	Gly	Lys	Gly	Leu 155	Glu	Gly	His	Glu	Phe 160
Val	Val	Gly	Phe	Gly 165	Gly	Pro	Gly	Glu	Ala 170	Trp	Gly	Pro	Trp	Gly 175	Gly
Leu	Gly	Ala	Gly 180	Gly	Leu	Arg	Pro	Arg 185	Ala	Ala	Trp	Leu	Ala 190	Leu	Gly
Gln	Gly	Arg 195	Val	Leu	Leu	Leu	Val 200	His	Pro	Cys	Ser	Leu 205	Phe	Tyr	Leu
Ser	Gly 210	Pro	Gly	Trp	Phe	Val 215	Ser	Gly	Ile	His	Ala 220	Pro	Thr	Ile	Met
Val 225	Gln	Gly	Leu	Pro	Val 230	Pro									

<210> 269

<211> 454

<212> PRT

<213> homo sapiens

<400> 269

Gly 1	Ala	Gly	Cys	Thr 5	Ser	Pro	Gly	Leu	Trp 10	Ala	Arg	Lys	Ala 15	Ala
Arg	Cys	Leu	Pro 20	Thr	Tyr	Pro	Ser	Arg 25	Ala	Gln	Pro	Ser	Asn 30	Gly
Arg	Arg	Arg 35	Arg	Arg	Arg	Pro	Gly 40	Leu	Gly	Ala	Leu	Ala 45	Ala	Val
Pro	Ala 50	Met	Ala	Glu	Ser	Val 55	Glu	Arg	Leu	Gln 60	Arg	Val	Gln	Glu
Leu 65	Glu	Arg	Glu	Leu	Ala 70	Gln	Glu	Arg	Ser	Leu 75	Gln	Val	Pro	Ser
Gly	Asp	Gly	Gly	Gly 85	Gly	Arg	Val	Arg	Ile 90	Glu	Lys	Met	Ser	Ser 95
Val	Val	Asp	Ser 100	Asn	Pro	Tyr	Ser	Arg 105	Leu	Met	Ala	Leu	Lys 110	Arg
Gly	Ile	Val	Ser	Asp	Tyr	Glu	Lys	Ile	Arg	Thr	Phe	Ala	Val	Ile

[illegible]

450

<210> 270
<211> 123
<212> PRT
<213> homo sapiens

<400> 270

Lys	Leu	Thr	Val	Pro	Lys	Phe	Asn	Arg	Asn	Phe	Asn	Thr	Phe	Cys	Thr
1				5					10					15	
Lys	Ile	Pro	Ala	Thr	Thr	Pro	Ile	Val	Val	Gly	Arg	Leu	Ala	Ala	Gln
			20					25					30		
Thr	Pro	Ser	Arg	Phe	Arg	Val	Phe	Ser	Ser	Ile	Phe	Ala	Ala	Thr	Thr
		35					40					45			
Ser	Gly	Gly	Ala	His	Ala	Lys	Gln	Ala	Asp	Ser	Pro	Gly	Ile	Ile	Ser
	50					55					60				
Cys	Ile	Cys	Pro	Glu	Thr	Ala	Phe	Ser	Leu	Thr	Pro	Asp	Ser	Ile	His
65					70					75					80
Val	Cys	Pro	Ser	Ser	Leu	Gln	Ala	Val	Phe	Ile	Val	Ile	Arg	Ala	Ser
				85					90					95	
Lys	Leu	Ser	Thr	Gln	Leu	Arg	Thr	Arg	Ser	Thr	Gly	Phe	Pro	Ser	Ser
			100					105					110		
Asn	Pro	Pro	Leu	Leu	Ile	Leu	Ser	Met	Lys	Cys					
			115				120								

<210> 271
<211> 176
<212> PRT
<213> homo sapiens

<400> 271

Cys	Ser	Ser	Glu	Tyr	Val	Leu	Leu	Leu	Glu	Leu	Tyr	Leu	Ile	Leu	Leu
1				5					10					15	
Asp	Glu	Val	Gly	Arg	Lys	Val	Tyr	Ser	Tyr	Trp	Leu	Val	Pro	Pro	Cys
			20					25					30		
His	Asn	Gln	Arg	Val	Ala	Thr	Tyr	Gln	Cys	His	Ile	Leu	Ser	Ala	Phe
		35					40					45			
Gln	Gln	Ser	His	Tyr	Leu	Leu	His	Gln	His	Leu	Leu	Leu	Leu	Arg	Gln
	50				55					60					
Arg	Tyr	Gly	Phe	Ser	His	Ser	Arg	Leu	Gln	Phe	Pro	Phe	Val	Ser	Met
65					70					75					80
Pro	Ser	Ser	Gly	Cys	Arg	Asp	Ser	Asn	Pro	Pro	Pro	Leu	Ser	Ser	Ser
				85					90					95	
Ser	Arg	Cys	Gly	Pro	Gly	Arg	Pro	Leu	Arg	Arg	Arg	Ser	Ser	Gly	Pro
			100					105					110		
Ala	Asp	Ser	Ser	Pro	Gly	Gln	Val	Pro	Ala	Pro	Ala	Pro	Gly	Pro	Ala
			115				120					125			

Ala	Ala	Gly	Ala	Pro	Gln	Thr	Pro	Pro	Trp	Leu	Gly	Leu	Arg	Pro	Pro
	130					135					140				
Thr	Leu	Pro	Ala	Arg	Ala	Phe	Ala	Ala	Ala	Phe	Ala	Pro	Arg	Cys	Ser
145					150					155				160	
Ala	Gly	Pro	Ala	Arg	Gly	Thr	Trp	Gly	Gly	Thr	Ser	Pro	Leu	Pro	Ser
				165					170					175	

<210> 272
 <211> 117
 <212> PRT
 <213> homo sapiens

<400> 272

Glu	Ala	Arg	Gln	Ala	Trp	Thr	Gly	Ala	Lys	Gly	Ala	Gly	Ser	Leu	Thr
1				5					10					15	
Phe	Ser	Ser	Leu	Gln	Ser	Gly	His	Leu	Ala	Ser	Gly	Ser	Gln	Ser	Pro
			20					25					30		
Glu	Ser	Thr	Lys	Ala	Pro	Gly	Thr	Pro	Pro	Thr	Pro	Ser	Tyr	Pro	Gly
		35					40					45			
Thr	Pro	Ser	Arg	Gln	Leu	Leu	Trp	Gln	Trp	Val	Gln	Pro	Arg	Pro	Ala
	50					55					60				
Leu	Pro	Ala	Ser	Ser	Pro	Cys	Ser	Arg	His	Gln	Leu	Tyr	Leu	Pro	Arg
65					70					75				80	
Gln	Ala	Met	Ser	Trp	Leu	Leu	Ser	Pro	Ala	Pro	Ser	Val	Pro	Leu	Asp
				85					90					95	
Phe	Ser	Gly	Ala	Ser	Pro	Val	Trp	Ala	Thr	Leu	Cys	Phe	Pro	His	Pro
			100					105					110		
Arg	Leu	Pro	His	Arg											
			115												

<210> 273
 <211> 86
 <212> PRT
 <213> homo sapiens

<400> 273

Ala	Pro	Ala	Leu	Pro	Pro	Pro	Ala	Gly	Asn	Val	Leu	Ala	Ser	Gln	Pro
1				5					10					15	
Ser	Thr	Ile	Cys	Ser	Pro	Arg	Leu	Leu	Arg	Gly	Gln	Pro	Ser	Leu	Gly
			20					25					30		
His	Pro	Leu	Phe	Pro	Ser	Ser	Ser	Ala	Pro	Thr	Gln	Val	Thr	Asp	Pro
		35					40					45			
Ala	Asp	Ser	Phe	Ser	Leu	Gly	Lys	Val	Gly	Cys	Cys	Leu	Thr	Ser	Pro
	50					55					60				
Ser	Ser	Pro	Pro	Pro	Ile	His	Thr	His	Arg	His	Pro	Pro	Thr	Pro	Gly
65					70					75					80

Arg Leu Val Ser His Met
85

<210> 274

<211> 177

<212> PRT

<213> homo sapiens

<400> 274

Glu 1	Ala	Arg	Thr	Leu 5	Pro	Ala	Gly	Gly	Gly 10	Arg	Ala	Gly	Ala	Tyr 15	Cys
Arg	Glu	Arg	Arg 20	Leu	Ala	Val	Leu	Ala 25	Trp	Ala	Gly	Pro	Thr 30	Ala	Ile
Thr	Val	Ala 35	Tyr	Leu	Gly	Ser	Leu 40	Gly	Arg	Met	Glu	Trp 45	Val	Gly	Cys
Gln	Gly 50	Leu	Trp	Cys	Phe	Leu 55	Val	Ile	Gly	Thr	Leu 60	Met	Pro	Ser	Ala
His 65	Phe	Ala	Lys	Lys	Lys 70	Lys	Leu	Met	Thr	Leu 75	Leu	Pro	Trp	Leu	Leu 80
Ser	Met	Leu	Ala	Trp 85	Pro	Pro	Arg	Val	Gly 90	Gly	Thr	Ser	Pro	Leu 95	Leu
Ala	Glu	Ala	Gly 100	Glu	Gln	Val	Leu	Ser 105	Tyr	Asp	Pro	Ile	His 110	Gln	Ala
Gly	Val	Leu 115	Ser	Pro	Ser	Gly	His 120	His	Ser	Ser	Gln	His 125	Gln	Gly	Pro
Val	Gly 130	Leu	Gly	Gln	Gly	Ser 135	Glu	Lys	Gly	Trp	Gln 140	Glu	Val	Pro	Arg
Ser 145	Ser	Gln	Pro	Gly	Arg 150	Gly	Thr	Asn	Ala	Leu 155	Asn	Thr	Ser	Lys	Leu 160
Arg	Asp	Pro	Lys	Val 165	Ser	Thr	Pro	Gly	Ser 170	Gly	Leu	Pro	Pro	His 175	Arg

His

<210> 275

<211> 71

<212> PRT

<213> homo sapiens

<400> 275

Gln 1	Phe	Pro	Gly	Pro 5	Ser	Val	Pro	Glu	Gln 10	Ser	Thr	Ser	Val	Ser 15	Val
Thr	Thr	Ser	Cys 20	Leu	Phe	Pro	Ser	Leu 25	His	Leu	Leu	Gln	Phe 30	Ile	Tyr
Met	Leu	Leu 35	Leu	Leu	Val	His	Phe 40	Cys	Leu	Pro	Tyr	Gln 45	Ala	Val	Asn
Glu	Gly 50	Arg	Asn	Leu	Val	Cys 55	Phe	Ile	His	His	His 60	Val	Pro	Ser	Ala

Trp His Ile Val Gly Leu His
65 70

<210> 276
<211> 102
<212> PRT
<213> homo sapiens

<400> 276

Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Cys	Leu	Ile
1				5					10					15	
Asn	Met	Ser	Ile	Tyr	Leu	Ala	Pro	Asp	Gly	Asn	Thr	Lys	Ser	Trp	Gln
			20					25					30		
Trp	Glu	Trp	Lys	Gly	Ser	Leu	Ser	Gln	Ile	Leu	Pro	Tyr	Tyr	Val	Asp
		35					40					45			
Pro	Lys	Ala	Gly	Leu	Gly	Ser	Lys	Ala	His	Lys	Pro	Pro	Lys	Gln	Ile
	50					55					60				
Phe	Ile	Glu	His	Leu	Asp	Tyr	Tyr	Arg	Pro	Ser	Ile	Leu	Leu	Gly	Thr
65					70					75					80
Met	Gly	Asp	Val	Lys	Glu	Val	Ile	Ser	His	Met	Ile	Cys	Leu	Gln	Gly
				85					90					95	
Ala	Lys	Asn	Ala	Ser	Gly										
			100												

<210> 277
<211> 65
<212> PRT
<213> homo sapiens

<400> 277

Gly	Val	Ile	Glu	Ser	Arg	Arg	Val	Leu	Ser	Arg	Gly	Val	Ile	Arg	Phe
1				5					10					15	
Ile	Phe	Lys	Gln	Pro	Asn	Pro	Gly	Arg	Cys	Gly	Pro	Ile	Leu	Ser	Ala
			20					25					30		
Leu	Lys	Lys	Ile	Pro	Phe	Pro	Tyr	Leu	Pro	Ala	Ser	Ile	Met	Ser	Val
		35					40					45			
Glu	Glu	Ser	Asn	Cys	Gly	Ser	Phe	Glu	Gly	Asp	Gly	Pro	Phe	Phe	Pro
	50					55					60				
Val															
65															

<210> 278
<211> 65
<212> PRT
<213> homo sapiens

<400> 278

Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Leu	Phe	Asn	Lys
1				5						10				15	

Tyr	Glu	His	Leu	Phe	Gly	Thr	Arg	Trp	Gln	Tyr	Lys	Ile	Leu	Ala	Val
			20					25					30		
Gly	Val	Glu	Arg	Phe	Ser	Leu	Ser	Asn	Thr	Ser	Ile	Leu	Cys	Arg	Pro
		35					40					45			
Lys	Gly	Arg	Thr	Trp	Gln	Gln	Gly	Ser	Gln	Thr	Thr	Gln	Thr	Asn	Ile
	50					55					60				
Tyr															
65															

<210> 279
 <211> 489
 <212> PRT
 <213> homo sapiens

<400> 279

Leu	Ala	Asp	Ser	Phe	Pro	Gly	Ser	Ser	Pro	Tyr	Glu	Gly	Tyr	Asn	Tyr
1				5					10					15	
Gly	Ser	Phe	Glu	Asn	Val	Ser	Gly	Ser	Thr	Asp	Gly	Leu	Val	Asp	Ser
			20					25					30		
Ala	Gly	Thr	Gly	Asp	Leu	Ser	Asp	Gly	Tyr	Gln	Gly	Arg	Ser	Phe	Glu
		35					40					45			
Pro	Val	Gly	Thr	Arg	Pro	Arg	Val	Asp	Ser	Met	Ser	Ser	Val	Glu	Glu
	50					55					60				
Asp	Asp	Tyr	Asp	Thr	Leu	Thr	Asp	Ile	Asp	Ser	Asp	Lys	Asn	Val	Ile
65					70					75					80
Arg	Thr	Lys	Gln	Tyr	Leu	Tyr	Val	Ala	Asp	Leu	Ala	Arg	Lys	Asp	Lys
				85					90					95	
Arg	Val	Leu	Arg	Lys	Lys	Tyr	Gln	Ile	Tyr	Phe	Trp	Asn	Ile	Ala	Thr
			100					105					110		
Ile	Ala	Val	Phe	Tyr	Ala	Leu	Pro	Val	Val	Gln	Leu	Val	Ile	Thr	Tyr
			115				120					125			
Gln	Thr	Val	Val	Asn	Val	Thr	Gly	Asn	Gln	Asp	Ile	Cys	Tyr	Tyr	Asn
	130					135					140				
Phe	Leu	Cys	Ala	His	Pro	Leu	Gly	Asn	Leu	Ser	Ala	Phe	Asn	Asn	Ile
145					150					155					160
Leu	Ser	Asn	Leu	Gly	Tyr	Ile	Leu	Leu	Gly	Leu	Leu	Phe	Leu	Leu	Ile
				165					170					175	
Ile	Leu	Gln	Arg	Glu	Ile	Asn	His	Asn	Arg	Ala	Leu	Leu	Arg	Asn	Asp
			180					185					190		
Leu	Cys	Ala	Leu	Glu	Cys	Gly	Ile	Pro	Lys	His	Phe	Gly	Leu	Phe	Tyr
		195					200					205			
Ala	Met	Gly	Thr	Ala	Leu	Met	Met	Glu	Gly	Leu	Leu	Ser	Ala	Cys	Asp
	210					215						220			
His	Val	Cys	Pro	Asn	Tyr	Thr	Asn	Phe	Gln	Phe	Asp	Thr	Ser	Phe	Met

225					230					235				240	
Tyr	Met	Ile	Ala	Gly 245	Leu	Cys	Met	Leu	Lys 250	Leu	Tyr	Gln	Lys	Arg 255	His
Pro	Asp	Ile	Asn 260	Ala	Ser	Ala	Tyr	Ser 265	Ala	Tyr	Ala	Cys	Leu 270	Ala	Ile
Val	Ile	Phe 275	Phe	Ser	Val	Leu	Gly 280	Val	Val	Phe	Gly	Lys 285	Gly	Asn	Thr
Ala	Phe 290	Trp	Ile	Val	Phe	Ser 295	Ile	Ile	His	Ile	Ile 300	Ala	Thr	Leu	Leu
Leu 305	Ser	Thr	Gln	Leu	Tyr 310	Tyr	Met	Gly	Arg	Trp 315	Lys	Leu	Asp	Ser	Gly 320
Ile	Phe	Arg	Arg	Ile 325	Leu	His	Val	Leu	Tyr 330	Thr	Asp	Cys	Ile	Arg 335	Gln
Cys	Ser	Gly	Pro 340	Leu	Tyr	Val	Asp	Arg 345	Met	Val	Leu	Leu	Val 350	Met	Gly
Asn	Val	Ile 355	Asn	Trp	Ser	Leu	Ala 360	Ala	Tyr	Gly	Leu	Ile 365	Met	Arg	Pro
Asn	Asp 370	Phe	Ala	Ser	Tyr	Leu 375	Leu	Ala	Ile	Gly	Ile 380	Cys	Asn	Leu	Leu
Leu 385	Tyr	Phe	Ala	Phe	Tyr 390	Ile	Ile	Met	Lys	Leu 395	Arg	Ser	Gly	Glu	Arg 400
Ile	Lys	Leu	Ile	Pro 405	Leu	Leu	Cys	Ile	Val 410	Cys	Thr	Ser	Val	Val 415	Trp
Gly	Phe	Ala	Leu 420	Phe	Phe	Phe	Phe	Gln 425	Gly	Leu	Ser	Thr	Trp 430	Gln	Lys
Thr	Pro	Ala 435	Glu	Ser	Arg	Glu	His 440	Asn	Arg	Asp	Cys	Ile 445	Leu	Leu	Asp
Phe	Phe 450	Asp	Asp	His	Asp	Ile 455	Trp	His	Phe	Leu	Ser 460	Ser	Ile	Ala	Met
Phe 465	Gly	Ser	Phe	Leu	Val 470	Leu	Leu	Thr	Leu	Asp 475	Asp	Asp	Leu	Asp	Thr 480
Val	Gln	Arg	Asp	Lys 485	Ile	Tyr	Val	Phe							

<210> 280

<211> 182

<212> PRT

<213> homo sapiens

<400> 280

Ala 1	Pro	Leu	Cys	His 5	Arg	Pro	Val	Thr	Leu 10	Ser	Cys	Cys	Gly	Asp 15	Glu
Ser	Gln	His	Arg 20	Cys	Pro	Ala	Leu	Asp 25	Gly	Ser	Arg	Thr	Ala 30	Arg	Ser

Ser	Leu	Gly	Leu	Ala	Trp	Asp	Ser	His	Gly	Val	Ala	Trp	Asn	Leu	Ala
		35					40					45			
Ala	Ala	Leu	Cys	Arg	Gly	Ala	Gly	Leu	Leu	Pro	Trp	Asp	Pro	Gln	Met
	50					55					60				
Leu	Ala	Lys	Leu	Leu	Leu	Ser	Ser	Gln	Cys	Trp	Gly	Leu	Pro	Trp	Ala
	65				70					75					80
Pro	Val	Leu	Trp	Leu	Ser	Ile	Cys	Pro	Phe	Ala	Arg	Gly	Arg	Met	Glu
				85					90					95	
Gly	Thr	Pro	Ser	Pro	Phe	His	Ala	Leu	His	Phe	Ala	Arg	Pro	Pro	Pro
			100					105					110		
His	Asn	Ala	Pro	Ala	Trp	Asp	Leu	Arg	Pro	Leu	Phe	Pro	Pro	Ile	Leu
		115					120					125			
Pro	Leu	Gln	Gly	Leu	Val	Trp	Gly	Leu	Asn	Leu	Cys	Pro	Val	Ser	Gly
	130					135					140				
Pro	Gln	Phe	Ser	Leu	Gly	Cys	Pro	Trp	Leu	Pro	Ser	Leu	Pro	Ile	Pro
	145				150					155					160
Val	Ser	Gln	Asp	Gly	Trp	Gly	Tyr	Glu	Ile	Leu	Gly	Val	Gly	Gln	Leu
				165					170					175	
Val	Pro	Asp	Phe	Trp	Cys										
			180												

<210> 281

<211> 536

<212> PRT

<213> homo sapiens

<400> 281

Ala	Arg	Pro	Gly	Cys	Pro	Ala	Ala	Ile	Gln	Cys	Trp	Ala	Ala	Val	Leu
	1			5					10					15	
Gly	Leu	Ile	Pro	Thr	Ala	Arg	Gln	Ser	Asp	Arg	Ser	Met	Thr	Gln	Arg
			20					25					30		
Ser	Ser	Gly	Pro	Leu	Glu	Val	Lys	Arg	Arg	Ala	Gln	Leu	Leu	Leu	Glu
		35					40					45			
Asp	Ile	Asp	Leu	Val	Pro	Leu	His	Ser	Ile	Gln	Val	Val	Ile	Gln	Cys
	50					55					60				
Gln	Gln	His	Gln	Glu	Gly	Pro	Glu	His	Gly	Asp	Gly	Gly	Glu	Glu	Val
	65				70					75					80
Pro	Asp	Val	Val	Val	Val	Lys	Glu	Val	Glu	Glu	Asp	Ala	Val	Pro	Val
				85					90					95	
Val	Leu	Pro	Arg	Leu	Cys	Arg	Gly	Phe	Leu	Pro	Gly	Ala	Glu	Ser	Leu
			100					105					110		
Glu	Glu	Glu	Glu	Glu	Arg	Glu	Ala	Pro	Asp	His	Gly	Gly	Ala	Asn	Asp
		115					120					125			
Ala	Glu	Gln	Gly	Asp	Glu	Leu	Asp	Pro	Leu	Pro	Thr	Pro	Glu	Leu	His
	130					135					140				

Asp 145	Asp	Val	Glu	Gly	Glu 150	Val	Lys	Glu	Gln	Val 155	Ala	Asp	Ala	Asn	Gly 160
Gln	Gln	Val	Gly	Ser 165	Glu	Ile	Ile	Gly	Ala 170	His	Asp	Lys	Pro	Ile 175	Gly
Ser	Gln	Arg	Pro 180	Val	Asp	Asp	Val	Ala 185	His	Asp	Gln	Gln	His 190	His	Ala
Val	His	Val 195	Glu	Arg	Pro	Ala	Ala 200	Leu	Pro	Asp	Ala	Val 205	Cys	Val	Glu
His	Val 210	Glu	Asp	Ala	Ala	Glu 215	Asp	Pro	Arg	Val	Gln 220	Phe	Pro	Pro	Ala
His 225	Val	Ile	Glu	Leu	Arg 230	Ala	Glu	Glu	Gln	Gly 235	Gly	Asp	Asp	Val	Asn 240
Asp	Gly	Glu	Asp	Asp 245	Pro	Glu	Arg	Arg	Val 250	Pro	Phe	Ala	Lys	Asp 255	His
Ala	Gln	His	Arg 260	Glu	Glu	Asp	Asp	Asn 265	Gly	Gln	Ala	Gly	Val 270	Gly	Thr
Val	Gly	Ala 275	Gly	Val	Asp	Val	Arg 280	Val	Pro	Leu	Leu	Val 285	Glu	Leu	Gln
His	Ala 290	Glu	Ser	Gly	Asp	His 295	Val	His	Glu	Arg	Cys 300	Val	Lys	Leu	Glu
Ile 305	Gly	Ile	Val	Gly	Ala 310	His	Met	Ile	Ala	Ser 315	Thr	Glu	Gln	Pro	Leu 320
His	His	Gln	Gly	Cys 325	Ala	His	Gly	Val	Glu 330	Lys	Pro	Lys	Val	Phe 335	Gly
Asp	Pro	Thr	Phe 340	Gln	Gly	Thr	Glu	Val 345	Ile	Ala	Gln	Gln	Gly 350	Pro	Val
Val	Val	Asp 355	Leu	Pro	Leu	Gln	Asp 360	Asp	Glu	Gln	Glu	Lys 365	Gln	Pro	Gln
Gln	Asp 370	Val	Pro	Gln	Val	Ala 375	Glu	Asp	Val	Val	Glu 380	Gly	Ala	Glu	Ile
Ala 385	Gln	Trp	Val	Gly	Ala 390	Glu	Glu	Val	Val	Val 395	Ala	Asp	Val	Leu	Ile 400
Pro	Cys	Asp	Ile	His 405	His	Arg	Leu	Val	Gly 410	Asp	His	Gln	Leu	His 415	His
Arg	Lys	Gly	Ile 420	Glu	Asp	Ser	Asn	Gly 425	Gly	Asn	Val	Pro	Glu 430	Val	Asp
Leu	Val	Leu 435	Phe	Pro	Gln	Asn	Thr 440	Leu	Val	Leu	Pro	Cys 445	Gln	Val	Ser
His	Ile 450	Glu	Val	Leu	Leu	Gly 455	Ala	Asn	Asp	Ile	Leu 460	Val	Gly	Ile	Asp
Val 465	Gly	Gln	Cys	Val	Val 470	Val	Ile	Leu	Leu	His 475	Arg	Ala	His	Gly	Val 480

His	Ser	Gly	Pro	Ser 485	Thr	Tyr	Arg	Phe	Lys 490	Gly	Ala	Ala	Leu	Val 495	Thr
Val	Arg	Glu	Val 500	Pro	Ser	Ala	Ser	Ala 505	Val	Asn	Gln	Thr	Ile 510	Gly	Arg
Ser	Arg	Asn 515	Ile	Leu	Lys	Gly	Ala 520	Ile	Val	Val	Thr	Leu 525	Ile	Arg	Gly
Thr	Ala 530	Arg	Lys	Arg	Ile	Ser 535	Gln								

<210> 282
 <211> 551
 <212> PRT
 <213> homo sapiens

<400> 282

Pro 1	Leu	Ser	Ser	Pro 5	Ser	Cys	Cys	Arg	Tyr 10	Arg	Arg	Cys	Cys	Arg 15	Arg
Leu	Arg	Pro	Pro 20	Leu	Arg	Ser	Val	Val 25	Gln	Pro	Gly	Pro	Arg 30	Thr	Met
Ser	Leu	Ser 35	Arg	Ser	Glu	Glu	Met 40	His	Arg	Leu	Thr	Glu 45	Asn	Val	Tyr
Lys	Thr 50	Ile	Met	Glu	Gln	Phe 55	Asn	Pro	Ser	Leu	Arg 60	Asn	Phe	Ile	Ala
Met 65	Gly	Lys	Asn	Tyr	Glu 70	Lys	Ala	Leu	Ala	Gly 75	Val	Thr	Tyr	Ala	Ala 80
Lys	Gly	Tyr	Phe	Asp 85	Ala	Leu	Val	Lys	Met 90	Gly	Glu	Leu	Ala	Ser 95	Glu
Ser	Gln	Gly	Ser 100	Lys	Glu	Leu	Gly	Asp 105	Val	Leu	Phe	Gln	Met 110	Ala	Glu
Val	His	Arg 115	Gln	Ile	Gln	Asn	Gln 120	Leu	Glu	Glu	Met	Leu 125	Lys	Ser	Phe
His	Asn 130	Glu	Leu	Leu	Thr	Gln 135	Leu	Glu	Gln	Lys	Val 140	Glu	Leu	Asp	Ser
Arg 145	Tyr	Leu	Ser	Ala	Ala 150	Leu	Lys	Lys	Tyr	Gln 155	Thr	Glu	Gln	Arg	Ser 160
Lys	Gly	Asp	Ala	Leu 165	Asp	Lys	Cys	Gln	Ala 170	Glu	Leu	Lys	Lys	Leu 175	Arg
Lys	Lys	Ser	Gln 180	Gly	Ser	Lys	Asn	Pro 185	Gln	Lys	Tyr	Ser	Asp 190	Lys	Glu
Leu	Gln	Tyr 195	Ile	Asp	Ala	Ile	Ser 200	Asn	Lys	Gln	Gly	Glu 205	Leu	Glu	Asn
Tyr	Val 210	Ser	Asp	Gly	Tyr	Lys 215	Thr	Ala	Leu	Thr	Glu 220	Glu	Arg	Arg	Arg
Phe	Cys	Phe	Leu	Val	Glu	Lys	Gln	Cys	Ala	Val	Ala	Lys	Asn	Ser	Ala

225				230				235				240			
Ala	Tyr	His	Ser	Lys 245	Gly	Lys	Glu	Leu	Leu 250	Ala	Gln	Lys	Leu	Pro 255	Leu
Trp	Gln	Gln	Ala 260	Cys	Ala	Asp	Pro	Ser 265	Lys	Ile	Pro	Glu	Arg 270	Ala	Val
Gln	Leu	Met 275	Gln	Gln	Val	Ala	Ser 280	Asn	Gly	Ala	Thr	Leu 285	Pro	Ser	Ala
Leu	Ser 290	Ala	Ser	Lys	Ser	Asn 295	Leu	Val	Ile	Ser	Asp 300	Pro	Ile	Pro	Gly
Ala 305	Lys	Pro	Leu	Pro	Val 310	Pro	Pro	Glu	Leu	Ala 315	Pro	Phe	Val	Gly	Arg 320
Met	Ser	Ala	Gln	Glu 325	Ser	Thr	Pro	Ile	Met 330	Asn	Gly	Val	Thr	Gly 335	Pro
Asp	Gly	Glu	Asp 340	Tyr	Ser	Pro	Trp	Ala 345	Asp	Arg	Lys	Ala	Ala 350	Gln	Pro
Lys	Ser	Leu 355	Ser	Pro	Pro	Gln	Ser 360	Gln	Ser	Lys	Leu	Ser 365	Asp	Ser	Tyr
Ser	Asn 370	Thr	Leu	Pro	Val	Arg 375	Lys	Ser	Val	Thr	Pro 380	Lys	Asn	Ser	Tyr
Ala 385	Thr	Thr	Glu	Asn	Lys 390	Thr	Leu	Pro	Arg	Ser 395	Ser	Ser	Met	Ala	Ala 400
Gly	Leu	Glu	Arg	Asn 405	Gly	Arg	Met	Arg	Val 410	Lys	Ala	Ile	Phe	Ser 415	His
Ala	Ala	Gly	Asp 420	Asn	Ser	Thr	Leu	Leu 425	Ser	Phe	Lys	Glu	Gly 430	Asp	Leu
Ile	Thr	Leu 435	Leu	Val	Pro	Glu	Ala 440	Arg	Asp	Gly	Trp	His 445	Tyr	Gly	Glu
Ser	Glu 450	Lys	Thr	Lys	Met	Arg 455	Gly	Trp	Phe	Pro	Phe 460	Ser	Tyr	Thr	Arg
Val 465	Leu	Asp	Ser	Asp	Gly 470	Ser	Asp	Arg	Leu	His 475	Met	Ser	Leu	Gln	Gln 480
Gly	Lys	Ser	Ser	Ser 485	Thr	Gly	Asn	Leu	Leu 490	Asp	Lys	Asp	Asp	Leu 495	Ala
Ile	Pro	Pro	Pro 500	Asp	Tyr	Gly	Ala	Ala 505	Ser	Arg	Ala	Phe	Pro 510	Ala	Gln
Thr	Ala	Ser 515	Gly	Phe	Lys	Gln	Arg 520	Pro	Tyr	Ser	Val	Ala 525	Val	Pro	Ala
Phe	Ser 530	Gln	Gly	Leu	Asp	Asp 535	Tyr	Gly	Ala	Arg	Ser 540	Met	Ser	Ser	Ala
Asp 545	Val	Glu	Val	Ala	Arg 550	Phe									

<211> 185
 <212> PRT
 <213> homo sapiens

<400> 283

Ala 1	Gly	Glu	Ala	Ala 5	Gly	Gln	Pro	Gly	Ser 10	Pro	Pro	Ser	His	Gln 15	Leu
Ala	Lys	Cys	Pro 20	Pro	Leu	Thr	Gln	Gly 25	Tyr	Pro	Arg	Leu	His 30	Gly	His
Val	Thr	Arg 35	Gly	Val	Tyr	Pro	Gln 40	Glu	Ala	Ala	Pro	Gln 45	Pro	Trp	Ala
Ala	Gln 50	Pro	Leu	Gly	Leu	Ala 55	Leu	Gln	Gly	Pro	Ala 60	Pro	His	Ser	Ala
Arg 65	Pro	Cys	Leu	Glu	Gln 70	Leu	Gly	Ser	Ser	Pro 75	Gly	Gln	Thr	Gln	Val 80
Gly	Gln	Asp	Gln	Ala 85	Ala	Gly	Ala	Trp	Met 90	Phe	Ser	Thr	Gln	Glu 95	Arg
Thr	Asp	Asp	Asp 100	Arg	Thr	Gly	Tyr	Met 105	Gly	Arg	Ala	Gly	Glu 110	Ala	Thr
Arg	Trp	Ala 115	Ala	Leu	Gln	Met	Trp 120	Pro	Ser	Ala	Glu	Glu 125	Gly	Gly	Arg
Pro	Val 130	Val	Gly	His	Cys	Arg 135	Leu	Gln	Leu	Asp	Val 140	Gly	Lys	Gly	Ile
Leu 145	Thr	Leu	Val	Arg	Arg 150	Leu	Arg	Ile	Trp	Pro 155	Leu	Pro	His	Arg	Arg 160
Cys	Ser	Trp	Thr	Ala 165	Leu	His	Ser	His	Pro 170	Gly	Pro	Gly	Arg	Arg 175	Arg
Ala	Arg	Pro	His 180	Cys	Arg	Ala	Ser	Ala 185							

<210> 284
 <211> 518
 <212> PRT
 <213> homo sapiens

<400> 284

Ser 1	Gly	Gly	Ser	Glu 5	Ser	Gly	His	Phe	His 10	Ile	Gly	Ala	Ala	His 15	Gly
Pro	Arg	Ser	Ile 20	Val	Ile	Gln	Ala	Leu 25	Gly	Glu	Gly	Gly	His 30	Gly	His
Thr	Val	Gly 35	Pro	Leu	Leu	Glu	Ala 40	Ala	Gly	Arg	Leu	Gly 45	Gly	Glu	Gly
Pro	Gly 50	Gly	Gly	Ala	Val	Ile 55	Gly	Gly	Trp	Asp	Gly 60	Gln	Val	Val	Leu
Val 65	Gln	Glu	Val	Ala	Arg 70	Ala	Ala	Ala	Leu	Pro 75	Leu	Leu	Gln	Ala	His 80

Val	Gln	Pro	Val	Thr 85	Ala	Ile	Ala	Val	Gln 90	Asp	Pro	Gly	Val	Gly 95	Glu	
Gly	Lys	Pro	Ala 100	Pro	His	Leu	Gly	Leu 105	Leu	Thr	Leu	Ser	Val 110	Val	Pro	
Ala	Ile	Ala 115	Gly	Leu	Arg	His	Gln 120	Gln	Gly	Asn	Glu	Val 125	Thr	Leu	Leu	
Glu	Ala 130	Gln	Glu	Gly	Ala	Val 135	Val	Pro	Ser	Ser	Val 140	Gly	Glu	Asp	Gly	
Leu 145	His	Pro	His	Thr	Ala 150	Ile	Ala	Leu	Gln	Ala 155	Gly	Cys	His	Gly	Ala 160	
Arg	Ala	Arg	Gln	Ser 165	Leu	Val	Leu	Gly	Gly 170	Gly	Ile	Ala	Val	Phe 175	Trp	
Gly	His	Ala	Leu 180	Ala	His	Gly	Glu	Cys 185	Val	Gly	Val	Gly	Val 190	Ala	Glu	
Leu	Ala	Leu 195	Arg	Leu	Arg	Arg	Arg 200	Gln	Gly	Phe	Gly	Leu 205	Gly	Ser	Leu	
Ala	Val 210	Ser	Pro	Arg	Ala	Val 215	Val	Leu	Ala	Ile	Arg 220	Ala	Cys	Asp	Ala	
Val 225	His	Asp	Gly	Cys	Ala 230	Leu	Leu	Gly	Arg	His 235	Pro	Pro	His	Glu	Arg 240	
Cys	Gln	Leu	Gly	Gly 245	His	Arg	Gln	Gly	Leu 250	Gly	Pro	Arg	Asn	Gly 255	Val	
Gly	Asn	Asp	Gln 260	Val	Gly	Leu	Gly	Gly 265	Arg	Gln	Gly	Ala	Gly 270	Glu	Gly	
Gly	Ala	Val 275	Ala	Gly	His	Leu	Leu 280	His	Glu	Leu	His	Arg 285	Ala	Leu	Arg	
Asp	Leu 290	Ala	Gly	Val	Gly	Thr 295	Gly	Leu	Leu	Pro	Gln 300	Arg	Gln	Leu	Leu	
Arg 305	Gln	Gln	Leu	Leu	Ala 310	Leu	Gly	Val	Val	Gly 315	Arg	Gly	Val	Leu	Gly 320	
His	Gly	Ala	Leu	Leu 325	Leu	His	Gln	Glu	Ala 330	Glu	Ala	Pro	Ala	Leu 335	Leu	
Cys	Gln	Cys	Gly 340	Leu	Val	Ala	Val	Gly 345	His	Val	Ile	Leu	Gln 350	Leu	Ala	
Leu	Leu	Val 355	Ala	Asp	Gly	Val	Asp 360	Val	Leu	Gln	Leu	Leu 365	Val	Arg	Val	
Leu 370	Leu	Arg	Ile	Leu	Ala	Ala 375	Leu	Ala	Leu	Leu	Pro 380	Lys	Leu	Leu	Gln	
Leu 385	Ser	Leu	Thr	Leu	Val 390	Gln	Gly	Val	Ala	Phe 395	Ala	Pro	Leu	Leu	Ser 400	
Leu	Val	Phe	Leu	Gln 405	Arg	Ser	Thr	Gln	Ile 410	Pro	Gly	Val	Gln	Leu 415	His	

Leu	Leu	Leu	Gln 420	Leu	Arg	Lys	Gln	Leu 425	Val	Val	Lys	Arg	Leu 430	Gln	His
Phe	Phe	Gln 435	Leu	Ile	Leu	Asp	Leu 440	Pro	Val	Asp	Phe	Ser 445	His	Leu	Glu
Glu	Asn 450	Val	Ser	Glu	Phe	Phe 455	Gly	Ala	Leu	Ala	Leu 460	Ala	Gly	Gln	Leu
Pro 465	His	Leu	His	Gln	Gly 470	Val	Lys	Val	Ala	Phe 475	Gly	Cys	Ile	Arg	His 480
Thr	Cys	Gln	Cys	Leu 485	Leu	Val	Ile	Leu	Pro 490	His	Gly	Asp	Glu	Val 495	Pro
Glu	Ala	Arg	Val 500	Glu	Leu	Leu	His	Asp 505	Gly	Leu	Ile	Asp	Ile 510	Phe	Arg
Glu	Pro	Val 515	His	Leu	Leu										

<210> 285
 <211> 217
 <212> PRT
 <213> homo sapiens

<400> 285

Val 1	Arg	Glu	Ala	Ala 5	Arg	Arg	Glu	Gln	Arg 10	Tyr	Gln	Glu	Gln	Gly 15	Gly
Glu	Ala	Ser	Pro 20	Gln	Arg	Thr	Trp	Glu 25	Gln	Gln	Gln	Glu	Val 30	Val	Ser
Arg	Asn	Arg 35	Asn	Glu	Gln	Glu	Ser 40	Ala	Val	His	Pro	Arg 45	Glu	Ile	Phe
Lys	Gln 50	Lys	Glu	Arg	Ala	Met 55	Ser	Thr	Thr	Ser	Ile 60	Ser	Ser	Pro	Gln
Pro 65	Gly	Lys	Leu	Arg	Ser 70	Pro	Phe	Leu	Gln	Lys 75	Gln	Leu	Thr	Gln	Pro 80
Glu	Thr	His	Phe	Gly 85	Arg	Glu	Pro	Ala	Ala 90	Ala	Ile	Ser	Arg	Pro 95	Arg
Ala	Asp	Leu	Pro 100	Ala	Glu	Glu	Pro	Ala 105	Pro	Ser	Thr	Pro	Pro 110	Cys	Leu
Val	Gln	Ala 115	Glu	Glu	Glu	Ala	Val 120	Tyr	Glu	Glu	Pro	Pro 125	Glu	Gln	Glu
Thr	Phe 130	Tyr	Glu	Gln	Pro	Pro 135	Leu	Val	Gln	Gln	Gln 140	Gly	Ala	Gly	Ser
Glu 145	His	Ile	Asp	His	His 150	Ile	Gln	Gly	Gln	Gly 155	Leu	Ser	Gly	Gln	Gly 160
Leu	Cys	Ala	Arg	Ala 165	Leu	Tyr	Asp	Tyr	Gln	Ala 170	Ala	Asp	Asp	Thr 175	Glu
Ile	Ser	Phe	Asp	Pro	Glu	Asn	Leu	Ile	Thr	Gly	Ile	Glu	Val	Ile	Asp

				180					185					190			
Glu	Gly	Trp	Trp	Arg	Gly	Tyr	Gly	Pro	Asp	Gly	His	Phe	Gly	Met	Phe		
		195					200					205					
Pro	Ala	Asn	Tyr	Val	Glu	Leu	Ile	Glu									
	210					215											

<210> 286
 <211> 162
 <212> PRT
 <213> homo sapiens

<400> 286

Ala	Gly	Ala	Ser	Gly	Arg	Leu	Trp	Leu	Pro	Ser	Ala	Phe	Ile	Cys	Leu		
1				5					10					15			
Phe	Ser	Phe	Ser	Leu	Ala	Ser	Lys	Gly	Trp	Trp	Pro	Pro	Leu	Phe	Arg		
			20					25					30				
Met	Thr	Leu	Gly	Asn	Ser	Glu	Arg	Arg	Glu	Leu	Phe	Leu	Ala	Glu	Phe		
		35					40					45					
Val	Thr	Lys	Val	Arg	Val	Asp	His	Gly	Gly	Leu	Ala	Ala	Gly	Asn	Leu		
	50					55					60						
Ser	Cys	Trp	Ser	Leu	Leu	Cys	Ala	Pro	His	Ser	Ile	Ser	Leu	Ser	Leu		
65					70					75					80		
Cys	Leu	Gly	Tyr	Gly	Lys	Trp	Gly	Cys	Arg	Trp	Pro	Ser	Ser	His	Pro		
				85					90					95			
Gly	Tyr	Ser	Lys	Thr	Ala	Asp	Thr	Thr	Cys	Ser	Ser	Thr	Arg	Leu	Thr		
			100					105					110				
Arg	Cys	Leu	Gln	Ala	Pro	Val	Cys	Ala	Ser	Thr	Asp	Ser	Asp	Phe	Arg		
		115					120					125					
Lys	Ser	Asn	Thr	Glu	Trp	Pro	Trp	Pro	Val	Val	Phe	Pro	Tyr	Phe	Leu		
	130					135					140						
Ser	Gln	Leu	Ile	Arg	Val	Ser	Glu	Glu	Gln	Ile	Cys	Phe	Trp	Thr	Lys		
145					150					155					160		
Lys	Lys																

<210> 287
 <211> 173
 <212> PRT
 <213> homo sapiens

<400> 287

Leu	Leu	Ala	Cys	Arg	Gly	Trp	Pro	Gly	Arg	Arg	Trp	Trp	Glu	Glu	Leu		
1				5					10					15			
Asn	Ser	Gly	Lys	Val	Met	Tyr	Ala	Phe	Cys	Arg	Val	Lys	Asp	Pro	Asn		
			20					25					30				
Ser	Gly	Leu	Pro	Lys	Phe	Val	Leu	Ile	Asn	Trp	Thr	Gly	Glu	Gly	Val		
		35					40					45					

Asn	Asp	Val	Arg	Lys	Gly	Ala	Cys	Ala	Ser	His	Val	Ser	Thr	Met	Ala
	50					55					60				
Ser	Phe	Leu	Lys	Gly	Ala	His	Val	Thr	Ile	Asn	Ala	Arg	Ala	Glu	Glu
65					70					75				80	
Asp	Val	Glu	Pro	Glu	Cys	Ile	Met	Glu	Lys	Val	Ala	Lys	Ala	Ser	Gly
				85					90					95	
Ala	Asn	Tyr	Ser	Phe	His	Lys	Glu	Ser	Gly	Arg	Phe	Gln	Asp	Val	Gly
			100					105				110			
Pro	Gln	Ala	Pro	Val	Gly	Ser	Val	Tyr	Gln	Lys	Thr	Asn	Ala	Val	Ser
		115					120					125			
Glu	Ile	Lys	Arg	Val	Gly	Lys	Asp	Ser	Phe	Trp	Ala	Lys	Ala	Glu	Lys
	130					135					140				
Glu	Glu	Glu	Asn	Arg	Arg	Leu	Glu	Glu	Lys	Arg	Arg	Ala	Glu	Glu	Ala
145					150					155					160
Gln	Arg	Gln	Trp	Ser	Arg	Ser	Ala	Gly	Ser	Val	Ser	Ala			
				165					170						

<210> 288

<211> 597

<212> PRT

<213> homo sapiens

<400> 288

Glu	Lys	Cys	Gly	Gln	Tyr	Ile	Gln	Lys	Gly	Tyr	Ser	Lys	Leu	Lys	Ile
1				5					10					15	
Tyr	Asn	Cys	Glu	Leu	Glu	Asn	Val	Ala	Glu	Phe	Glu	Gly	Leu	Thr	Asp
			20					25					30		
Phe	Ser	Asp	Thr	Phe	Lys	Leu	Tyr	Arg	Gly	Lys	Ser	Asp	Glu	Asn	Glu
		35					40					45			
Asp	Pro	Ser	Val	Val	Gly	Glu	Phe	Lys	Gly	Ser	Phe	Arg	Ile	Tyr	Pro
	50				55						60				
Leu	Pro	Asp	Asp	Pro	Ser	Val	Pro	Ala	Pro	Pro	Arg	Gln	Phe	Arg	Glu
65					70				75					80	
Leu	Pro	Asp	Ser	Val	Pro	Gln	Glu	Cys	Thr	Val	Arg	Ile	Tyr	Ile	Val
				85					90					95	
Arg	Gly	Leu	Glu	Leu	Gln	Pro	Gln	Asp	Asn	Asn	Gly	Leu	Cys	Asp	Pro
			100					105					110		
Tyr	Ile	Lys	Ile	Thr	Leu	Gly	Lys	Lys	Val	Ile	Glu	Asp	Arg	Asp	His
		115					120					125			
Tyr	Ile	Pro	Asn	Thr	Leu	Asn	Pro	Val	Phe	Gly	Arg	Met	Tyr	Glu	Leu
	130					135					140				
Ser	Cys	Tyr	Leu	Pro	Gln	Glu	Lys	Asp	Leu	Lys	Ile	Ser	Val	Tyr	Asp
145					150					155					160
Tyr	Asp	Thr	Phe	Thr	Arg	Asp	Glu	Lys	Val	Gly	Glu	Thr	Ile	Ile	Asp
				165					170					175	

Leu	Glu	Asn	Arg	Phe	Leu	Ser	Arg	Phe	Gly	Ser	His	Cys	Gly	Ile	Pro
			180					185					190		
Glu	Glu	Tyr	Cys	Val	Ser	Gly	Val	Asn	Thr	Trp	Arg	Asp	Gln	Leu	Arg
		195					200					205			
Pro	Thr	Gln	Leu	Leu	Gln	Asn	Val	Ala	Arg	Phe	Lys	Gly	Phe	Pro	Gln
	210					215					220				
Pro	Ile	Leu	Ser	Glu	Asp	Gly	Ser	Arg	Ile	Arg	Tyr	Gly	Gly	Arg	Asp
225					230					235					240
Tyr	Ser	Leu	Asp	Glu	Phe	Glu	Ala	Asn	Lys	Ile	Leu	His	Gln	His	Leu
				245					250					255	
Gly	Ala	Pro	Glu	Glu	Arg	Leu	Ala	Leu	His	Ile	Leu	Arg	Thr	Gln	Gly
			260					265					270		
Leu	Val	Pro	Glu	His	Val	Glu	Thr	Arg	Thr	Leu	His	Ser	Thr	Phe	Gln
		275					280					285			
Pro	Asn	Ile	Ser	Gln	Gly	Lys	Leu	Gln	Met	Trp	Val	Asp	Val	Phe	Pro
	290					295					300				
Lys	Ser	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Phe	Asn	Ile	Thr	Pro	Arg	Lys
305					310					315					320
Ala	Lys	Lys	Tyr	Tyr	Leu	Arg	Val	Ile	Ile	Trp	Asn	Thr	Lys	Asp	Val
			325						330					335	
Ile	Leu	Asp	Glu	Lys	Ser	Ile	Thr	Gly	Glu	Glu	Met	Ser	Asp	Ile	Tyr
			340					345					350		
Val	Lys	Gly	Trp	Ile	Pro	Gly	Asn	Glu	Glu	Asn	Lys	Gln	Lys	Thr	Asp
		355					360					365			
Val	His	Tyr	Arg	Ser	Leu	Asp	Gly	Glu	Gly	Asn	Phe	Asn	Trp	Arg	Phe
	370					375					380				
Val	Phe	Pro	Phe	Asp	Tyr	Leu	Pro	Ala	Glu	Gln	Leu	Cys	Ile	Val	Ala
385					390					395					400
Lys	Lys	Glu	His	Phe	Trp	Ser	Ile	Asp	Gln	Thr	Glu	Phe	Arg	Ile	Pro
				405					410					415	
Pro	Arg	Leu	Ile	Ile	Gln	Ile	Trp	Asp	Asn	Asp	Lys	Phe	Ser	Leu	Asp
			420					425					430		
Asp	Tyr	Leu	Gly	Phe	Leu	Glu	Leu	Asp	Leu	Arg	His	Thr	Ile	Ile	Pro
		435					440					445			
Ala	Lys	Ser	Pro	Glu	Lys	Cys	Arg	Leu	Asp	Met	Ile	Pro	Asp	Leu	Lys
	450					455					460				
Ala	Met	Asn	Pro	Leu	Lys	Ala	Lys	Thr	Ala	Ser	Leu	Phe	Glu	Gln	Lys
465					470					475					480
Ser	Met	Lys	Gly	Trp	Trp	Pro	Cys	Tyr	Ala	Glu	Lys	Asp	Gly	Ala	Arg
			485						490					495	
Val	Met	Ala	Gly	Lys	Val	Glu	Met	Thr	Leu	Glu	Ile	Leu	Asn	Glu	Lys
			500					505					510		

Glu	Ala	Asp	Glu	Arg	Pro	Ala	Gly	Lys	Gly	Arg	Asp	Glu	Pro	Asn	Met
		515					520					525			
Asn	Pro	Lys	Leu	Asp	Leu	Pro	Asn	Arg	Pro	Glu	Thr	Ser	Phe	Leu	Trp
	530					535					540				
Phe	Thr	Asn	Pro	Cys	Lys	Thr	Met	Lys	Phe	Ile	Val	Trp	Arg	Arg	Phe
545					550					555					560
Lys	Trp	Val	Ile	Ile	Gly	Leu	Leu	Phe	Leu	Leu	Ile	Leu	Leu	Leu	Phe
			565						570					575	
Val	Ala	Val	Leu	Leu	Tyr	Ser	Leu	Pro	Asn	Tyr	Leu	Ser	Met	Lys	Ile
			580					585					590		
Val	Lys	Pro	Asn	Val											
		595													

<210> 289
 <211> 120
 <212> PRT
 <213> homo sapiens

<400> 289

Asp	Gln	His	Ser	Cys	Phe	Lys	Met	Ser	Pro	Asp	Ser	Lys	Ala	Ser	His
1				5					10					15	
Asn	Pro	Ser	Phe	Pro	Lys	Met	Gly	Val	Glu	Ser	Asp	Met	Glu	Asp	Glu
			20					25					30		
Thr	Thr	Ala	Trp	Met	Asn	Leu	Lys	Pro	Thr	Lys	Ser	Cys	Thr	Ser	Thr
		35					40					45			
Ser	Gly	Pro	Leu	Lys	Ser	Gly	Leu	Leu	Phe	Thr	Ser	Ser	Gly	Leu	Arg
	50					55					60				
Gly	Trp	Ser	Leu	Ser	Thr	Trp	Lys	Gln	Gly	Leu	Cys	Thr	Ala	Pro	Ser
65					70				75					80	
Ser	Pro	Thr	Phe	Pro	Arg	Glu	Asn	Phe	Arg	Cys	Gly	Trp	Met	Phe	Ser
				85					90					95	
Pro	Arg	Val	Trp	Gly	His	Gln	Ala	Leu	Leu	Ser	Thr	Ser	His	Pro	Gly
			100					105					110		
Lys	Pro	Arg	Asn	Thr	Thr	Cys	Val								
		115					120								

<210> 290
 <211> 289
 <212> PRT
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<400> 290

Glu	Thr	Gln	Val	Val	Ile	Gln	Arg	Lys	Leu	Val	Ile	Val	Pro	Tyr	Leu
1				5					10					15	
Asn	Asp	Gln	Pro	Gly	Trp	Asp	Ser	Lys	Phe	Arg	Leu	Val	Asn	Thr	Pro
			20					25					30		

Glu	Met	Leu	Phe	Phe	Arg	Asn	Asp	Thr	Glu	Leu	Phe	Gly	Trp	Lys	Val
		35					40					45			
Val	Lys	Arg	Glu	Asn	Lys	Ser	Pro	Val	Lys	Ile	Pro	Phe	Thr	Ile	Gln
	50					55					60				
Arg	Ser	Val	Met	Asp	Ile	Cys	Phe	Leu	Phe	Val	Phe	Phe	Ile	Ala	Arg
	65				70					75					80
Asn	Pro	Ala	Phe	Asp	Val	Asp	Val	Thr	His	Phe	Leu	Ser	Cys	Asp	Ala
				85					90					95	
Phe	Leu	Val	Gln	Asp	Asn	Val	Leu	Gly	Val	Pro	Asp	Asp	His	Thr	Gln
			100					105					110		
Val	Val	Phe	Leu	Gly	Phe	Pro	Gly	Cys	Asp	Val	Glu	Arg	Ala	Trp	
		115					120					125			
Trp	Pro	Gln	Thr	Leu	Gly	Glu	Asn	Ile	His	Pro	His	Leu	Lys	Phe	Ser
	130					135					140				
Leu	Gly	Asn	Val	Gly	Leu	Gly	Ala	Val	Gln	Ser	Pro	Cys	Phe	His	
	145				150				155					160	
Val	Leu	Arg	Asp	Gln	Pro	Leu	Ser	Pro	Glu	Asp	Val	Lys	Ser	Lys	Pro
				165					170					175	
Leu	Phe	Arg	Gly	Pro	Glu	Val	Leu	Val	Gln	Asp	Phe	Val	Gly	Phe	Lys
			180					185					190		
Phe	Ile	Gln	Ala	Val	Val	Ser	Ser	Ser	Ile	Ser	Asp	Ser	Thr	Pro	Ile
		195					200					205			
Phe	Gly	Lys	Asp	Gly	Leu	Trp	Glu	Ala	Phe	Glu	Ser	Gly	Asp	Ile	Leu
	210					215					220				
Lys	Gln	Leu	Cys	Trp	Ser	Gln	Leu	Ile	Ser	Pro	Gly	Ile	Asp	Ser	Arg
	225				230					235					240
Asn	Thr	Val	Leu	Leu	Trp	Tyr	Ala	Ala	Val	Gly	Pro	Lys	Ala	Gly	Lys
				245					250					255	
Glu	Ser	Val	Phe	Gln	Ile	Asn	Asn	Cys	Phe	Ser	Tyr	Phe	Phe	Ile	Pro
			260					265					270		
Gly	Lys	Gly	Val	Ile	Ile	Ile	Asp	Arg	Asn	Phe	Gln	Val	Phe	Phe	Leu
		275					280					285			

Arg

<210> 291

<211> 201

<212> PRT

<213> homo sapiens

<400> 291

Gly	Thr	Gly	Asp	Gly	Ser	Lys	Glu	Ile	Asn	Ile	Val	Trp	Gly	Ile	Gln
	1			5					10					15	
Val	Pro	Ile	Phe	His	Asn	Gly	Pro	Trp	Val	Ser	Thr	Asn	His	Pro	Val
			20					25					30		

Ala	Arg	Phe 35	Pro	Arg	Ile	Thr	Ser 40	Leu	Ala	Ser	Glu	Gly 45	Ile	Ile	Val
Pro	Ser 50	Thr	Ser	Thr	Ile	Arg 55	Gly	Met	Gly	Val	Trp 60	Arg	Ala	Ser	Cys
Gly 65	Asp	Cys	Arg	Ala	Asp 70	Ser	Thr	Ser	Ser	Ile 75	Ala	Gln	Asp	Arg	Gly 80
Pro	Gly	Leu	Thr	Ile 85	Gly	His	Gln	Ala	Leu 90	Gly	Ser	Leu	Val	Trp 95	Val
Gly	Glu	Ser	Trp 100	Gly	Gln	Thr	Trp	Gly 105	Glu	Tyr	Leu	Gly	Gly 110	Pro	Arg
Trp	Leu	Gly 115	Trp	Leu	Asp	Leu	Arg 120	Gln	Ser	Trp	Ala	Leu 125	Ser	Ile	Ser
Glu	Glu 130	Val	Val	Lys	Lys	Arg 135	Asp	Phe	Leu	Phe	His 140	Phe	Leu	Asn	Phe
Leu 145	Cys	Met	Leu	Val	Glu 150	Asp	Met	Phe	Ala	His 155	Lys	Leu	Arg	Thr	Leu 160
Glu	Phe	Leu	Ala	Thr 165	Glu	Arg	Thr	Gln	Pro 170	Leu	Ile	Leu	Ala	Gln 175	Phe
Leu	Arg	Val	Gly 180	Gly	Asp	Glu	Leu	Leu 185	His	Phe	Leu	Leu	Trp 190	Val	Phe
Ala	Pro	His 195	Leu	Leu	Gly	Leu	Phe 200	Leu							

<210> 292

<211> 171

<212> PRT

<213> homo sapiens

<400> 292

Ser 1	Val	Ile	Phe	Phe 5	Lys	Ile	Gly	Phe	Cys 10	Glu	Gly	Arg	Leu	Val 15	Gly
Arg	Gly	Gly	Val 20	Pro	Gly	Ser	Glu	Ala 25	Gln	Ser	Cys	Val	Leu 30	Ser	Ser
Ser	Val	Trp 35	Ile	Ser	Leu	Ala	Ala 40	Ser	Leu	Met	Ser	Leu 45	Arg	Thr	Ile
Cys	Leu 50	Cys	Trp	Val	Met	Pro 55	Leu	Met	Leu	Arg	Thr 60	Arg	Arg	Val	Arg
Ser 65	Leu	Phe	Thr	Pro	Gly 70	Leu	Ser	Ser	His	Ser 75	Arg	Arg	Arg	Met	Phe 80
Cys	Arg	Phe	Gln	Gln 85	Ile	Ser	Leu	Met	Leu 90	Thr	Leu	Arg	Ser	Lys 95	Val
Thr	Gln	Pro	Arg 100	Arg	Lys	Asn	Leu	Leu 105	Ser	Gly	Trp	Gly	Ser 110	Glu	Ser
Ala	Thr	Arg 115	Ile	Lys	Pro	Gly	Tyr 120	Leu	Leu	Gln	Arg	Glu 125	Met	Ile	Ser

Ala	Arg	Glu	Met	Leu	Gly	Ala	Met	Leu	Arg	Met	Lys	Arg	Glu	Gln	Val
	130					135					140				
Leu	Cys	Ser	Gly	Arg	Gly	Leu	His	Ser	Ser	Pro	Ala	Ala	Ser	Leu	Gly
145					150					155					160
Phe	Ser	His	Ser	Ser	Ser	Leu	Gly	Phe	Ser	Phe					
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Glu	Lys	Glu	Lys	Pro	Lys	Glu	Glu	Glu	Trp	Glu	Lys	Pro	Lys	Asp	Ala
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Ala	Gly	Leu	Glu	Cys	Lys	Pro	Arg	Pro	Leu	His	Lys	Thr	Cys	Ser	Leu
			20					25					30		
Phe	Met	Arg	Asn	Ile	Ala	Pro	Asn	Ile	Ser	Arg	Ala	Glu	Ile	Ile	Ser
		35					40					45			
Leu	Cys	Lys	Arg	Tyr	Pro	Gly	Phe	Met	Arg	Val	Ala	Leu	Ser	Glu	Pro
	50					55					60				
Gln	Pro	Glu	Arg	Arg	Phe	Phe	Arg	Arg	Gly	Trp	Val	Thr	Phe	Asp	Arg
65					70					75				80	
Ser	Val	Asn	Ile	Lys	Glu	Ile	Cys	Trp	Asn	Leu	Gln	Asn	Ile	Arg	Leu
				85					90					95	
Arg	Glu	Cys	Glu	Leu	Ser	Pro	Gly	Val	Asn	Arg	Asp	Leu	Thr	Arg	Arg
			100					105					110		
Val	Arg	Asn	Ile	Asn	Gly	Ile	Thr	Gln	His	Lys	Gln	Ile	Val	Arg	Asn
		115					120					125			
Asp	Ile	Lys	Leu	Ala	Ala	Lys	Leu	Ile	His	Thr	Leu	Asp	Asp	Arg	Thr
	130					135					140				
Gln	Leu	Trp	Ala	Ser	Glu	Pro	Gly	Thr	Pro	Pro	Leu	Pro	Thr	Ser	Leu
145					150					155					160
Pro	Ser	Gln	Asn	Pro	Ile	Leu	Lys	Asn	Ile	Thr	Asp	Tyr	Leu	Ile	Glu
				165					170					175	
Glu	Val	Ser	Ala	Glu	Glu	Glu	Glu	Leu	Gly	Ser	Ser	Gly	Gly	Ala	
			180					185					190		
Pro	Pro	Glu	Glu	Pro	Pro	Lys	Glu	Gly	Asn	Pro	Ala	Glu	Ile	Asn	Val
		195					200					205			
Glu	Arg	Asp	Glu	Lys	Leu	Ile	Lys	Val	Leu	Asp	Lys	Leu	Leu	Leu	Tyr
	210					215					220				
Leu	Arg	Ile	Val	His	Ser	Leu	Asp	Tyr	Tyr	Asn	Thr	Cys	Glu	Tyr	Pro
225					230					235					240
Asn	Glu	Asp	Glu	Met	Pro	Asn	Arg	Cys	Gly	Ile	Ile	His	Val	Arg	Gly

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Pro	Met	Pro	Pro 260	Asn	Arg	Ile	Ser	His 265	Gly	Glu	Val	Leu	Glu 270	Trp	Gln				
Lys	Thr	Phe 275	Glu	Glu	Lys	Leu	Thr 280	Pro	Leu	Leu	Ser	Val 285	Arg	Glu	Ser				
Leu	Ser 290	Glu	Glu	Glu	Ala	Gln 295	Lys	Met	Gly	Arg	Lys 300	Asp	Pro	Glu	Gln				
Glu 305	Val	Glu	Lys	Phe 310	Val	Thr	Ser	Asn	Thr	Gln 315	Glu	Leu	Gly	Lys	Asp 320				
Lys	Trp	Leu	Cys	Pro 325	Leu	Ser	Gly	Lys	Lys 330	Phe	Lys	Gly	Pro	Glu 335	Phe				
Val	Arg	Lys	His 340	Ile	Phe	Asn	Lys	His 345	Ala	Glu	Lys	Ile	Glu 350	Glu	Val				
Lys	Lys	Glu 355	Val	Ala	Phe	Phe	Asn 360	Asn	Phe	Leu	Thr	Asp 365	Ala	Lys	Arg				
Pro	Ala 370	Leu	Pro	Glu	Ile	Lys 375	Pro	Ala	Gln	Pro	Pro 380	Gly	Pro	Ala	Gln				
Ile 385	Leu	Pro	Pro	Gly	Leu 390	Thr	Pro	Gly	Leu	Pro 395	Tyr	Pro	His	Gln	Thr 400				
Pro	Gln	Gly	Leu	Met 405	Pro	Tyr	Gly	Gln	Pro 410	Arg	Pro	Pro	Ile	Leu 415	Gly				
Tyr	Gly	Ala	Gly 420	Ala	Val	Arg	Pro	Ala 425	Val	Pro	Thr	Gly	Gly 430	Pro	Pro				
Tyr	Pro	His 435	Ala	Pro	Tyr	Gly	Ala 440	Gly	Arg	Gly	Asn	Tyr 445	Asp	Ala	Phe				
Arg	Gly 450	Gln	Gly	Gly	Tyr	Pro 455	Gly	Lys	Pro	Arg	Asn 460	Arg	Met	Val	Arg				
Gly 465	Asp	Pro	Arg	Ala	Ile 470	Val	Glu	Tyr	Arg	Asp 475	Leu	Asp	Ala	Pro	Asp 480				
Asp	Val	Asp	Phe	Phe 485															

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Glu 1	Ser	Ser	Gly	Phe 5	Gln	Ala	Ile	Gly	Arg 10	Ala	Glu	Asp	Asp	Ala 15	Arg				
Ser	Cys	Trp	Val 20	Lys	Thr	Ser	Glu	Ser 25	Thr	Arg	Pro	Tyr	Gln 30	Leu	Leu				
Arg	Arg	Arg 35	Arg	Pro	Thr	Leu	Ile 40	Thr	Tyr	Arg	Ile	Phe 45	Arg	His	Arg				

Arg	His 50	Lys	Asp	Thr	Ser	Ser 55	Gly	Asp	His	Leu	Thr 60	Cys	Arg	Leu	Asp
Pro 65	Gln	Ala	Lys	Asp	Leu 70	Lys	Asp	Gly	Thr	Gln 75	Glu	Glu	Ala	Thr	Lys 80
Arg	Gln	Glu	Ala	Pro 85	Val	Asp	Pro	Arg	Pro 90	Glu	Gly	Asp	Pro	Gln 95	Arg
Thr	Val	Ile	Ser 100	Trp	Arg	Gly	Ala	Val 105	Ile	Glu	Pro	Glu	Gln 110	Gly	Thr
Glu	Leu	Pro 115	Ser	Arg	Arg	Ala	Glu 120	Val	Pro	Thr	Lys	Pro 125	Pro	Leu	Pro
Pro	Ala 130	Arg	Thr	Gln	Gly	Thr 135	Pro	Val	His	Leu	Asn 140	Tyr	Arg	Gln	Lys
Gly 145	Val	Ile	Asp	Val	Phe 150	Leu	His	Ala	Trp	Lys 155	Gly	Tyr	Arg	Lys	Phe 160
Ala	Trp	Gly	His	Asp 165	Glu	Leu	Lys	Pro	Val 170	Ser	Arg	Ser	Phe	Ser 175	Glu
Trp	Phe	Gly	Leu 180	Gly	Leu	Thr	Leu	Ile 185	Asp	Ala	Leu	Asp	Thr 190	Met	Trp
Ile	Leu	Gly 195	Leu	Arg	Lys	Glu	Phe 200	Glu	Glu	Ala	Arg	Lys 205	Trp	Val	Ser
Lys	Lys 210	Leu	His	Phe	Glu	Lys 215	Asp	Val	Asp	Val	Asn 220	Leu	Phe	Glu	Ser
Thr 225	Ile	Arg	Ile	Leu	Gly 230	Gly	Leu	Leu	Ser	Ala 235	Tyr	His	Leu	Ser	Gly 240
Asp	Ser	Leu	Phe	Leu 245	Arg	Lys	Ala	Glu	Asp 250	Phe	Gly	Asn	Arg	Leu 255	Met
Pro	Ala	Phe	Arg 260	Thr	Pro	Ser	Lys	Ile 265	Pro	Tyr	Ser	Asp	Val 270	Asn	Ile
Gly	Thr	Gly 275	Val	Ala	His	Pro	Pro 280	Arg	Trp	Thr	Ser	Asp 285	Ser	Thr	Val
Ala	Glu 290	Val	Thr	Ser	Ile	Gln 295	Leu	Glu	Phe	Arg	Glu 300	Leu	Ser	Arg	Leu
Thr 305	Gly	Asp	Lys	Lys	Phe 310	Gln	Glu	Ala	Val	Glu 315	Lys	Val	Thr	Gln	His 320
Ile	His	Gly	Leu	Ser 325	Gly	Lys	Lys	Asp	Gly 330	Leu	Val	Pro	Met	Phe 335	Ile
Asn	Thr	His	Ser 340	Gly	Pro	Val	Ser	Pro 345	Thr	Trp	Gly	Val	Phe 350	His	Gly
Gly	Ala	Pro 355	Gly	Ala	Asp	Ser	Leu 360	Leu	Leu	Ser	Tyr	Leu 365	Phe	Glu	Arg

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<212> PRT

<213> homo sapiens

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Ala 1	Leu	Arg	Ser	Pro 5	Pro	Arg	Met	Arg	Ile 10	Val	Leu	Ser	Asn	Arg 15	Leu
Thr	Ser	Thr	Ser 20	Phe	Ser	Lys	Cys	Asn 25	Phe	Phe	Asp	Thr	His 30	Phe	Leu
Ala	Ser	Ser 35	Asn	Ser	Phe	Leu	Arg 40	Pro	Lys	Ile	His	Met 45	Val	Ser	Ser
Ala	Ser 50	Ile	Ser	Val	Arg	Pro 55	Arg	Pro	Asn	His	Ser 60	Leu	Lys	Asp	Leu
Asp 65	Thr	Gly	Phe	Ser	Ser 70	Ser	Trp	Pro	His	Ala 75	Asn	Leu	Arg	Tyr	Pro 80
Phe	His	Ala	Cys	Arg 85	Lys	Thr	Ser	Ile	Thr 90	Pro	Phe	Trp	Arg		

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Leu 1	Leu	Arg	His	Pro 5	Leu	Pro	Gly	Phe	Leu 10	Lys	Phe	Phe	Pro	Gln 15	Thr
Gln	Asp	Pro	His 20	Gly	Val	Gln	Arg	Val 25	Asp	Gln	Cys	Glu	Thr 30	Glu	Ala
Lys	Pro	Leu 35	Thr	Glu	Gly	Pro	Gly 40	His	Arg	Leu	Gln	Leu 45	Val	Met	Ala
Pro	Cys 50	Lys	Leu	Ala	Val	Ser 55	Phe	Pro	Cys	Met	Gln 60	Glu	Asp	Val	Asn
His 65	Ala	Leu	Leu	Ala	Ile 70	Val	Gln	Met	His	Trp 75	Cys	Ala	Leu	Cys	Pro 80
Gly	Arg	Trp	Gln	Gly 85	Arg	Leu	Gly	Gly	His 90	Phe	Cys	Ser	Ser		

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Ser 1	Gly	Pro	Leu	Leu 5	Ala	Gly	Pro	Ala	Thr 10	Leu	Thr	Gly	Arg	Met 15	Ser
Glu	Val	Arg	Leu 20	Pro	Pro	Leu	Arg	Ala 25	Leu	Asp	Asp	Phe	Val 30	Leu	Gly
Ser	Ala	Arg 35	Leu	Ala	Ala	Pro	Asp 40	Pro	Cys	Asp	Pro	Gln 45	Arg	Trp	Cys

His	Arg	Val	Ile	Asn	Asn	Leu	Leu	Tyr	Tyr	Gln	Thr	Asn	Tyr	Leu	Leu
	50					55					60				
Cys	Phe	Gly	Ile	Gly	Leu	Ala	Leu	Ala	Gly	Tyr	Val	Arg	Pro	Leu	His
65					70					75					80
Thr	Leu	Leu	Ser	Ala	Leu	Val	Val	Ala	Val	Ala	Leu	Gly	Val	Leu	Val
				85					90					95	
Trp	Ala	Ala	Glu	Thr	Arg	Ala	Leu	Cys	Ala	Ala	Ala	Ala	Ala	Ala	Thr
			100					105					110		
Leu	Gln	Pro	Ala	Trp	Pro	Gln	Cys	Leu	Pro	Ser	Ala	Ser	Trp	Cys	Ser
		115					120					125			
Gly	Ser	Arg	Ala	Ala	Leu	Ala	Pro	Ser	Cys	Ser	Ala	Ser	Pro	Gly	Arg
	130					135					140				
Cys	Phe														
145															
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Thr	Gln	Arg	His	Ser	His	Pro	Pro	Phe	Ser	Met	Leu	Ile	Pro	Lys	Leu
1				5					10					15	
Gly	Pro	Gly	Ala	Arg	His	Ser	Gln	Ile	Leu	Asn	Pro	Gly	Pro	Lys	Leu
			20					25					30		
Phe	Gln	Thr	Pro	Pro	Tyr	Leu	Pro	Thr	Gln	Val	Lys	Thr	Leu	Pro	Asn
		35					40					45			
Leu	Glu	Leu	Arg	Thr	Gln	Val	Phe	His	Ala	Pro	Val	Trp	Met	Glu	Ser
	50					55					60				
Gly	Ile	Leu	Thr	Val	Gly	Pro	Leu	Val	Gln	Val	Ile	Pro	Thr	Leu	Thr
65					70					75					80
Ser	Pro	Ile	Cys	Leu	Pro	Pro	Ala	Leu	Leu	Arg	His	Phe	Ala	Pro	His
				85					90					95	
Pro	Asn	Val	Pro	His	His	Arg	Gln	Pro	Arg	Gly	Glu	Val	Gly	Thr	Gly
			100					105					110		
Leu	Ser	Arg	Glu	Trp	Gly	Val	Tyr	Val	Ser	Val	Ala	Ala	Thr	Ile	Lys
		115					120					125			
Pro	Val	Ala	Ser	Leu	Met	Pro	Lys	Lys	Lys	Lys	Lys	Ser	Thr	Gly	Arg
	130					135					140				
Lys	Tyr	Ser	Ser	Ser	Ser	Arg	Pro								
145					150										

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Arg 1	Thr	Thr	Thr	Thr 5	Thr	Ile	Phe	Ala	Ala 10	Gly	Arg	Leu	Phe	Phe 15	Phe
Phe	Trp	His	Glu 20	Arg	Cys	Asn	Arg	Leu 25	Tyr	Cys	Cys	Ser	Asn 30	Thr	Asn
Ile	Tyr	Ala 35	Pro	Phe	Pro	Ala	Glu 40	Ala	Cys	Pro	His	Leu 45	Thr	Pro	Trp
Leu	Ser 50	Met	Val	Trp	Asn	Ile 55	Gly	Val	Arg	Gly	Lys 60	Met	Pro	Lys	Gln
Ser 65	Trp	Arg	Glu	Ala	Asn 70	Gly	Thr	Gly	Glu	Gly 75	Arg	Asp	His	Leu	Asp 80
Gln	Gly	Ser	Asn	Ser 85	Gln	Asp	Thr	Arg	Leu 90	His	Pro	His	Arg	Gly 95	Met
Glu	His	Leu	Gly 100	Ser	Glu	Phe	Lys	Ile 105	Trp	Gln	Cys	Leu	Asp 110	Leu	Gly
Trp	Lys	Val 115	Gly	Trp	Gly	Leu	Glu 120	Lys	Leu	Trp	Ser	Arg 125	Val	Gln	Asp
Leu	Arg 130	Val	Pro	Cys	Ser	Arg 135	Pro	Gln	Phe	Gly	Asp 140	Glu	His	Gly	Glu
Gly 145	Trp	Met	Gly	Val	Ser	Leu	Gly	Ser	Gln	Phe 155	Glu	Ile	Gly	His	Gly 160
Cys	Ser	Gly	Leu	Lys 165	Pro	Gln	Phe	Trp	Gly 170	Trp	Met				

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Trp 1	Phe	Trp	Arg	Glu 5	Ser	Tyr	Trp	Gln	Thr 10	Ile	Lys	Val	Asp	Leu 15	Gln
Val	Glu	His	Pro 20	Tyr	Gln	Phe	Leu	Leu 25	Lys	Tyr	Ala	Lys	Gln 30	Leu	Lys
Gly	Asp	Lys 35	Asn	Lys	Ile	Gln	Lys 40	Leu	Val	Gln	Met	Ala 45	Trp	Thr	Phe
Val	Asn 50	Asp	Ser	Leu	Cys	Thr 55	Thr	Leu	Ser	Leu	Gln 60	Trp	Glu	Pro	Glu
Ile 65	Ile	Ala	Val	Ala	Val 70	Met	Tyr	Leu	Ala	Gly 75	Arg	Leu	Cys	Lys	Phe 80
Glu	Ile	Gln	Glu	Trp 85	Thr	Ser	Lys	Pro	Met 90	Tyr	Arg	Arg	Trp	Trp 95	Glu
Gln	Phe	Val	Gln 100	Asp	Val	Pro	Val	Asp 105	Val	Leu	Glu	Asp	Ile 110	Cys	His

Gln	Ile	Leu	Asp	Leu	Tyr	Ser	Gln	Gly	Lys	Gln	Gln	Met	Pro	His	His
		115					120					125			
Thr	Pro	His	Gln	Leu	Gln	Gln	Pro	Pro	Ser	Pro	Glu	Pro	Pro	Thr	Pro
		130				135					140				
Leu	Pro	Gly	Pro	Cys	Gly	Cys	Trp	Ala	Ser	His	Leu	Lys	Glu	Gly	Lys
		145			150					155					160
Val	Val	Gln	Pro	Glu	Pro	Val	Glu	Gln	Cys	Pro	Val	Trp	Pro	Pro	Lys
				165					170					175	
Pro	Lys														

<210> 301

<211> 113

<212> PRT

<213> homo sapiens

<400> 301

Cys	Ile	Ser	Gln	Asp	Val	Cys	Ala	Asn	Leu	Lys	Tyr	Lys	Asn	Gly	Pro
1				5					10					15	
Pro	Asn	Pro	Cys	Ile	Gly	Asp	Gly	Gly	Ser	Ser	Leu	Phe	Lys	Met	Ser
			20					25					30		
Arg	Ser	Thr	Phe	Trp	Lys	Thr	Ser	Ala	Thr	Lys	Ser	Trp	Ile	Phe	Thr
		35					40					45			
His	Lys	Glu	Asn	Asn	Arg	Cys	Leu	Ile	Thr	Pro	Pro	Ile	Ser	Cys	Asn
	50					55					60				
Ser	Pro	His	Leu	Leu	Ser	Leu	Pro	Pro	Arg	Cys	Leu	Gly	Pro	Val	Val
	65				70					75					80
Ala	Gly	Pro	Pro	Thr	Ser	Arg	Arg	Gly	Arg	Leu	Tyr	Ser	Pro	Asn	Pro
				85					90					95	
Trp	Ser	Asn	Ala	Leu	Ser	Gly	Leu	Gln	Asn	Gln	Asn	Lys	Thr	Gly	Ser
			100					105					110		
Leu															

<210> 302

<211> 90

<212> PRT

<213> homo sapiens

<400> 302

Gly	Gly	Arg	Pro	Ser	Asn	His	Arg	Ala	Gln	Ala	Ala	Gly	Trp	Glu	Ala
1				5					10					15	
Gln	Glu	Met	Gly	Ala	Val	Ala	Ala	Asp	Gly	Gly	Cys	Asp	Glu	Ala	Ser
			20					25					30		
Val	Val	Phe	Leu	Val	Ser	Lys	Asp	Pro	Gly	Phe	Gly	Gly	Arg	Cys	Leu
		35					40					45			
Pro	Lys	Arg	Arg	Pro	Gly	His	Leu	Glu	Gln	Thr	Ala	Pro	Thr	Ile	Ser
	50					55					60				

Tyr 65	Thr	Trp	Val	Trp	Arg 70	Ser	Ile	Leu	Val	Phe 75	Gln	Ile	Cys	Thr	Asn 80
Val	Leu	Arg	Asp	Thr 85	Ser	Leu	Leu	Leu	Leu 90						

<210> 303
 <211> 158
 <212> PRT
 <213> homo sapiens

<400> 303

Thr 1	Gln	Val	Met	Val 5	Gln	Ser	Met	Phe	Ala 10	Pro	Thr	Asp	Thr	Ser 15	Asp
Met	Glu	Ala	Val 20	Trp	Lys	Glu	Ala	Lys 25	Pro	Glu	Asp	Leu	Met 30	Asp	Ser
Lys	Leu	Arg 35	Cys	Val	Phe	Glu	Leu 40	Pro	Ala	Glu	Asn	Asp 45	Lys	Pro	His
Asp	Val 50	Glu	Ile	Asn	Lys	Ile 55	Ile	Ser	Thr	Thr	Ala 60	Ser	Lys	Thr	Glu
Thr 65	Pro	Ile	Val	Ser	Lys 70	Ser	Leu	Ser	Ser	Ser 75	Leu	Asp	Asp	Thr	Glu 80
Val	Lys	Lys	Val	Met 85	Glu	Glu	Cys	Lys	Arg 90	Leu	Gln	Gly	Glu	Val 95	Gln
Arg	Leu	Arg	Glu 100	Glu	Asn	Lys	Gln	Phe 105	Lys	Glu	Glu	Asp	Gly 110	Leu	Arg
Met	Arg	Lys 115	Thr	Val	Gln	Ser	Asn 120	Ser	Pro	Ile	Ser	Ala 125	Leu	Ala	Pro
Thr	Gly 130	Lys	Glu	Glu	Gly	Leu 135	Ser	Thr	Arg	Leu	Leu 140	Ala	Leu	Val	Val
Leu 145	Phe	Phe	Ile	Val	Gly 150	Val	Ile	Ile	Gly	Lys 155	Ile	Ala	Leu		

<210> 304
 <211> 112
 <212> PRT
 <213> homo sapiens

<400> 304

Val 1	Asn	Lys	Ala	Leu 5	Pro	Phe	Ile	Ser	Lys 10	Ala	Leu	Gly	Gln	Ser 15	Val
Asn	Thr	Arg	Leu 20	Ser	Leu	Met	Thr	Ser 25	Thr	Ser	Asp	Ala	Ala 30	Thr	Val
Gln	Phe	Leu 35	Trp	Ala	Ser	Asp	Ser 40	Val	His	Gln	Ser	Gln 45	Gly	Ala	Asp
Gly	Leu 50	Asp	Arg	Thr	Glu	Asp 55	Thr	Glu	Ser	Ser	Leu 60	Gly	Arg	Glu	Trp

Ala 65	Thr	Trp	Gly	Leu	Leu 70	Cys	Gly	Ala	Asp	Arg 75	Thr	Pro	Gln	His	Ala 80
Gly	Leu	Gln	Leu	Pro 85	Lys	Gly	Gln	His	Gln 90	Gln	Ala	Arg	Lys	Gly 95	Val
Ile	Leu	Arg	Glu 100	Val	Ile	Gln	His	His 105	Val	Pro	Arg	Pro	Thr 110	Asn	Val

<210> 305
 <211> 105
 <212> PRT
 <213> homo sapiens

<400> 305

Phe 1	Lys	Gly	Lys	Thr 5	Cys	Glu	Met	Ser	Ser 10	Tyr	Ile	Asn	Phe	Phe 15	Leu
His	Met	Val	Met 20	Ile	Asn	Leu	Asn	Pro 25	Met	Ile	Trp	Trp	Ile 30	His	Gln
Ser	Asn	Leu 35	Pro	Ser	Cys	Ala	Cys 40	Tyr	Leu	Tyr	Lys	Ala 45	Ile	Phe	Pro
Ile	Ile 50	Thr	Pro	Thr	Ile	Lys 55	Asn	Lys	Thr	Thr	Arg 60	Ala	Lys	Ser	Arg
Val 65	Leu	Arg	Pro	Ser	Ser 70	Phe	Pro	Val	Gly	Ala 75	Asn	Ala	Glu	Met	Gly 80
Leu	Leu	Leu	Cys	Thr 85	Val	Phe	Leu	Ile	Arg 90	Ser	Pro	Ser	Ser	Ser 95	Leu
Asn	Cys	Leu	Phe 100	Ser	Ser	Arg	Ser	Leu 105							

<210> 306
 <211> 126
 <212> PRT
 <213> homo sapiens

<400> 306

Arg 1	Pro	Pro	Gln	Arg 5	Thr	Leu	Arg	His	Ser 10	Ala	Gln	Leu	Gly	Ala 15	Ala
Pro	Ala	Ala	Leu 20	Pro	Gln	Pro	Leu	Trp 25	Glu	Leu	Pro	Arg	Ala 30	His	Gly
Ser	Gln	Arg 35	Gln	Pro	Gly	Pro	Gly 40	Glu	Ala	Ala	Asp	His 45	Ala	Glu	Gln
Glu	Arg 50	Glu	Glu	Ala	Ala	Glu 55	Arg	Pro	Gly	Ser	Ser 60	Pro	Glu	Glu	Gly
Gln 65	Glu	Gly	Ser	Gly	Ala 70	Phe	Gly	Gly	His	Thr 75	Gly	His	Arg	Ala	Cys 80
Ala	Arg	Cys	Leu	Gly 85	Arg	Gly	Ala	Leu	Gly 90	Gly	Arg	Ile	Pro	Cys 95	Gly
Leu	Leu	Cys	Gln	Leu	Phe	Arg	Arg	Asp	Gly	Cys	Pro	Ala	Asp	Ser	Glu

Lys 1	Ala	Gly	Ile	Glu 5	Gly	His	Arg	Gly	Ser 10	Cys	Leu	Pro	Glu	Arg 15	Arg
Ala	Gln	Gly	Thr 20	Trp	His	Arg	Pro	Cys 25	Asp	Pro	Tyr	Val	His 30	Gln	Arg
Leu	Arg	Phe 35	Leu	Leu	Val	Pro	Leu 40	Pro	Gly	Ser	Phe	Gln 45	Val	Phe	Leu
Leu 50	Leu	Pro	Phe	Pro	Ala 55	Gln	His	Gly	Leu	Gln 60	Leu	Pro	Gln	Val	
Gln 65	Ala	Asp	Val	Gly	Phe 70	His	Glu	Pro	Leu	Glu 75	Val	Pro	Lys	Glu	Ala 80
Val	Glu	Glu	Pro	Leu 85	Val	Leu	Leu	Gln	Ala 90	Ala	Leu	Ser	Gly	Glu 95	Glu
Cys	Val	Val	Glu 100	Ala	Val	Lys	Gly	Gly 105	Val	Glu	Gly	Gly	Gly 110	Pro	Gly
Pro	Gly	Leu 115	Gly	Leu	Ala	Ala	Pro 120	Pro	Asp	Ile					

<210> 309
 <211> 84
 <212> PRT
 <213> homo sapiens

<400> 309

Pro 1	Thr	Thr	Thr	Leu 5	Val	Ile	Pro	Leu	Phe 10	Phe	Leu	Ser	Ser	Arg 15	Lys
Arg	Lys	Gln	Lys 20	Asp	Ser	Phe	Gln	Thr 25	Ala	Leu	Cys	Ser	Leu 30	His	Cys
Ser	Phe	Pro 35	Lys	Gln	Ala	Ala	Ser 40	Thr	Gly	Lys	Ala	His 45	Val	Val	Thr
Pro 50	Tyr	Phe	Ser	Glu	Val	Leu 55	Leu	Phe	His	Gly	Val 60	Thr	Leu	Leu	Ser
Glu 65	Ser	Lys	Phe	Arg	Lys 70	Gln	Val	Leu	Pro	Leu 75	Ala	Asp	Lys	Asn	His 80
Thr	Ser	Phe	Leu												

<210> 310
 <211> 128
 <212> PRT
 <213> homo sapiens

<400> 310

Cys 1	Asp	Arg	Val	Pro 5	Leu	Phe	Leu	Ser	Tyr 10	Trp	Cys	Ala	Val	Ala 15	Asp
Ser	Trp	Leu	Thr 20	Ala	Ser	Ser	Val	Ser 25	His	Val	Lys	Gly	Ile 30	Leu	Ser
Pro	Gln	Pro	Thr	Glu	Cys	Ala	Pro	Pro	Gly	Pro	Ala	Asn	Cys	Phe	Phe

35					40					45					
Asn	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Leu	Val	Glu	Thr	Gly	Ser	Pro	Ser
	50					55					60				
Val	Ala	Gln	Asp	Gly	Leu	Glu	Leu	Leu	Gly	Ser	Ser	Asn	Pro	Pro	Thr
65					70					75					80
Leu	Ala	Ser	Gln	Ser	Ala	Glu	Ile	Thr	Gly	Met	Ser	His	Tyr	Ala	Gln
				85					90					95	
Pro	Glu	Gln	Asp	Asp	Leu	Asn	Leu	Ile	Asn	Ser	Thr	Pro	Lys	Gln	Gln
			100					105					110		
Leu	Ser	Leu	Ser	Gln	Gly	Cys	Gln	Gly	Gly	Leu	Cys	Glu	Gly	Lys	Asp
		115					120					125			

<210> 311

<211> 96

<212> PRT

<213> homo sapiens

<400> 311

Trp	Val	Ala	Gly	Arg	Arg	His	Leu	Leu	Ser	Val	Gln	Thr	Lys	Ser	Leu
1				5					10					15	
Gln	Val	Leu	Gly	Leu	Asp	Leu	Cys	Val	Thr	Pro	Glu	Ser	Gln	Cys	Ile
			20					25					30		
Arg	Tyr	Leu	Tyr	Lys	Lys	Leu	Val	Trp	Phe	Leu	Ser	Ala	Lys	Gly	Lys
		35					40					45			
Thr	Cys	Phe	Leu	Asn	Leu	Leu	Ser	Asp	Asn	Lys	Val	Thr	Pro	Trp	Lys
	50					55					60				
Arg	Arg	Thr	Ser	Glu	Lys	Tyr	Gly	Val	Thr	Thr	Trp	Ala	Phe	Pro	Val
65					70					75					80
Leu	Ala	Ala	Cys	Phe	Gly	Lys	Leu	Gln	Cys	Arg	Leu	Gln	Arg	Ala	Val
				85					90					95	

<210> 312

<211> 57

<212> PRT

<213> homo sapiens

<400> 312

Ile	Ser	Thr	Ser	Ile	Ala	Ala	Leu	Trp	Leu	Pro	Gly	Gly	Gln	Asp	Ala
1				5					10					15	
Gly	Gly	Gly	Ala	Leu	Trp	Pro	Leu	Cys	Gly	Ser	Arg	Gly	Leu	Cys	Val
			20					25					30		
Ser	Asp	Arg	Phe	Pro	Gly	Asn	Phe	Arg	Ala	Arg	Leu	Thr	Ser	Trp	Lys
		35					40					45			
Phe	Lys	Tyr	Ser	Ile	Ala	Leu	Glu	Phe							
	50					55									

<210> 313

<211> 52

<212> PRT
<213> homo sapiens

<400> 313

Ser	Ala	His	Gln	Leu	Gln	His	Cys	Gly	Tyr	Gln	Gly	Val	Arg	Met	Arg
1				5					10					15	
Ala	Val	Glu	Pro	Ser	Gly	Leu	Cys	Val	Val	Ala	Glu	Asp	Ser	Val	Ser
			20					25					30		
Ala	Thr	Val	Phe	Arg	Glu	Thr	Ser	Gly	Arg	Asp	Ser	His	Leu	Gly	Asn
		35					40					45			
Ser	Asn	Thr	Gln												
	50														

<210> 314
<211> 43
<212> PRT
<213> homo sapiens

<400> 314

Asn	Ser	Arg	Ala	Ile	Glu	Tyr	Leu	Asn	Phe	Gln	Asp	Val	Ser	Leu	Ala
1				5					10					15	
Arg	Lys	Phe	Pro	Gly	Lys	Arg	Ser	Leu	Thr	Gln	Ser	Pro	Arg	Leu	Pro
			20					25					30		
His	Lys	Gly	Gln	Arg	Ala	Pro	Pro	Pro	Ala	Ser					
		35					40								

<210> 315
<211> 247
<212> PRT
<213> homo sapiens

<400> 315

Gly	Ser	Ser	Gly	Ser	Arg	Phe	Glu	Val	Val	Val	Val	Leu	Glu	Glu	Arg
1				5					10					15	
Arg	Gly	Gly	Arg	Gly	Arg	Gly	Met	Gly	Arg	Gly	Asp	Gly	Phe	Asp	Ser
			20					25					30		
Arg	Gly	Lys	Arg	Glu	Phe	Asp	Arg	His	Ser	Gly	Ser	Asp	Arg	Ser	Gly
		35					40					45			
Leu	Lys	His	Glu	Asp	Lys	Arg	Gly	Gly	Ser	Gly	Ser	His	Asn	Trp	Gly
	50					55					60				
Thr	Val	Lys	Asp	Glu	Leu	Thr	Glu	Ser	Pro	Lys	Tyr	Ile	Gln	Lys	Gln
65					70					75				80	
Ile	Ser	Tyr	Asn	Tyr	Ser	Asp	Leu	Asp	Gln	Ser	Asn	Val	Thr	Glu	Glu
			85						90					95	
Thr	Pro	Glu	Gly	Glu	Glu	His	His	Pro	Val	Ala	Asp	Thr	Glu	Asn	Lys
			100					105					110		
Glu	Asn	Glu	Val	Glu	Glu	Val	Lys	Glu	Glu	Gly	Pro	Lys	Glu	Met	Thr
		115					120					125			

Leu	Asp	Glu	Trp	Lys	Ala	Ile	Gln	Asn	Lys	Asp	Arg	Ala	Lys	Val	Glu
130						135					140				
Phe	Asn	Ile	Arg	Lys	Pro	Asn	Glu	Gly	Ala	Asp	Gly	Gln	Trp	Lys	Lys
145					150					155					160
Gly	Phe	Val	Leu	His	Lys	Ser	Lys	Ser	Glu	Glu	Ala	His	Ala	Glu	Asp
				165					170					175	
Ser	Val	Met	Asp	His	His	Phe	Arg	Lys	Pro	Ala	Asn	Asp	Ile	Thr	Ser
			180					185					190		
Gln	Leu	Glu	Ile	Asn	Phe	Gly	Asp	Leu	Gly	Arg	Pro	Gly	Arg	Gly	Gly
		195					200					205			
Arg	Gly	Gly	Arg	Gly	Gly	Arg	Gly	Arg	Gly	Gly	Arg	Pro	Asn	Arg	Gly
	210					215					220				
Ser	Arg	Thr	Asp	Lys	Ser	Ser	Ala	Ser	Ala	Pro	Asp	Val	Asp	Asp	Pro
225					230					235					240
Glu	Ala	Phe	Pro	Ala	Leu	Ala									
				245											

<210> 316
 <211> 75
 <212> PRT
 <213> homo sapiens

<400> 316

Phe	Met	Lys	Asn	Lys	Ser	Leu	Leu	Pro	Leu	Pro	Ile	Ser	Thr	Phe	Ile
1				5					10					15	
Trp	Phe	Ser	Asp	Ile	Lys	Phe	Tyr	Phe	Cys	Pro	Val	Leu	Ile	Leu	Asn
			20					25					30		
Ser	Leu	Pro	Leu	Ile	Gln	Ser	His	Leu	Phe	Trp	Thr	Leu	Leu	Phe	Tyr
		35					40					45			
Leu	Phe	Asn	Phe	Ile	Leu	Leu	Ile	Phe	Ser	Val	Cys	His	Trp	Met	Met
	50					55					60				
Phe	Phe	Thr	Phe	Arg	Cys	Phe	Leu	Ser	His	Ile					
65					70					75					

<210> 317
 <211> 78
 <212> PRT
 <213> homo sapiens

<400> 317

Ser	Phe	Gly	Ile	Leu	Lys	His	Ala	Lys	Ala	Leu	Asn	Arg	Arg	Val	His
1				5					10					15	
Lys	Gly	Thr	Arg	Val	Val	Leu	Trp	His	Pro	Val	Lys	Pro	Glu	Leu	Gly
			20					25					30		
Met	Pro	Leu	Gly	His	Pro	His	Gln	Glu	Gln	Lys	His	Leu	Thr	Cys	Arg
		35					40					45			

Ser	Cys	Cys	His	Gly	Leu	Gly	Ala	His	His	Ala	His	Val	His	Leu	Val
	50					55					60				
Leu	Pro	Cys	Arg	His	Val	Leu	Gly	Gly	Gln	Gly	Leu	Gln	Asn		
65					70					75					

<210> 318

<211> 235

<212> PRT

<213> homo sapiens

<400> 318

Leu	His	Leu	Gly	Ala	Gln	Arg	Ala	Leu	Ala	Pro	Gly	Leu	Phe	Arg	Leu
1				5					10					15	
Gln	Gly	Met	Leu	Arg	Ala	Leu	Leu	Gly	Arg	Gln	Leu	Phe	Arg	Ala	Arg
			20					25					30		
Gly	Pro	Pro	Val	Val	Arg	Glu	Pro	Leu	Pro	Arg	Thr	Thr	Arg	Leu	Ala
		35					40					45			
Val	Arg	His	Val	Trp	Pro	Pro	Cys	Asp	Arg	Pro	Leu	Arg	Val	Gly	Pro
	50					55					60				
Gly	Ser	Pro	Leu	Pro	Pro	Gly	Pro	Leu	His	Met	His	Leu	Leu	Pro	Ala
65					70					75					80
Pro	Ala	His	Gln	Gly	Val	Leu	Pro	Gly	Ala	Arg	Arg	Gln	Ala	Leu	Leu
				85					90					95	
Pro	Ala	Leu	Leu	Pro	Glu	Ala	Leu	Arg	Leu	Thr	Ala	Arg	Ser	Ala	Arg
			100					105					110		
Pro	Leu	Pro	Arg	Arg	Pro	Arg	Pro	Pro	Gly	Lys	Ala	Gly	Ser	Ser	Arg
		115					120					125			
Pro	Arg	Gly	Leu	Ala	Leu	Arg	Ala	Gly	Gly	Pro	Thr	His	Trp	Arg	Ala
	130					135					140				
Pro	Pro	Leu	Arg	Tyr	Tyr	Glu	Ser	Ser	Gly	Val	Lys	Phe	Arg	Asn	Gly
145					150					155					160
Pro	Ala	Arg	Pro	Lys	Pro	Thr	Arg	Pro	Gln	Ser	Gly	Leu	His	Thr	Asp
				165					170					175	
Lys	Asn	Ser	Arg	Ala	Gly	Leu	His	Ser	Ile	Pro	Thr	Leu	Glu	Gly	Ala
			180					185					190		
Pro	Leu	Leu	Gly	Glu	Gly	Pro	Cys	Asn	Ser	Ser	Glu	Ser	Glu	Ala	Arg
		195					200					205			
Pro	Gly	Arg	Pro	Cys	Ser	Leu	His	Pro	His	Cys	Ser	Val	His	Phe	Phe
	210					215					220				
Tyr	Leu	His	Lys	His	Thr	His	Ser	Thr	Ser	Lys					
225					230					235					

<210> 319

<211> 478

<212> PRT

<213> homo sapiens

<400> 319

Gly 1	Ser	Arg	Pro	Pro 5	Pro	Cys	Ser	Pro	Arg 10	Ala	Thr	Gly	Pro	Arg 15	Pro
Ala	Met	Glu	Asp 20	Leu	Asp	Ala	Leu	Leu 25	Ser	Asp	Leu	Glu	Thr 30	Thr	Thr
Ser	His	Met 35	Pro	Arg	Ser	Gly	Ala 40	Pro	Lys	Glu	Arg	Pro 45	Ala	Glu	Pro
Leu	Thr 50	Pro	Pro	Pro	Ser	Tyr 55	Gly	His	Gln	Pro	Gln 60	Thr	Gly	Ser	Gly
Glu 65	Ser	Ser	Gly	Ala	Ser 70	Gly	Asp	Lys	Asp	His 75	Leu	Tyr	Ser	Thr	Val 80
Cys	Lys	Pro	Arg	Ser 85	Pro	Lys	Pro	Ala	Ala 90	Pro	Ala	Ala	Pro	Pro 95	Phe
Ser	Ser	Ser	Ser 100	Gly	Val	Leu	Gly	Thr 105	Gly	Leu	Cys	Glu	Leu 110	Asp	Arg
Leu	Leu	Gln 115	Glu	Leu	Asn	Ala	Thr 120	Gln	Phe	Asn	Ile	Thr 125	Asp	Glu	Ile
Met 130	Ser	Gln	Phe	Pro	Ser	Ser 135	Lys	Val	Ala	Ser	Gly 140	Glu	Gln	Lys	Glu
Asp 145	Gln	Ser	Glu	Asp	Lys 150	Lys	Arg	Pro	Ser	Leu 155	Pro	Ser	Ser	Pro	Ser 160
Pro	Gly	Leu	Pro	Lys 165	Ala	Ser	Ala	Thr	Ser 170	Ala	Thr	Leu	Glu	Leu 175	Asp
Arg	Leu	Met	Ala 180	Ser	Leu	Ser	Asp	Phe 185	Arg	Val	Gln	Asn	His 190	Leu	Pro
Ala	Ser	Gly 195	Pro	Thr	Gln	Pro	Pro 200	Val	Val	Ser	Ser	Thr 205	Asn	Glu	Gly
Ser	Pro 210	Ser	Pro	Pro	Glu	Pro 215	Thr	Gly	Lys	Gly	Ser 220	Leu	Asp	Thr	Met
Leu 225	Gly	Leu	Leu	Gln	Ser 230	Asp	Leu	Ser	Arg	Arg 235	Gly	Val	Pro	Thr	Gln 240
Ala	Lys	Gly	Leu	Cys 245	Gly	Ser	Cys	Asn	Lys 250	Pro	Ile	Ala	Gly	Gln 255	Val
Val	Thr	Ala	Leu 260	Gly	Arg	Ala	Trp	His 265	Pro	Glu	His	Phe	Val 270	Cys	Gly
Gly	Cys	Ser 275	Thr	Ala	Leu	Gly	Gly 280	Ser	Ser	Phe	Phe	Glu 285	Lys	Asp	Gly
Ala	Pro 290	Phe	Cys	Pro	Glu	Cys 295	Tyr	Phe	Glu	Arg	Phe 300	Ser	Pro	Arg	Cys
Gly 305	Phe	Cys	Asn	Gln	Pro 310	Ile	Arg	His	Lys	Met 315	Val	Thr	Ala	Leu	Gly 320
Thr	His	Trp	His	Pro	Glu	His	Phe	Cys	Cys	Val	Ser	Cys	Gly	Glu	Pro

F11
 G12
 H13
 I14
 J15
 K16
 L17
 M18
 N19
 O20
 P21
 Q22
 R23
 S24
 T25
 U26
 V27
 W28
 X29
 Y30
 Z31
 aa1
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325										330					335				
Phe	Gly	Asp	Glu	Gly	Phe	His	Glu	Arg	Glu	Gly	Arg	Pro	Tyr	Cys	Arg				
			340					345					350						
Arg	Asp	Phe	Leu	Gln	Leu	Phe	Ala	Pro	Arg	Cys	Gln	Gly	Cys	Gln	Gly				
		355					360					365							
Pro	Ile	Leu	Asp	Asn	Tyr	Ile	Ser	Ala	Leu	Ser	Ala	Leu	Trp	His	Pro				
	370					375					380								
Asp	Cys	Phe	Val	Cys	Arg	Glu	Cys	Phe	Ala	Pro	Phe	Ser	Gly	Gly	Ser				
385					390					395					400				
Phe	Phe	Glu	His	Glu	Gly	Arg	Pro	Leu	Cys	Glu	Asn	His	Phe	His	Ala				
				405					410					415					
Arg	Arg	Gly	Ser	Leu	Cys	Ala	Thr	Cys	Gly	Leu	Pro	Val	Thr	Gly	Arg				
			420					425					430						
Cys	Val	Ser	Ala	Leu	Gly	Arg	Arg	Phe	His	Pro	Asp	His	Phe	Thr	Cys				
		435					440					445							
Thr	Phe	Cys	Leu	Arg	Pro	Leu	Thr	Lys	Gly	Ser	Phe	Gln	Glu	Arg	Ala				
	450					455					460								
Gly	Lys	Pro	Tyr	Cys	Gln	Pro	Cys	Phe	Leu	Lys	Leu	Phe	Gly						
465					470					475									
<210> 320																			
<211> 285																			
<212> PRT																			
<213> homo sapiens																			
<400> 320																			
Glu	Gln	Gly	Leu	Gly	Val	Trp	Arg	Thr	Arg	Leu	Phe	Arg	Glu	Gly	Ala				
1				5					10					15					
Ala	Ser	Gly	Gly	Glu	Gly	Glu	Pro	Ser	Gly	Leu	Ser	Ala	Glu	Glu	Leu				
			20					25					30						
Gln	Glu	Ala	Gly	Leu	Ala	Val	Gly	Leu	Ala	Gly	Ala	Leu	Leu	Glu	Gly				
		35					40					45							
Pro	Leu	Gly	Glu	Arg	Ala	Gln	Ala	Glu	Gly	Ala	Cys	Glu	Val	Val	Arg				
	50					55					60								
Val	Glu	Ala	Ala	Thr	Gln	Gly	Arg	His	Ala	Ala	Ala	Gly	His	Arg	Glu				
65					70				75						80				
Ala	Thr	Arg	Gly	Ala	Gln	Arg	Ala	Ala	Ser	Cys	Val	Glu	Val	Val	Leu				
				85					90					95					
Ala	Gln	Arg	Ala	Ala	Leu	Val	Leu	Glu	Lys	Ala	Ala	Ser	Arg	Glu	Gly				
			100					105					110						
Arg	Glu	Ala	Phe	Pro	Ala	Asp	Glu	Thr	Val	Arg	Val	Pro	Glu	Arg	Ala				
		115					120					125							
Glu	Arg	Arg	Asp	Val	Val	Ile	Gln	Asp	Gly	Ala	Leu	Ala	Ala	Leu	Ala				
130						135					140								

Ala 145	Arg	Gly	Glu	Gln	Leu 150	Gln	Glu	Val	Pro	Ala 155	Ala	Val	Gly	Ala	Ala 160
Leu	Ala	Leu	Val	Glu 165	Thr	Leu	Ile	Ser	Glu 170	Gly	Leu	Pro	Ala	Thr 175	Asp
Ala	Ala	Glu	Met 180	Leu	Trp	Val	Pro	Val 185	Ser	Ala	Gln	Gly	Gly 190	His	His
Leu	Val	Ser 195	Asp	Gly	Leu	Val	Ala 200	Glu	Ala	Thr	Ser	Trp 205	Arg	Glu	Ala
Leu	Lys 210	Val	Ala	Leu	Gly	Ala 215	Glu	Gly	Gly	Ser	Ile 220	Leu	Leu	Glu	Glu
Ala 225	Ala	Ala	Ser	Gln	Gly 230	Gly	Gly	Thr	Ala	Ser 235	Ala	Asn	Glu	Val	Leu 240
Gly	Val	Pro	Gly	Ala 245	Ala	Gln	Ser	Arg	His 250	His	Leu	Pro	Ser	Asn 255	Arg
Phe	Ile	Ala	Gly 260	Ala	Thr	Glu	Ala	Phe 265	Gly	Leu	Gly	Gly	Asn 270	Thr	Pro
Ala	Ala	Glu 275	Val	Gly	Leu	Gln	Gln 280	Pro	Gln	His	Gly	Val 285			

<210> 321
 <211> 99
 <212> PRT
 <213> homo sapiens

<400> 321

Gly 1	Leu	His	Leu	Gln 5	Pro	Leu	Leu	Trp	Arg 10	Gln	Ser	Thr	Glu	Glu 15	Glu
Val	Arg	Glu	Glu 20	Gly	Gln	Ala	Leu	Thr 25	Glu	Pro	Lys	Ser	Cys 30	Gly	Ala
Gln	Gly	Gly 35	Ala	Gln	His	Arg	Gly 40	Leu	Thr	Pro	Cys	Pro 45	Thr	Gly	Asn
Gly	Leu 50	Gly	Leu	Ala	Gln	Pro 55	Lys	Ile	Pro	Ala	Leu 60	Ser	Asn	Ser	Trp
Arg 65	Val	Asp	Ser	Val	Leu 70	Ala	Cys	Leu	Val	Ser 75	Ser	Asp	Ile	Phe	His 80
Thr	Val	Glu	Gln	Asn 85	His	Gln	Pro	Cys	Thr 90	Asp	Val	Thr	Leu	Cys 95	Arg

Lys Arg Pro

<210> 322
 <211> 99
 <212> PRT
 <213> homo sapiens

<400> 322

Glu 1	Thr	Gln	Ser	Ser 5	Gln	Arg	Leu	Thr	Cys 10	Pro	Arg	Ser	Leu	Gly 15	Leu
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Asp	Leu	Ser	Leu 20	Arg	Leu	Arg	Leu	Gln 25	Asn	Pro	His	Ser	Ile 30	Cys	Tyr
Ile	Ser	Gln 35	Gly	Trp	Gly	Gln	Gly 40	Ser	Cys	Glu	Gln	Lys 45	Glu	Lys	Tyr
Gln	Leu 50	Leu	Lys	Gly	Leu	Gly 55	Phe	Val	Gly	Arg	Ala 60	Arg	Gln	Gly	Gln
Arg 65	Gly	Ile	Gln	Asn	Lys 70	Gly	Ala	Ser	Thr	Ser 75	Ala	Trp	Asp	Gly	Pro 80
Ile	His	Ser	Gly	Arg 85	Gly	Cys	Gly	Val	Ser 90	Pro	Val	Leu	Arg	Asn 95	His

Leu Ala Ser

<210> 323
 <211> 83
 <212> PRT
 <213> homo sapiens

<400> 323

Ser 1	Asn	Pro	Lys	Ala 5	Pro	Val	Ser	Met	Trp 10	Val	Lys	Gly	Pro	Thr 15	Met
Gly	Thr	Tyr	Thr 20	Gln	Glu	Asp	Glu	Ser 25	Ser	Leu	Ala	Ser	Glu 30	Ser	Asp
Cys	Leu 35	Pro	Gln	Thr	Pro	Pro	Gln 40	Asn	Arg	Leu	Leu	Ser 45	His	Leu	Pro
Leu 50	His	Ser	Asp	Lys	Thr	Gln 55	Ala	His	Ile	Pro	Gly 60	Pro	Gly	Val	Phe
Ala 65	Cys	Ile	Cys	Ile	Asp 70	Gly	Asn	Ala	Gly	Pro 75	Ala	Lys	Ala	Phe	Phe 80

Tyr Ile Lys

<210> 324
 <211> 111
 <212> PRT
 <213> homo sapiens

<400> 324

Val 1	Phe	Pro	Thr	Val 5	Leu	Arg	Gly	Val	Leu 10	Val	Pro	Ser	Ser	Val 15	Thr
Ser	Lys	Pro	Gly 20	Leu	Ile	Val	Pro	Ile 25	Gly	Asp	Glu	Gly	Gly 30	Met	Arg
Arg	Ser	His 35	Leu	Gln	Leu	Leu	Ser 40	Val	Glu	Arg	Thr	Ser 45	Gly	Thr	Glu
Lys	Asn 50	Arg	Gly	Pro	His	Gly 55	Ser	Leu	Glu	Gly	Arg 60	Gly	Thr	Arg	Val
Gly 65	Glu	Leu	Ile	Ala	Glu 70	Arg	Arg	Asp	Val	Gln 75	Arg	Pro	Ser	Ala	Pro 80

Leu	Ser	Trp	Asp	Val 85	Asn	Arg	Ile	Phe	Pro 90	Ser	Thr	Pro	Ser	Leu 95	Pro
Pro	Val	Leu	Pro 100	Leu	Phe	Phe	Phe	Pro 105	Ser	Ile	Lys	Arg	Cys 110	Ile	

<210> 325

<211> 272

<212> PRT

<213> homo sapiens

<400> 325

Ser 1	Ser	Arg	Ala	Ser 5	Gly	Ile	Thr	Arg	Ala 10	Ala	Arg	Pro	Cys	Pro 15	Ala
Lys	Asn	Glu	Gly 20	Pro	Ser	Lys	Ala	Phe 25	Val	Asn	Cys	Asp	Glu 30	Asn	Ser
Arg	Leu	Val 35	Ser	Leu	Thr	Leu	Asn 40	Leu	Val	Thr	Arg	Ala 45	Asp	Glu	Gly
Trp	Tyr 50	Trp	Cys	Gly	Val	Lys 55	Gln	Gly	His	Phe	Tyr 60	Gly	Glu	Thr	Ala
Ala 65	Val	Tyr	Val	Ala	Val 70	Glu	Glu	Arg	Lys	Ala 75	Ala	Gly	Ser	Arg	Asp 80
Val	Ser	Leu	Ala	Lys 85	Ala	Asp	Ala	Ala	Pro 90	Asp	Glu	Lys	Val	Leu 95	Asp
Ser	Gly	Phe	Arg 100	Glu	Ile	Glu	Asn	Lys 105	Ala	Ile	Gln	Asp	Pro 110	Arg	Leu
Phe	Ala	Glu 115	Glu	Lys	Ala	Val	Ala 120	Asp	Thr	Arg	Asp	Gln 125	Ala	Asp	Gly
Ser 130	Arg	Ala	Ser	Val	Asp	Ser 135	Gly	Ser	Ser	Glu	Glu 140	Gln	Gly	Gly	Ser
Ser 145	Arg	Ala	Leu	Val	Ser 150	Thr	Leu	Val	Pro	Leu 155	Gly	Leu	Val	Leu	Ala 160
Val	Gly	Ala	Val	Ala 165	Val	Gly	Val	Ala	Arg 170	Ala	Arg	His	Arg	Lys 175	Asn
Val	Asp	Arg	Val 180	Ser	Ile	Arg	Ser	Tyr 185	Arg	Thr	Asp	Ile	Ser 190	Met	Ser
Asp	Phe	Glu 195	Asn	Ser	Arg	Glu	Phe 200	Gly	Ala	Asn	Asp	Asn 205	Met	Gly	Ala
Ser 210	Ser	Ile	Thr	Gln	Glu	Thr 215	Ser	Leu	Gly	Gly	Lys 220	Glu	Glu	Phe	Val
Ala 225	Thr	Thr	Glu	Ser	Thr 230	Thr	Glu	Thr	Lys	Glu 235	Pro	Lys	Lys	Ala	Lys 240
Arg	Ser	Ser	Lys 245	Glu	Ala	Glu	Met	Ala 250	Tyr	Lys	Asp	Phe	Leu 255	Leu	
Gln	Ser	Ser	Thr	Val	Ala	Ala	Glu	Ala	Gln	Asp	Gly	Pro	Gln	Glu	Ala

<210> 326
 <211> 241
 <212> PRT
 <213> homo sapiens

<400> 326

Thr 1	Leu	Val	Phe	Gly 5	Arg	Leu	Arg	Thr	Lys 10	Pro	Phe	Arg	Ile	Pro 15	Gly
Phe	Leu	Gln	Arg 20	Lys	Arg	Arg	Trp	Gln 25	Ile	Gln	Glu	Ile	Lys 30	Pro	Met
Gly	Ala	Glu 35	His	Leu	Trp	Ile	Pro 40	Ala	Ala	Leu	Arg	Asn 45	Lys	Val	Glu
Ala	Pro 50	Glu	Arg	Trp	Ser	Pro 55	Pro	Trp	Cys	Pro	Trp 60	Ala	Trp	Cys	Trp
Gln 65	Trp	Glu	Pro	Trp	Leu 70	Trp	Gly	Trp	Pro	Glu 75	Pro	Gly	Thr	Gly	Arg 80
Thr	Ser	Thr	Glu	Phe 85	Gln	Ser	Glu	Ala	Thr 90	Gly	Gln	Thr	Leu	Ala 95	Cys
Gln	Thr	Ser	Arg 100	Thr	Pro	Gly	Asn	Leu 105	Glu	Pro	Met	Thr	Thr 110	Trp	Glu
Pro	Leu	Arg 115	Ser	Leu	Arg	Arg	His 120	Pro	Ser	Glu	Glu	Lys 125	Lys	Ser	Leu
Leu 130	Pro	Pro	Leu	Arg	Ala	Pro 135	Gln	Arg	Pro	Lys	Asn 140	Pro	Arg	Arg	Gln
Lys 145	Gly	His	Pro	Arg	Arg 150	Lys	Pro	Arg	Trp	Pro 155	Thr	Lys	Thr	Ser	Cys 160
Ser	Ser	Pro	Ala	Pro 165	Trp	Pro	Pro	Arg	Pro 170	Arg	Thr	Ala	Pro	Arg 175	Lys
Pro	Arg	Arg	Cys 180	Arg	Arg	Leu	Leu	Pro 185	Ala	Pro	Met	Thr	Ile 190	Thr	Phe
Arg	Ile	Met 195	Ser	Ile	Leu	Gly	Pro 200	Ser	Ala	Pro	Gly	Asp 205	Pro	Thr	Pro
Cys	Ser 210	Asn	Thr	Cys	Leu	Gly 215	Phe	Ser	Tyr	Cys	Pro 220	Gln	Arg	Arg	Ala
Gly 225	Pro	Leu	Leu	Ser	Asp 230	Ile	Lys	Ala	Trp	Pro 235	Asn	Cys	Ser	Tyr	Trp 240

Gly

<210> 327
 <211> 121
 <212> PRT
 <213> homo sapiens

<400> 327

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Ala	Val	Val	Arg	Val	Thr	Trp	Tyr	Lys	Gly	Glu	Gly	Ile	Thr	Leu	Pro
1				5					10					15	
Pro	Val	Leu	Thr	Pro	Ala	Leu	Val	Arg	Gly	Glu	Ser	Ile	Pro	Ile	Arg
			20					25					30		
Leu	Phe	Leu	Ala	Gly	Tyr	Glu	Leu	Thr	Pro	Thr	Met	Arg	Asp	Ile	Asn
		35					40					45			
Lys	Lys	Phe	Ser	Val	Arg	Tyr	Tyr	Leu	Asn	Leu	Val	Leu	Ile	Asp	Glu
	50					55					60				
Glu	Glu	Arg	Arg	Tyr	Phe	Lys	Gln	Gln	Glu	Val	Val	Leu	Trp	Arg	Lys
65					70					75					80
Gly	Asp	Ile	Val	Arg	Lys	Ser	Met	Ser	His	Gln	Ala	Ala	Ile	Ala	Ser
				85					90					95	
Gln	Arg	Phe	Glu	Gly	Thr	Thr	Ser	Leu	Gly	Glu	Val	Arg	Thr	Pro	Ser
			100					105					110		
Gln	Leu	Ser	Asp	Asn	Asn	Cys	Arg	Gln							
		115					120								

<210> 328
 <211> 140
 <212> PRT
 <213> homo sapiens

<400> 328

Gly	Glu	Thr	Arg	Val	His	Ser	Gln	Gln	Gly	Gly	Gly	Ile	Lys	Ala	Pro
1				5					10					15	
Ser	Trp	Asp	Trp	Phe	Phe	Arg	Glu	Pro	Gly	Pro	Leu	Val	Lys	Gly	Leu
			20					25					30		
Leu	Gly	His	Val	Lys	Gln	Tyr	Leu	Glu	Gln	Pro	Arg	Pro	Trp	Gly	Tyr
		35					40					45			
Gln	Val	Glu	Arg	Arg	Glu	Gly	Arg	Arg	Leu	Pro	Cys	Thr	His	Leu	Pro
	50					55					60				
Trp	Trp	Ala	Gly	Phe	Ser	Leu	Leu	Gly	Ser	Thr	Leu	Pro	Pro	Ser	Val
65					70					75					80
His	Asp	Thr	Asp	Pro	Arg	Ala	Ser	Pro	Cys	Pro	Arg	Pro	Ser	Tyr	Arg
				85					90					95	
Leu	Leu	Phe	Gln	Asp	Ile	Thr	Asp	Asn	Pro	Glu	Arg	Met	Glu	Lys	Gly
			100					105					110		
Gly	Ala	Trp	Val	Pro	Ala	Val	Ser	Gly	Gln	Lys	Glu	Val	Ala	Cys	Gly
		115					120					125			
Asn	Leu	Arg	Ser	Pro	His	Pro	Arg	Phe	Pro	Lys	Arg				
	130					135					140				

<210> 329
 <211> 127
 <212> PRT
 <213> homo sapiens

<400> 329

Val 1	Phe	Pro	Cys	His 5	Leu	Val	Gly	Ala	Gly 10	Pro	Thr	Pro	Ala	Thr 15	Thr
Ser	Gly	Thr	Ala 20	Lys	Gly	Ser	Thr	Arg 25	Cys	Asp	Tyr	Pro	Gly 30	Pro	Cys
Trp	Gln	Leu 35	Arg	Ile	Pro	Gly	Thr 40	Cys	Ser	Asp	Pro	Val 45	Ser	Gly	Ser
Ser	Glu 50	Ser	Gln	Glu	Pro	Arg 55	Met	Arg	Ala	Leu	Cys 60	Ser	Pro	Ser	Ser
Lys 65	Thr	Gln	Gly	Ser	Pro 70	Pro	Arg	Lys	Gly	Ala 75	His	Val	Pro	Gln	Arg 80
Gly	Trp	Leu	Pro	Gly 85	Cys	Tyr	Leu	Phe	Tyr 90	Pro	Thr	Ser	Ala	Ala 95	Glu
Ser	Gln	Gly	Glu 100	Thr	Ala	Ser	His	Pro 105	Lys	Pro	Leu	Gly	Phe 110	Ser	Arg
Glu	Lys	Asn 115	Leu	Ser	Gln	Lys	His 120	Asp	Leu	Phe	Ser	Gly 125	Cys	Lys	

<210> 330

<211> 418

<212> PRT

<213> homo sapiens

<400> 330

Gly 1	Ser	Thr	Ser	Thr 5	Lys	Asn	Thr	Lys	Ile 10	Ser	Gln	Ala	Cys	Gly 15	Val
Ile	Val	Glu	Leu 20	Ile	Lys	Ser	Lys	Lys 25	Met	Ala	Gly	Gly	Ala 30	Val	Leu
Leu	Ala	Gly 35	Pro	Pro	Gly	Thr	Gly 40	Lys	Thr	Ala	Leu	Ala 45	Leu	Ala	Ile
Ala	Gln	Glu	Leu	Gly	Ser	Lys 55	Val	Pro	Phe	Cys	Pro 60	Met	Val	Gly	Ser
Glu 65	Val	Tyr	Ser	Thr	Glu 70	Ile	Lys	Lys	Thr	Glu 75	Val	Leu	Met	Glu	Asn 80
Phe	Arg	Arg	Ala	Ile 85	Gly	Leu	Arg	Ile	Lys 90	Glu	Thr	Lys	Glu	Val 95	Tyr
Glu	Gly	Glu	Val 100	Thr	Glu	Leu	Thr	Pro 105	Cys	Glu	Thr	Glu	Asn 110	Pro	Met
Gly	Gly	Tyr 115	Gly	Lys	Thr	Ile	Ser 120	His	Val	Ile	Ile	Gly 125	Leu	Lys	Thr
Ala	Lys 130	Gly	Thr	Lys	Gln	Leu 135	Lys	Leu	Asp	Pro	Ser 140	Ile	Phe	Glu	Ser
Leu 145	Gln	Lys	Glu	Arg	Val 150	Glu	Ala	Gly	Asp	Val 155	Ile	Tyr	Ile	Glu	Ala 160

Asn	Ser	Gly	Ala	Val 165	Lys	Arg	Gln	Gly	Arg 170	Cys	Asp	Thr	Tyr	Ala 175	Thr	
Glu	Phe	Asp	Leu 180	Glu	Ala	Glu	Glu	Tyr 185	Val	Pro	Leu	Pro	Lys 190	Gly	Asp	
Val	His	Lys 195	Lys	Lys	Glu	Ile	Ile 200	Gln	Asp	Val	Thr	Leu 205	His	Asp	Leu	
Asp	Val 210	Ala	Asn	Ala	Arg	Pro 215	Gln	Gly	Gly	Gln	Asp 220	Ile	Leu	Ser	Met	
Met 225	Gly	Gln	Leu	Met	Lys 230	Pro	Lys	Lys	Thr	Glu 235	Ile	Thr	Asp	Lys	Leu 240	
Arg	Gly	Glu	Ile	Asn 245	Lys	Val	Val	Asn	Lys 250	Tyr	Ile	Asp	Gln	Gly 255	Ile	
Ala	Glu	Leu	Val 260	Pro	Gly	Val	Leu	Phe 265	Val	Asp	Glu	Val	His 270	Met	Leu	
Asp	Ile	Glu 275	Cys	Phe	Thr	Tyr	Leu 280	His	Arg	Ala	Leu	Glu 285	Ser	Ser	Ile	
Ala	Pro 290	Ile	Val	Ile	Phe	Ala 295	Ser	Asn	Arg	Gly	Asn 300	Cys	Val	Ile	Arg	
Gly 305	Thr	Glu	Asp	Ile	Thr 310	Ser	Pro	His	Gly	Ile 315	Pro	Leu	Asp	Leu	Leu 320	
Asp	Arg	Val	Met	Ile 325	Ile	Arg	Thr	Met	Leu 330	Tyr	Thr	Pro	Gln	Glu 335	Met	
Lys	Gln	Ile	Ile 340	Lys	Ile	Arg	Ala	Gln 345	Thr	Glu	Gly	Ile	Asn 350	Ile	Ser	
Glu	Glu	Ala 355	Leu	Asn	His	Leu	Gly 360	Glu	Ile	Gly	Thr	Lys 365	Thr	Thr	Leu	
Arg	Tyr 370	Ser	Val	Gln	Leu	Leu 375	Thr	Pro	Ala	Asn	Leu 380	Leu	Ala	Lys	Ile	
Asn 385	Gly	Lys	Asp	Ser	Ile 390	Glu	Lys	Glu	His	Val 395	Glu	Glu	Ile	Ser	Glu 400	
Leu	Phe	Tyr	Asp	Ala 405	Lys	Ser	Ser	Ala	Lys 410	Ile	Leu	Gly	Leu	Thr 415	Arg	

Gln Gly

<210> 331

<211> 142

<212> PRT

<213> homo sapiens

<400> 331

Val 1	Pro	Gln	Cys	Gly 5	Leu	Gly	Ala	Asn	Leu 10	Pro	Gln	Val	Val	Gln 15	Cys	
Leu	Leu	Thr	Asp 20	Val	Asp	Ser	Phe	Arg 25	Leu	Gly	Thr	Asp	Phe 30	Asn	Asp	

Leu	Phe	His 35	Phe	Leu	Trp	Ser	Ile 40	Gln	His	Gly	Pro	Asp 45	Tyr	His	His	
Ser	Val 50	Gln	Lys	Val	Lys	Arg 55	Asp	Ala	Val	Arg	Gly 60	Cys	Asp	Val	Leu	
Ser 65	Ala	Ser	Asp	Asp	Thr 70	Val	Ala	Ser	Val	Gly 75	Cys	Lys	Asp	Asp	Asp 80	
Gly	Ser	Asp	Arg	Arg 85	Leu	Gln	Gly	Ala	Val 90	Gln	Val	Gly	Glu	Ala 95	Leu	
Asn	Val	Gln	His 100	Val	Asp	Leu	Ile	Asn 105	Lys	Gln	His	Thr	Arg 110	Asp	Gln	
Leu	Ser	Asn 115	Ala	Leu	Val	Asp	Val 120	Leu	Val	His	His	Leu 125	Ile	Asn	Leu	
Pro	Ser 130	Lys	Phe	Val	Cys	Asp 135	Phe	Cys	Leu	Leu	Trp 140	Leu	His			

<210> 332

<211> 124

<212> PRT

<213> homo sapiens

<400> 332

Leu 1	Ala	His	His	Gly 5	Gln	Asp	Ile	Leu	Ser 10	Pro	Leu	Gly	Pro	Arg 15	Ile	
Ser	His	Ile	Gln 20	Val	Met	Gln	Gly	His 25	Ile	Leu	Asp	Asp	Phe 30	Phe	Leu	
Phe	Val	His 35	Ile	Pro	Phe	Trp	Gln 40	Gly	Asp	Ile	Leu	Phe 45	Ser	Phe	Lys	
Val	Glu 50	Phe	Cys	Gly	Ile	Gly 55	Ile	Thr	Pro	Ala	Leu 60	Pro	Leu	His	Gly	
Pro 65	Thr	Val	Gly	Phe	Asn 70	Val	Asn	His	Ile	Ser 75	Ser	Phe	Tyr	Ser	Leu 80	
Phe	Leu	Gln	Thr	Phe 85	Lys	Asn	Ala	Gly	Val 90	Gln	Phe	Gln	Leu	Phe 95	Gly	
Ser	Phe	Gly	Cys 100	Phe	Glu	Ser	Tyr	Asp 105	His	Met	Ala	Asn	Gly 110	Phe	Ala	
Ile	Ser	Ser 115	His	Gly	Ile	Leu	Cys 120	Leu	Thr	Arg	Ser					

<210> 333

<211> 176

<212> PRT

<213> homo sapiens

<400> 333

Gln 1	Ala	Met	Gly	Lys 5	Lys	Gln	Lys	Asn	Lys 10	Ser	Glu	Asp	Ser	Thr 15	Lys	
Asp	Asp	Ile	Asp	Leu	Asp	Ala	Leu	Ala	Ala	Glu	Ile	Glu	Gly	Ala	Gly	

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Year	Country	Age	Gender	Occupation	Education	Income	Health	Family	Community	Environment	Policy	Outcome
1990	USA	25	Male	Teacher	High School	\$15,000	Good	2 Children	Suburban	Urban	Public	Good
1995	USA	30	Female	Nurse	College	\$20,000	Good	1 Child	Suburban	Urban	Public	Good
2000	USA	35	Male	Engineer	College	\$25,000	Good	2 Children	Suburban	Urban	Public	Good
2005	USA	40	Female	Manager	College	\$30,000	Good	2 Children	Suburban	Urban	Public	Good
2010	USA	45	Male	Doctor	College	\$35,000	Good	2 Children	Suburban	Urban	Public	Good
2015	USA	50	Female	Lawyer	College	\$40,000	Good	2 Children	Suburban	Urban	Public	Good
2020	USA	55	Male	Executive	College	\$45,000	Good	2 Children	Suburban	Urban	Public	Good
2025	USA	60	Female	Retired	College	\$50,000	Good	2 Children	Suburban	Urban	Public	Good
2030	USA	65	Male	Retired	College	\$55,000	Good	2 Children	Suburban	Urban	Public	Good
2035	USA	70	Female	Retired	College	\$60,000	Good	2 Children	Suburban	Urban	Public	Good
2040	USA	75	Male	Retired	College	\$65,000	Good	2 Children	Suburban	Urban	Public	Good
2045	USA	80	Female	Retired	College	\$70,000	Good	2 Children	Suburban	Urban	Public	Good
2050	USA	85	Male	Retired	College	\$75,000	Good	2 Children	Suburban	Urban	Public	Good
2055	USA	90	Female	Retired	College	\$80,000	Good	2 Children	Suburban	Urban	Public	Good
2060	USA	95	Male	Retired	College	\$85,000	Good	2 Children	Suburban	Urban	Public	Good
2065	USA	100	Female	Retired	College	\$90,000	Good	2 Children	Suburban	Urban	Public	Good
2070	USA	105	Male	Retired	College	\$95,000	Good	2 Children	Suburban	Urban	Public	Good
2075	USA	110	Female	Retired	College	\$100,000	Good	2 Children	Suburban	Urban	Public	Good
2080	USA	115	Male	Retired	College	\$105,000	Good	2 Children	Suburban	Urban	Public	Good
2085	USA	120	Female	Retired	College	\$110,000	Good	2 Children	Suburban	Urban	Public	Good
2090	USA	125	Male	Retired	College	\$115,000	Good	2 Children	Suburban	Urban	Public	Good
2095	USA	130	Female	Retired	College	\$120,000	Good	2 Children	Suburban	Urban	Public	Good
2100	USA	135	Male	Retired	College	\$125,000	Good	2 Children	Suburban	Urban	Public	Good
2105	USA	140	Female	Retired	College	\$130,000	Good	2 Children	Suburban	Urban	Public	Good
2110	USA	145	Male	Retired	College	\$135,000	Good	2 Children	Suburban	Urban	Public	Good
2115	USA	150	Female	Retired	College	\$140,000	Good	2 Children	Suburban	Urban	Public	Good
2120	USA	155	Male	Retired	College	\$145,000	Good	2 Children	Suburban	Urban	Public	Good
2125	USA	160	Female	Retired	College	\$150,000	Good	2 Children	Suburban	Urban	Public	Good
2130	USA	165	Male	Retired	College	\$155,000	Good	2 Children	Suburban	Urban	Public	Good
2135	USA	170	Female	Retired	College	\$160,000	Good	2 Children	Suburban	Urban	Public	Good
2140	USA	175	Male	Retired	College	\$165,000	Good	2 Children	Suburban	Urban	Public	Good
2145	USA	180	Female	Retired	College	\$170,000	Good	2 Children	Suburban	Urban	Public	Good
2150	USA	185	Male	Retired	College	\$175,000	Good	2 Children	Suburban	Urban	Public	Good
2155	USA	190	Female	Retired	College	\$180,000	Good	2 Children	Suburban	Urban	Public	Good
2160	USA	195	Male	Retired	College	\$185,000	Good	2 Children	Suburban	Urban	Public	Good
2165	USA	200	Female	Retired	College	\$190,000	Good	2 Children	Suburban	Urban	Public	

<211> 193

<212> PRT

<213> homo sapiens

<400> 334

Arg 1	Phe	Lys	Ile	Lys 5	Lys	Asp	Cys	Lys	Thr 10	Glu	Ser	Gly	Asn	Val 15	Leu
Trp	Glu	Phe	Asn 20	Lys	Leu	Pro	Lys	Lys 25	Ala	Lys	Gly	Lys	Ala 30	Gln	Lys
Ser	Asn	Lys 35	Lys	Trp	Asp	Gly	Ser 40	Glu	Glu	Asp	Glu	Asp 45	Asn	Ser	Lys
Lys	Ile 50	Lys	Glu	Arg	Ser	Arg 55	Ile	Asn	Ser	Ser	Gly 60	Glu	Ser	Gly	Asp
Glu 65	Ser	Asp	Glu	Phe	Leu 70	Gln	Ser	Arg	Lys	Gly 75	Gln	Lys	Lys	Asn	Gln 80
Lys	Asn	Lys	Pro	Gly 85	Pro	Asn	Ile	Glu	Ser 90	Gly	Asn	Glu	Asp	Asp 95	Asp
Ala	Ser	Phe	Lys 100	Ile	Lys	Thr	Val	Ala 105	Gln	Lys	Lys	Ala	Glu 110	Lys	Lys
Glu	Arg	Glu 115	Arg	Lys	Lys	Arg	Asp 120	Glu	Glu	Lys	Ala	Lys 125	Leu	Arg	Lys
Leu 130	Lys	Glu	Lys	Glu	Glu	Leu 135	Glu	Thr	Gly	Lys	Lys 140	Asp	Gln	Ser	Lys

Gln 145	Lys	Glu	Ser	Gln	Arg 150	Lys	Phe	Glu	Glu	Glu 155	Thr	Val	Lys	Ser	Lys 160
Val	Thr	Val	Asp	Thr 165	Gly	Val	Ile	Pro	Ala 170	Ser	Glu	Glu	Lys	Ala 175	Glu
Thr	Pro	Thr	Ala 180	Ala	Glu	Asp	Asp	Asn 185	Glu	Gly	Asp	Lys	Lys 190	Asn	Glu

Arg

<210> 335
 <211> 118
 <212> PRT
 <213> homo sapiens

<400> 335

Glu 1	Thr	Val	Ala	Phe 5	Ala	Arg	Pro	Phe	Phe 10	Pro	Ser	Leu	Phe	Ser 15	Phe
Pro	Pro	Leu	Ser 20	Ser	Phe	Leu	Phe	Leu 25	Leu	Ile	Phe	Arg	Ser 30	Phe	Cys
Leu	Leu	His 35	Cys	His	Leu	Leu	Gln 40	Leu	Trp	Glu	Ser	Leu 45	Leu	Ser	Leu
Gln	Arg 50	Gln	Glu	Leu	Leu	Gln 55	Tyr	Gln	Gln	Ser	Leu 60	Trp	Ile	Leu	Gln
Phe 65	Leu	Leu	Gln	Ile	Ser 70	Phe	Glu	Ile	Pro	Phe 75	Val	Tyr	Ser	Asp	Pro 80
Phe	Tyr	Leu	Phe	Leu 85	Thr	Leu	Leu	Phe	Leu 90	Ser	Ala	Ser	Ala	Val 95	Ser
Leu	Phe	Leu	His 100	Leu	Ala	Phe	Phe	Ser 105	Arg	Ala	Pro	Ser	Phe 110	Leu	Pro
Ser	Phe	Gly 115	Pro	Leu	Ser										

<210> 336
 <211> 230
 <212> PRT
 <213> homo sapiens

<400> 336

Leu 1	Gln	Arg	Leu	Leu 5	Pro	Pro	Gly	Ala	Glu 10	Arg	Pro	Ala	His	Leu 15	Cys
Thr	Gly	Pro	Gly 20	Gly	Glu	Asp	Gly	Ala 25	Gly	Gly	Arg	Val	Pro 30	Gly	Thr
Arg	Pro	Gln 35	Arg	Pro	Pro	Ala	Leu 40	Gln	Arg	Ala	Glu	Asp 45	Gly	Arg	Gln
Gly	Gly 50	Leu	Arg	Val	Ala	Gly 55	Thr	Ala	Gly	Pro	Pro 60	Pro	Gly	Val	Pro
Leu 65	Arg	Pro	Gly	Gln	Gly 70	Ser	Gly	His	Gln 75	Glu	Gln	Gly	Ala	Ser 80	

His	Pro	Gly	Ser	Leu 85	Asp	Gln	Gly	Leu	Thr 90	Gly	Ala	Lys	Arg	Pro 95	Gln
Gly	Cys	Pro	Ala 100	Cys	Gly	Arg	Arg	Pro 105	Pro	Cys	Val	Gly	Gly 110	Val	Pro
Gly	Ser	Ala 115	His	Arg	Pro	Gln	Pro 120	Glu	Gly	Ala	Ala	Leu 125	Arg	Arg	Gly
Arg	Ser 130	Arg	Leu	Gln	Gln	Ala 135	Gly	Pro	Cys	Cys	Cys 140	Arg	Val	Leu	Trp
Leu 145	Arg	Arg	Cys	His	Pro 150	Ala	Gly	Leu	Pro	Arg 155	Arg	Pro	Pro	Ala	Ala 160
Asp	Pro	Gly	Ala	Arg 165	Ala	Ala	Ala	Gly	Gly 170	Arg	His	Val	Leu	Cys 175	Arg
Ser	Pro	Leu	His 180	Pro	Gly	Leu	Arg	Pro 185	Pro	Leu	Pro	Gln	Trp 190	Gly	Leu
Leu	Arg	Pro 195	Glu	Gly	Gly	Cys	Leu 200	Cys	Val	Pro	Val	Ser 205	Arg	Gly	Ile
Leu	Arg 210	Thr	Ala	Leu	Arg	Glu 215	Gly	Ala	Gly	Gly	Glu 220	Val	Ser	Gly	Gly
Arg 225	Gly	Tyr	Leu	Gly	Leu 230										

<210> 337

<211> 416

<212> PRT

<213> homo sapiens

<400> 337

Gln 1	Asp	Gly	Ser	Gly 5	Pro	Phe	Leu	Ala	Asp 10	Phe	Asn	Gly	Phe	Ser 15	His
Leu	Glu	Leu	Arg 20	Gly	Leu	His	Thr	Phe 25	Ala	Arg	Asp	Leu	Gly 30	Glu	Lys
Met	Ala	Leu 35	Glu	Val	Val	Phe	Leu 40	Ala	Arg	Gly	Pro	Ser 45	Gly	Leu	Leu
Leu	Tyr 50	Asn	Gly	Gln	Lys	Thr 55	Asp	Gly	Lys	Gly	Asp 60	Phe	Val	Ser	Leu
Ala 65	Leu	Arg	Asp	Arg	Arg 70	Leu	Glu	Phe	Arg	Tyr 75	Asp	Leu	Gly	Lys	Gly 80
Ala	Ala	Val	Ile	Arg 85	Ser	Arg	Glu	Pro	Val 90	Thr	Leu	Gly	Ala	Trp 95	Thr
Arg	Val	Ser	Leu 100	Glu	Arg	Asn	Gly	Arg 105	Lys	Gly	Ala	Leu	Arg 110	Val	Gly
Asp	Gly	Pro 115	Arg	Val	Leu	Gly	Glu 120	Ser	Pro	Val	Pro	His 125	Thr	Val	Leu
Asn	Leu	Lys	Glu	Pro	Leu	Tyr	Val	Gly	Gly	Ala	Pro	Asp	Phe	Ser	Lys

130					135					140					
Leu 145	Ala	Arg	Ala	Ala 150	Val	Ser	Ser	Gly	Phe 155	Asp	Gly	Ala	Ile	Gln 160	
Leu	Val	Ser	Leu	Gly 165	Gly	Arg	Gln	Leu	Leu 170	Thr	Pro	Glu	His	Val 175	Leu
Arg	Gln	Val	Asp 180	Val	Thr	Ser	Phe	Ala 185	Gly	His	Pro	Cys	Thr 190	Arg	Ala
Ser	Gly	His 195	Pro	Cys	Leu	Asn	Gly 200	Ala	Ser	Cys	Val	Pro 205	Arg	Glu	Ala
Ala	Tyr 210	Val	Cys	Leu	Cys	Pro 215	Gly	Gly	Phe	Ser	Gly 220	Pro	His	Cys	Glu
Lys 225	Gly	Leu	Val	Glu	Lys 230	Ser	Ala	Gly	Asp	Val 235	Asp	Thr	Leu	Ala	Phe 240
Asp	Gly	Arg	Thr	Phe 245	Val	Glu	Tyr	Leu	Asn 250	Ala	Val	Thr	Glu	Ser 255	Glu
Lys	Ala	Leu	Gln 260	Ser	Asn	His	Phe	Glu 265	Leu	Ser	Leu	Arg	Thr 270	Glu	Ala
Thr	Gln	Gly 275	Leu	Val	Leu	Trp	Ser 280	Gly	Lys	Ala	Thr	glu 285	Arg	Ala	Asp
Tyr	Val 290	Ala	Leu	Ala	Ile	Val 295	Asp	Gly	His	Leu	Gln 300	Leu	Ser	Tyr	Asn
Leu 305	Gly	Ser	Gln	Pro	Val 310	Val	Leu	Arg	Ser	Thr 315	Val	Pro	Val	Asn	Thr 320
Asn	Arg	Trp	Leu	Arg 325	Val	Val	Ala	His	Arg 330	Glu	Gln	Arg	Glu	Gly 335	Ser
Leu	Gln	Val	Gly 340	Asn	Glu	Ala	Pro	Val 345	Thr	Gly	Ser	Ser	Pro 350	Leu	Gly
Ala	Thr	Gln 355	Leu	Asp	Thr	Asp	Gly 360	Ala	Leu	Trp	Leu	Gly 365	Gly	Leu	Pro
Glu	Leu 370	Pro	Val	Gly	Pro	Ala 375	Leu	Pro	Lys	Ala	Tyr 380	Gly	Thr	Gly	Phe
Val 385	Gly	Cys	Leu	Arg	Asp 390	Val	Val	Val	Gly	Arg 395	His	Pro	Leu	His	Leu 400
Leu	Glu	Asp	Ala	Val 405	Thr	Lys	Pro	Glu	Leu 410	Arg	Pro	Cys	Pro	Thr 415	Pro

<210> 338

<211> 241

<212> FRT

<213> homo sapiens

<400> 338

Asn 1	Gln	His	Met	Lys 5	Asn	Thr	Ala	Met	Ala 10	Arg	Pro	Arg	Tyr	Pro 15	Gly
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Arg	Arg	Gln	Arg 20	Ser	Thr	Pro	Ser	His 25	Ser	Glu	Leu	Leu	Ser 30	Ile	Ala	
Pro	Arg	Arg 35	Ala	Trp	Gly	Val	Ala 40	Glu	Gly	Tyr	Gly	His 45	Val	Gln	Gly	
Gly	Trp 50	Ala	Gly	Pro	Ala	Glu 55	Gly	Gln	Asp	Thr	Gln 60	Ile	Gly	Pro	Gly	
Leu 65	Ala	Ser	Ala	Pro	Gln 70	Gln	Pro	Gly	Leu	Ala 75	Gln	Ala	Ala	Arg	Glu 80	
Gln	Arg	Arg	Ala	Val 85	Pro	Ser	Ser	Asn	Ile 90	Val	Trp	Lys	Ser	Gln 95	Tyr	
Trp	Arg	Arg	Arg 100	Pro	Arg	Gln	Gly	Pro 105	Glu	His	Thr	Gln	Glu 110	Gly	Ala	
Ala	Gln	Ile 115	Gly	Ala	Trp	Lys	Gly 120	Pro	Val	Gly	Ser	Pro 125	Gly	Gly	Arg	
Ala	Pro 130	Ser	Asp	Leu	Ser	Ser 135	Pro	Phe	Leu	Ser	Gly 140	Thr	Arg	Val	Pro	
Pro 145	Asp	Gly	Ala	Arg	Val 150	Ile	Gln	Glu	Pro	Gly 155	Leu	Leu	Pro	Gly	Gly 160	
Asp	Thr	Val	Gly	Gln 165	Ala	Gln	Cys	Lys	Ala 170	Gly	Ala	Gln	His	Leu 175	Glu	
Ala	Gly	Val	Cys 180	Val	Leu	Arg	Leu	Pro 185	Ser	Thr	Pro	Ser	Pro 190	Pro	Arg	
Cys	His	Leu 195	Ala	Cys	Pro	Ser	Leu 200	Ser	Thr	Arg	Ser	Val 205	Cys	Ser	Thr	
Ala	Ala 210	Trp	Thr	Glu	Gly	Arg 215	Pro	Gly	Gln	Gln	Ser 220	Leu	Arg	Pro	Thr	
Leu 225	Arg	Gln	Glu	Asn	His 230	Ile	Lys	Lys	Arg	Gln 235	Val	Tyr	Lys	Asn	Arg 240	
Lys																

<210> 339

<211> 79

<212> PRT

<213> homo sapiens

<400> 339

Leu 1	Leu	Gln	Pro	Gln 5	Gly	Glu	Met	Pro	Pro 10	Gly	Asn	Pro	Pro	Met 15	Ser	
Thr	Arg	Gly	Gln 20	Glu	Ala	Thr	Val	Leu 25	Arg	Thr	Pro	Glu	Asn 30	Leu	Ala	
Gly	Glu	Leu 35	Phe	Leu	Val	His	Pro 40	Ser	Leu	Gln	Leu	Tyr 45	Leu	Cys	Pro	
Ala	Asp 50	Asn	Val	Lys	Asp	Trp 55	Ser	Lys	Val	Val	Leu 60	Ala	Tyr	Glu	Pro	

Val	Trp	Ala	Ile	Gly	Thr	Gly	Lys	Thr	Ala	Thr	Pro	Gln	Gln	Gly
65					70					75				

<210> 340

<211> 62

<212> PRT

<213> homo sapiens

<400> 340

Phe	Pro	Val	Gly	Val	Leu	Gln	Ser	Cys	Gln	Tyr	Gln	Trp	Pro	Thr	Gln
1				5					10					15	

Ala	His	Arg	Pro	Gly	Arg	Pro	Cys	Ser	Ser	Pro	Ser	Arg	Tyr	Leu	Gln
			20					25					30		

Gly	Arg	Asp	Thr	Ala	Gly	Gly	Lys	Gly	Glu	Gln	Glu	Arg	Ala	Leu	Gln
		35					40					45			

Pro	Gly	Ser	Pro	Glu	Tyr	Glu	Glu	Arg	Trp	Pro	Pro	Ala	Pro
	50					55					60		

<210> 341

<211> 80

<212> PRT

<213> homo sapiens

<400> 341

Ser	Leu	Leu	Gly	Cys	Cys	Ser	Leu	Ala	Ser	Thr	Asn	Gly	Pro	His	Arg
1				5					10					15	

Leu	Ile	Gly	Gln	Asp	Asp	Leu	Ala	Pro	Val	Leu	His	Val	Ile	Cys	Arg
			20					25					30		

Ala	Glu	Ile	Gln	Leu	Glu	Gly	Arg	Val	Asn	Lys	Lys	Glu	Leu	Ser	Ser
		35					40					45			

Gln	Val	Leu	Arg	Ser	Thr	Lys	Asn	Gly	Gly	Leu	Leu	Pro	Pro	Ser	Gly
	50					55					60				

His	Trp	Gly	Ile	Ser	Arg	Trp	His	Leu	Pro	Leu	Gly	Leu	Glu	Lys	Ser
65					70					75					80

<210> 342

<400> 342

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<210> 343

<400> 343

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<210> 344

<400> 344

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<210> 345

<211> 257

<212> PRT

<213> homo sapiens

<400> 345

Lys 1	Asn	Leu	Ser	Gln 5	Leu	Glu	Pro	Arg	Glu 10	Asn	Ala	Lys	Glu	Glu 15	Val
Arg	Lys	Glu	Arg 20	Gly	Met	Gly	Trp	Val 25	Ala	Ala	Gly	Ala	Ala 30	Gln	Leu
Leu	Ser	Leu 35	Leu	Ser	Thr	Ser	Thr 40	Ala	Ser	Asp	Ser	Ser 45	Val	Ile	Ser
Ser	Ser 50	Ala	Cys	Thr	Ser	Gly 55	Leu	Leu	Pro	Arg	Arg 60	Arg	Ser	Pro	Ala
Ser 65	Pro	Arg	Ser	Ala	His 70	Leu	His	His	Leu	Gly 75	Gly	Leu	Glu	His	Phe 80
His	Leu	Ala	Leu	Ala 85	Asp	Leu	Leu	Asp	Val 90	Glu	Gly	Glu	Gly	Trp 95	His
Leu	Val	Asp	Arg 100	Gly	Leu	Gly	Ala	Arg 105	Val	His	His	Val	Val 110	Gly	Arg
Glu	Gly	Phe 115	Ala	Gln	Leu	Val	Pro 120	Arg	Arg	Leu	Gln	Phe 125	Leu	Ala	Pro
Leu	Gly 130	Gly	His	Gln	Ala	Arg 135	Ala	Gln	Leu	Val	His 140	Ala	Leu	Leu	Gln
Gly 145	Val	Pro	Arg	Leu	Leu 150	Gln	Val	Phe	Leu	Gly 155	Leu	Glu	Ala	Arg	Leu 160
Leu	Gln	Val	Leu	Ala 165	Gly	Thr	His	Leu	Gly 170	Leu	Leu	His	Leu	Leu 175	Leu
Gly	Glu	Gly	Leu 180	Leu	Glu	Val	Val	His 185	Ala	Pro	Gln	Ala	Leu 190	Arg	Leu
Ile	Arg	Ser 195	Ala	Arg	Asp	Ser	Ser 200	Ile	Thr	Ser	Ser	Thr 205	Ser	Thr	Ala
Ser	Ser 210	Asp	Glu	Ser	Ser	Ser 215	Ala	Ala	Ala	Ser	Ser 220	Ser	Gly	Arg	Ser
Pro 225	Ser	Pro	Ser	Ser	Ser 230	Pro	Ser	Phe	Ser	Gly 235	Ser	Ala	Ser	Asp	Ser 240
Phe	Ser	Asp	Leu	Leu 245	Met	Leu	Ser	Leu	Ala 250	Gly	Ser	Phe	Thr	Ser 255	Ser

Trp

<210> 346

<211> 237

<212> PRT

<213> homo sapiens

<400> 346

Lys 1	Ser	Arg	Arg	Arg 5	Cys	Gln	Arg	Arg	Arg 10	Ala	Arg	Ser	Trp	Ala 15	Arg
Ala	Ser	Gly	Pro 20	Arg	Arg	Thr	Gln	Arg 25	Arg	Trp	Ser	Phe	Arg 30	Arg	Thr

Arg	Arg	Trp 35	Arg	Leu	Arg	Arg	Leu 40	Leu	Arg	Ser	Pro	Ala 45	Gln	Ser	Val
Ser	Ser 50	Ala	Gly	Pro	Ala	Ala 55	Arg	Gly	Arg	Leu	Gln 60	Glu	Gly	Leu	Leu
Gln 65	Gly	Glu	Asp	Gly	Glu 70	Asp	Gln	Gly	Ala	Tyr 75	Pro	Arg	Glu	Pro	Gly 80
Glu	Asp	Ala	Pro	Gln 85	Asp	Gln	Gly	Lys	Pro 90	Gly	Glu	Asp	Ala	Ala 95	His
Pro	Gly	Glu	Ala 100	His	Glu	Gln	Ala	Gly 105	His	Ala	Pro	Gly	Ala 110	Arg	Arg
Ala	Ala	Arg 115	Glu	Thr	Glu	Asp	Val 120	Ala	Gly	Gln	Val	Ala 125	Gln	Ile	Leu
His	Ala 130	Arg	Pro	Arg	Gly	Val 135	Arg	Ala	Leu	Gln	Asp 140	Arg	Gly	Leu	Gln
Gly 145	Ala	Thr	Leu	His	Leu 150	Pro	Arg	Gln	Glu	Asp 155	Pro	Arg	Gly	Pro	Gly 160
Gly	Ser	Ala	Gln	Gly 165	His	Arg	Asp	Gly	Gly 170	Gly	Gly	Arg	Ser	Gly 175	Gly
Arg	Pro	Ala	Thr 180	Cys	Gly	Ala	Gly	Ala 185	Ala	Pro	Thr	Cys	Thr 190	Arg	Cys
Trp	Arg	Ser 195	Pro	Arg	Ser	Arg	Thr 200	Pro	Cys	Trp	Trp	Thr 205	Arg	Ala	Thr
Ala	Thr 210	Glu	Arg	Pro	Pro	Leu 215	Pro	Pro	Thr	Pro	Phe 220	Leu	Ala	Pro	Ser
Glu 225	Leu	Pro	Leu	Ser	His 230	Ser	Leu	Ser	Ala	Arg 235	Ala	Gly			

<210> 347

<211> 263

<212> PRT

<213> homo sapiens

<400> 347

Gly 1	Arg	Leu	Pro	Gly 5	Tyr	Pro	Asp	Arg	Arg 10	Gly	Pro	Gly	Ala	Ser 15	Ser
Ala	Gly	Ala	Gln 20	Ala	Ala	Glu	Glu	Pro 25	Ser	Gly	Ala	Gly	Ser 30	Glu	Glu
Leu	Ile	Lys 35	Ser	Asp	Gln	Val	Asn 40	Gly	Val	Leu	Val	Leu 45	Ser	Leu	Leu
Asp	Lys 50	Ile	Ile	Gly	Ala	Val 55	Asp	Gln	Ile	Gln	Leu 60	Thr	Gln	Ala	Gln
Leu 65	Glu	Glu	Arg	Gln	Ala 70	Glu	Met	Glu	Gly	Ala 75	Val	Gln	Ser	Ile	Gln 80
Gly	Glu	Leu	Ser	Lys 85	Leu	Gly	Lys	Ala	His 90	Ala	Thr	Thr	Ser	Asn 95	Thr

Val	Ser	Lys	Leu 100	Leu	Glu	Lys	Val	Arg 105	Lys	Val	Ser	Val	Asn 110	Val	Lys	
Thr	Val	Arg 115	Gly	Ser	Leu	Glu	Arg 120	Gln	Ala	Gly	Gln	Ile 125	Lys	Lys	Leu	
Glu	Val 130	Asn	Glu	Ala	Glu	Leu 135	Leu	Arg	Arg	Arg	Asn 140	Phe	Lys	Val	Met	
Ile 145	Tyr	Gln	Asp	Glu	Val 150	Lys	Leu	Pro	Ala	Lys 155	Leu	Ser	Ile	Ser	Lys 160	
Ser	Leu	Lys	Glu	Ser 165	Glu	Ala	Leu	Pro	Glu 170	Lys	Glu	Gly	Glu	Glu 175	Leu	
Gly	Glu	Gly	Glu 180	Arg	Pro	Glu	Glu	Asp 185	Ala	Ala	Ala	Leu	Glu 190	Leu	Ser	
Ser	Asp	Glu 195	Ala	Val	Glu	Val	Glu 200	Glu	Val	Ile	Glu	Glu 205	Ser	Arg	Ala	
Glu	Arg 210	Ile	Lys	Arg	Arg	Ala 215	Cys	Gly	Ala	Trp	Thr 220	Thr	Ser	Arg	Arg	
Pro 225	Ser	Pro	Arg	Arg	Arg 230	Trp	Arg	Arg	Pro	Arg 235	Cys	Val	Pro	Ala	Arg 240	
Thr	Trp	Arg	Arg 245	Ala	Ser	Arg	Pro	Arg 250	Lys	Thr	Trp	Arg	Arg 255	Arg		
Gly	Thr	Pro	Trp 260	Arg	Ser	Ala										

<210> 348

<211> 106

<212> PRT

<213> homo sapiens

<400> 348

Ser 1	Ser	Gly	Ser	Ser 5	Arg	Phe	Gly	Ser	Ser 10	Gly	Ser	Arg	Arg	Arg 15	Tyr	
Ala	Ser	Leu	Tyr 20	Phe	Cys	Cys	Ala	Ile 25	Glu	Asp	Gln	Asp	Asn 30	Glu	Leu	
Ile	Thr 35	Leu	Glu	Ile	Ile	His	Arg 40	Tyr	Val	Glu	Leu	Leu 45	Asp	Lys	Tyr	
Phe 50	Gly	Ser	Val	Cys	Glu	Leu 55	Asp	Ile	Ile	Phe	Asn 60	Phe	Glu	Lys	Ala	
Tyr 65	Phe	Ile	Leu	Asp	Glu 70	Phe	Leu	Leu	Gly	Gly 75	Glu	Val	Gln	Glu	Thr 80	
Ser	Lys	Lys	Asn 85	Val	Leu	Lys	Ala	Ile	Glu 90	Gln	Ala	Asp	Leu	Leu 95	Gln	
Glu	Glu	Ala	Glu 100	Thr	Pro	Arg	Ser	Gly 105	Ser							

<210> 349

<211> 78
 <212> PRT
 <213> homo sapiens

<400> 349

Leu 1	Phe	Leu	Met	Pro 5	Gln	Asn	Lys	Val	Arg 10	Met	Val	Ile	Cys	Gln 15	Glu
Phe	Phe	Ile 20	Thr	Val	Ser	Tyr	Lys	Lys 25	Arg	Val	Ala	Leu	Phe 30	Thr	Val
Leu	Cys	Val 35	Lys	Ser	Leu	Phe	Lys 40	Ala	Arg	Met	Phe	Pro 45	Leu	Gly	Tyr
Leu 50	Leu	Lys	Leu	Asn	Leu	Phe 55	Cys	Phe	Pro	Pro	Leu 60	Arg	Ser	Ala	Ala
His 65	Phe	Thr	Ala	Ala	Ser 70	Phe	Leu	Ser	Met	Ala 75	Leu	Pro	Ser		

<210> 350
 <211> 65
 <212> PRT
 <213> homo sapiens

<400> 350

Thr 1	Cys	Leu	His	Gly 5	Leu	Tyr	Phe	His	Leu 10	Tyr	Met	Leu	Gly	Trp 15	Ile
Lys	Leu	Cys	Cys 20	Asp	Cys	Asp	Gln	His 25	Ser	Gly	His	Val	Ser 30	Thr	Val
Leu	Ser	His 35	Arg	Gln	Leu	Val	Val 40	Ile	Asn	Val	Gln	Arg 45	Thr	Lys	Lys
Lys 50	Lys	Gly	Ala	Ala	Ser	Leu 55	Gly	Gly	Ile	Thr	Gly 60	Ser	Gly	Val	Lys
Arg 65															

<210> 351
 <211> 196
 <212> PRT
 <213> homo sapiens

<400> 351

Leu 1	Pro	Gly	Leu	Pro 5	Leu	Arg	Gln	Leu	Gly 10	Gly	Val	Cys	His	Gly 15	His
Arg	Pro	Gly	Leu 20	Leu	Leu	His	Gln	Gln 25	His	Gly	Gly	Gly	Ala 30	Gly	Ala
Val	Gln	Gln 35	Pro	Gln	Arg	Glu	Glu 40	Glu	Ala	Leu	His	Asp 45	Pro	Gly	Gln
Gly 50	Ser	Ala	Pro	Ala	Glu	Leu 55	Cys	Gln	Phe	Gln	Gln 60	His	Val	Pro	Arg
Phe	Pro	Leu	Gln	Gln	Pro	Gln	Ala	Val	Gln	Glu	Gly	Gly	Gly	Ala	Gly

65				70				75				80			
Ala	Gly	Gln	Gly	Leu 85	Val	Leu	Trp	Gln	Pro 90	Gly	Ala	Gly	Leu	Gln 95	Gly
Val	Gln	Pro	Gly 100	Asp	Asp	Gly	Ala	Pro 105	Asp	Leu	Gln	His	Gly 110	Asp	Ala
Ala	Gly	Asp 115	Ser	His	His	Asp	Asp 120	Pro	Ala	Gln	Glu	Leu 125	Pro	Ala	Ala
Glu	His 130	Arg	Ala	Gln	Gly	Pro 135	Gly	Gly	Pro	Arg	Pro 140	Ala	Leu	Arg	Gly
Gly 145	Ala	Arg	Ser	Asn	Cys 150	Arg	Val	Cys	Leu	Val 155	Gln	Met	Cys	Pro	Glu 160
Ala	Pro	Glu	Gly	Ser 165	His	Gln	Leu	Met	Pro 170	Ala	Ser	Asp	Pro	Gln 175	Gln
Gly	Trp	Phe	Ala 180	Ala	Ala	Ala	Gln	Gly 185	Glu	Pro	Val	Ser	Asp 190	Pro	Gly
His	His	His	His 195												

<210> 352
 <211> 361
 <212> PRT
 <213> homo sapiens
 <400> 352

Ser 1	Leu	Ala	Ser	Leu 5	Ser	Asp	Ser	Leu	Gly 10	Val	Ser	Val	Met	Ala 15	Thr
Asp	Gln	Asp	Ser 20	Tyr	Ser	Thr	Ser	Ser 25	Thr	Glu	Glu	Glu	Leu 30	Glu	Gln
Phe	Ser	Ser 35	Pro	Ser	Val	Lys	Lys 40	Lys	Pro	Ser	Met	Ile 45	Leu	Gly	Lys
Ala	Arg 50	His	Arg	Leu	Ser	Phe 55	Ala	Ser	Phe	Ser	Ser 60	Met	Phe	His	Ala
Phe 65	Leu	Ser	Asn	Asn	Arg 70	Lys	Leu	Tyr	Lys 75	Val	Val	Glu	Leu	Ala 80	
Gln	Asp	Lys	Gly	Ser 85	Tyr	Phe	Gly	Ser	Leu 90	Val	Gln	Asp	Tyr	Lys 95	Val
Tyr	Ser	Leu 100	Glu	Met	Met	Ala	Arg	Gln 105	Thr	Ser	Ser	Thr	Glu 110	Met	Leu
Gln	Glu	Ile 115	Arg	Thr	Met	Met	Thr 120	Gln	Leu	Lys	Ser	Tyr 125	Leu	Leu	Gln
Ser	Thr 130	Glu	Leu	Lys	Ala	Leu 135	Val	Asp	Pro	Ala	Leu 140	His	Ser	Glu	Glu
Glu 145	Leu	Glu	Ala	Ile	Val 150	Glu	Ser	Ala	Leu	Tyr 155	Lys	Cys	Val	Leu	Lys 160

Pro	Leu	Lys	Glu	Ala 165	Ile	Asn	Ser	Cys	Leu 170	His	Gln	Ile	His	Ser 175	Lys
Asp	Gly	Ser	Leu 180	Gln	Gln	Leu	Lys	Glu 185	Asn	Gln	Leu	Val	Ile 190	Leu	Ala
Thr	Thr	Thr 195	Thr	Asp	Leu	Gly	Val 200	Thr	Thr	Ser	Val	Pro 205	Glu	Val	Pro
Met	Met 210	Glu	Lys	Ile	Leu	Gln 215	Lys	Phe	Thr	Ser	Met 220	His	Lys	Ala	Tyr
Ser 225	Pro	Glu	Lys	Lys	Ile 230	Ser	Ile	Leu	Leu	Lys 235	Thr	Cys	Lys	Leu	Ile 240
Tyr	Asp	Ser	Met	Ala 245	Leu	Gly	Asn	Pro	Gly 250	Lys	Pro	Tyr	Gly	Ala 255	Asp
Asp	Phe	Leu	Pro 260	Val	Leu	Met	Tyr	Val 265	Leu	Ala	Arg	Ser	Asn 270	Leu	Thr
Glu	Met	Leu 275	Leu	Asn	Val	Glu	Tyr 280	Met	Met	Glu	Leu	Met 285	Asp	Pro	Ala
Leu	Gln 290	Leu	Gly	Glu	Gly	Ser 295	Tyr	Tyr	Leu	Thr	Thr 300	Thr	Tyr	Gly	Ala
Leu 305	Glu	His	Ile	Lys	Ser 310	Tyr	Asp	Lys	Ile	Thr 315	Val	Thr	Arg	Gln	Leu 320
Ser	Val	Glu	Val	Gln 325	Asp	Ser	Ile	His	Arg 330	Trp	Glu	Arg	Arg	Arg 335	Thr
Leu	Asn	Lys	Ala 340	Arg	Ala	Ser	Arg	Ser 345	Ser	Val	Gln	Pro	Leu 350	His	Leu
Arg	Val	Val 355	Pro	Gly	Ala	Arg	Ala 360	Ala							

<210> 353

<211> 161

<212> PRT

<213> homo sapiens

<400> 353

Val 1	Asp	Gly	Phe	Leu 5	Gln	Gly	Leu	Gln	Asp 10	Thr	Phe	Val	Gln	Gly 15	Arg
Leu	Tyr	Asn	Cys 20	Phe	Glu	Leu	Leu	Leu 25	Gly	Val	Gln	Gly	Gly 30	Val	His
Gln	Gly	Leu 35	Glu	Leu	Gly	Ala	Leu 40	Gln	Gln	Val	Ala	Leu 45	Glu	Leu	Gly
His	His 50	Gly	Ala	Asn	Leu	Leu 55	Gln	His	Leu	Arg	Ala 60	Gly	Gly	Leu	Ala
Arg 65	His	His	Leu	Gln	Ala 70	Val	His	Leu	Val	Val 75	Leu	His	Gln	Ala	Ala 80
Lys	Val	Arg	Ala	Leu 85	Val	Leu	Arg	Gln	Leu 90	His	His	Leu	Leu	Val 95	Gln

<210> 355
 <211> 253
 <212> PRT
 <213> homo sapiens

<400> 355

Ala 1	Gly	Glu	Gly	Val 5	Asp	Gly	Leu	Thr	Gln 10	Glu	Thr	Pro	Leu	Lys 15	Pro
Val	Ser	Gln	Leu 20	Pro	Gly	Pro	Ala	Gly 25	Ala	Pro	Thr	Gly	Arg 30	Arg	Gly
Gln	Ala	Glu 35	Asp	Pro	Gly	Ser	Val 40	Met	Ala	Ser	Ala	Leu 45	Arg	Pro	Pro
Arg	Val 50	Pro	Lys	Pro	Lys	Gly 55	Val	Leu	Pro	Ser	His 60	Tyr	Tyr	Glu	Ser
Phe 65	Leu	Glu	Lys	Lys	Gly 70	Pro	Cys	Asp	Arg	Asp 75	Tyr	Lys	Lys	Phe	Trp 80
Ala	Gly	Leu	Gln	Gly 85	Leu	Thr	Ile	Tyr	Phe 90	Tyr	Asn	Ser	Asn	Arg 95	Asp
Phe	Gln	His	Val 100	Glu	Lys	Leu	Asn	Leu 105	Gly	Ala	Phe	Glu	Lys 110	Leu	Thr
Asp	Glu	Ile 115	Pro	Trp	Gly	Ser	Ser 120	Arg	Asp	Pro	Gly	Thr 125	His	Phe	Ser
Leu 130	Leu	Arg	Asn	Gln	Glu 135	Ile	Lys	Phe	Lys	Val 140	Glu	Thr	Leu	Glu	
Cys 145	Arg	Glu	Met	Trp	Lys 150	Gly	Phe	Ile	Leu	Thr 155	Val	Val	Glu	Leu	Arg 160
Val	Pro	Thr	Asp	Leu 165	Thr	Leu	Leu	Pro	Gly 170	His	Leu	Tyr	Met	Met 175	Ser
Glu	Val	Leu	Ala 180	Lys	Glu	Glu	Ala	Arg 185	Arg	Ala	Leu	Glu	Thr 190	Pro	Ser
Cys	Phe	Leu 195	Lys	Val	Ser	Arg	Leu 200	Glu	Ala	Gln	Leu	Leu 205	Leu	Glu	Arg
Tyr	Pro 210	Glu	Cys	Gly	Asn	Leu 215	Leu	Leu	Arg	Pro	Ser 220	Gly	Asp	Gly	Ala
Asp 225	Gly	Val	Gly	His	His 230	Ala	Ala	Asp	Ala	Gln 235	Arg	Asp	Ala	Arg	Gly 240
Pro	Ala	Leu	Gln	Gly 245	Glu	Ala	Gly	Gly	Ala 250	Pro	Ser	Thr			

<210> 356
 <211> 118
 <212> PRT
 <213> homo sapiens

<400> 356

Leu 1	Thr	Thr	Ala	Ser 5	Arg	Glu	Val	Gln	Glu 10	Asn	Gly	Cys	Ser	Thr 15	Ser	
Ile	Thr	Tyr	Leu 20	Gly	Pro	Leu	Pro	Leu 25	His	Leu	Val	Met	Pro 30	Asp	His	
Val	Arg	Pro 35	Val	Val	His	Leu	Pro 40	Arg	Gly	Asp	Arg	His 45	Arg	Arg	Arg	
Arg	Pro 50	Arg	Trp	Ala	Ala	Ala 55	Ala	Gly	Ser	Arg	Thr 60	Arg	Gly	Ser	Ala	
Pro 65	Gly	Ala	Val	Val	Pro 70	Pro	Ala	Gly	Ser	Pro 75	Ser	Gly	Ser	Thr	Arg 80	
Val	Ser	Pro	Val	His 85	Gly	Ala	Pro	Pro	Leu 90	Trp	Pro	Arg	Leu	Gln 95	Thr	
Ser	Cys	Ile	Gly 100	Ala	Gln	Glu	Ala	Gly 105	Ser	Ser	Arg	Ser	Gly 110	His	Gly	
Ala	Pro	Pro 115	Pro	Leu	Arg											

<210> 357
 <211> 223
 <212> PRT
 <213> homo sapiens

<400> 357

Asp 1	His	Thr	Cys	Gly 5	Cys	Ala	Gly	Asn	Leu 10	Gln	Glu	Ala	Ile	Met 15	Leu	
Arg	Ser	Gly	Val 20	Thr	Ser	Gln	Gly	Ile 25	His	Pro	Gly	Ser	Pro 30	Trp	Cys	
Cys	Thr	Pro 35	Thr	Gln	Ala	Glu	Leu 40	Ile	Val	Gly	Asp	Gln 45	Ser	Gly	Ala	
Ile 50	His	Ile	Trp	Asp	Leu	Lys 55	Thr	Asp	His	Asn	Glu 60	Gln	Leu	Ile	Pro	
Glu 65	Pro	Glu	Val	Ser	Ile 70	Thr	Ser	Ala	His	Ile 75	Asp	Pro	Asp	Ala	Ser 80	
Tyr	Met	Ala	Ala	Val 85	Asn	Ser	Thr	Gly	Asn 90	Cys	Tyr	Val	Trp	Asn 95	Leu	
Thr	Gly	Gly	Ile 100	Gly	Asp	Glu	Val	Thr 105	Gln	Leu	Ile	Pro	Lys 110	Thr	Lys	
Ile	Pro	Ala 115	His	Thr	Arg	Tyr	Ala 120	Leu	Gln	Cys	Arg	Phe 125	Ser	Pro	Asp	
Ser	Thr 130	Leu	Leu	Ala	Thr	Cys 135	Ser	Ala	Asp	Gln	Thr 140	Cys	Lys	Ile	Trp	
Arg 145	Thr	Ser	Asn	Phe	Ser 150	Leu	Met	Thr	Glu	Leu 155	Ser	Ile	Lys	Ser	Gly 160	
Asn	Pro	Gly	Glu	Ser 165	Ser	Arg	Gly	Trp	Met 170	Trp	Gly	Cys	Ala	Phe 175	Ser	

Gly	Asp	Ser	Gln 180	Tyr	Ile	Val	Thr	Ala 185	Ser	Ser	Asp	Asn	Leu 190	Ala	Arg
Leu	Trp	Cys 195	Val	Glu	Thr	Gly	Glu 200	Ile	Lys	Arg	Glu	Tyr 205	Gly	Gly	His
Gln	Lys 210	Ala	Val	Val	Cys	Leu 215	Ala	Phe	Asn	Asp	Ser 220	Val	Leu	Gly	

<210> 358

<211> 193

<212> PRT

<213> homo sapiens

<400> 358

Phe 1	Phe	Phe	Phe	Phe 5	Phe	Phe	Phe	Phe	Pro 10	Glu	Gln	His	Leu	Arg 15	Val
Gly	Leu	Leu	Leu 20	Leu	Pro	Pro	Arg	Leu 25	Ser	Pro	Arg	Pro	Gly 30	Pro	Ala
Trp	Pro	Val 35	Pro	Asn	Pro	Val	Gly 40	Trp	Pro	Gly	His	Leu 45	His	Gln	Gly
Gly	Gln 50	Leu	Leu	Ala	Gly	Thr 55	Asn	Lys	Pro	Phe	His 60	Leu	Ala	Met	Val
Val 65	Val	Phe	Ser	Met	Asp 70	Arg	Gly	Pro	Glu	Thr 75	Arg	Ala	Gly	Arg	Gly 80
Arg	Glu	His	Thr	Ser 85	Leu	Gly	Val	Gly	Thr 90	Ser	Leu	Arg	Pro	Leu 95	Ser
Ser	Phe	Gly	Pro 100	Ser	Ala	Asp	Phe	Pro 105	Arg	Gln	Cys	Arg	Leu 110	Ala	Gln
Ser	Arg	Ser 115	Val	Gln	Pro	Gly	Leu 120	Gly	Arg	Ala	Leu	Ser 125	His	Leu	Asp
Lys	Gln 130	Leu	Gly	Ala	Glu	Ser 135	Pro	Arg	Ala	Ala	Trp 140	Pro	Ser	Arg	Ser
Arg 145	Arg	His	Arg	Gly	Pro 150	Ser	Gly	Pro	Val	Ala 155	Gln	Ala	Gly	Arg	Gly 160
Gly	Ser	Ala	Leu	Thr 165	Trp	Val	Leu	His	Gly 170	Ser	Leu	Gln	Leu	Pro 175	Pro
Pro	Ala	Pro	Gly 180	Ser	Pro	Glu	Gly	Ser 185	Gln	Ala	Ser	Pro	Ala 190	His	Cys

His

<210> 359

<211> 251

<212> PRT

<213> homo sapiens

<400> 359

Pro Gly Cys Cys Met Gly Pro Ser Ser Cys His His Leu His Gln Ala

1				5				10				15			
Val	Pro	Arg	Gly 20	His	Arg	Leu	Ala	Gln 25	His	Thr	Val	Ile	Glu 30	Gly	Gln
Ala	Asp	Asn 35	Ser	Leu	Leu	Val	Ala 40	Ala	Ile	Leu	Ser	Leu 45	Asp	Leu	Ser
Ser	Leu 50	His	Thr	Pro	Glu	Pro 55	Gly	Gln	Val	Val	Arg 60	Gly	Ser	Ser	Asp
Asp 65	Val	Leu	Gly	Val	Pro 70	Arg	Glu	Gly	Ala	Ala 75	Pro	His	Pro	Ala	Ala 80
Gly	Gly	Leu	Pro	Gly 85	Val	Ala	Ala	Leu	Asp 90	Ala	Gln	Leu	Arg	His 95	Gln
Gly	Glu	Val	Gly 100	Arg	Pro	Pro	Asp	Leu 105	Ala	Arg	Leu	Ile	Ser 110	Arg	Ala
Gly	Gly	Glu 115	Glu	Arg	Gly	Val	Gly 120	Ala	Glu	Ala	Thr	Leu 125	Gln	Gly	Val
Ala	Arg 130	Val	Gly	Arg	Asp	Leu 135	Ser	Leu	Gly	Asp	Glu 140	Leu	Gly	His	Leu
Val 145	Thr	Asn	Ala	Pro	Arg 150	Gln	Ile	Pro	Asp	Ile 155	Ala	Val	Ser	Gly	Ala 160
Ile	Asp	Ser	Cys	His 165	Val	Ala	Gly	Val	Gly 170	Ile	Asp	Val	Gly	Gly 175	Arg
Asp	Gly	Asp	Leu 180	Gly	Leu	Arg	Asp	Gln 185	Leu	Leu	Val	Val	Val 190	Cys	Phe
Gln	Val	Pro 195	Asp	Val	Asp	Ser	Pro 200	Ala	Leu	Val	Thr	His 205	Asp	Glu	Leu
Cys	Leu 210	Gly	Trp	Gly	Ala	Ala 215	Pro	Gly	Thr	Pro	Arg 220	Val	Asn	Ala	Leu
Gly 225	Gly	His	Thr	Gly	Pro 230	Gln	His	Asp	Cys	Phe 235	Leu	Gln	Val	Thr	Ser 240
Thr	Ser	Ala	Cys	Met 245	Ile	Leu	Thr	Ser	Ser 250	Cys					

<210> 360

<211> 50

<212> PRT

<213> homo sapiens

<400> 360

Gly 1	Asn	Ile	Pro	His 5	Ser	Asn	Leu	Thr	Asp 10	Ala	Ser	Ser	Pro	Lys 15	Arg
Ile	Lys	Ile	Val 20	Ala	Cys	Thr	Asp	Gln 25	Glu	Asn	Ile	Leu	Gly 30	Arg	Met
Lys	Tyr 35	Val	Cys	Leu	Phe	Phe	Phe 40	Lys	Asn	Lys	Gly	Phe 45	Trp	Asn	Ser

Gly Glu
50

<210> 361

<211> 59

<212> PRT

<213> homo sapiens

<400> 361

Lys 1	Gly	Asn	Gln	Leu 5	Tyr	Gln	Gly	Glu	Thr 10	Arg	Ala	Leu	Gly	Thr 15	Met
Thr	Thr	Arg	Thr 20	Ala	Phe	Ile	Leu	His 25	His	Ser	Asp	Cys	Phe 30	Gln	Ser
Ser	Asn	Asp 35	Cys	Gln	Ala	Thr	Ser 40	Gln	Met	Thr	Asp	Asn 45	Phe	Cys	Cys
Ser	Phe 50	Leu	Tyr	Lys	Met	Leu 55	Arg	Gln	Gln	Ala					

<210> 362

<211> 67

<212> PRT

<213> homo sapiens

<400> 362

Asp 1	Lys	Ile	Leu	Leu 5	Ser	Pro	Arg	Met	Glu 10	Cys	Ser	Gly	Met	Ile 15	Met
Ala	His	Cys	Ser 20	Leu	Asp	Leu	Pro	Gly 25	Ser	His	Leu	Ser	Leu 30	Pro	Ser
Ser	Trp	Asp 35	His	Arg	His	Val	Pro 40	Pro	Cys	Pro	Ala	Asn 45	Phe	Tyr	Phe
Gly	Arg 50	Asp	Lys	Val	Ser	Pro 55	Cys	Cys	Leu	Gly	Arg 60	Phe	Gln	Thr	Pro
Gly 65	Leu	Lys													

<210> 363

<211> 84

<212> PRT

<213> homo sapiens

<400> 363

Met 1	Arg	Arg	Cys	Ile 5	His	Pro	Ser	His	Ser 10	Leu	Ser	Gly	Ser	Arg 15	Gln
Thr	Gln	Ser	Pro 20	Leu	Ser	His	Ser	Ala 25	Ser	Asn	Gly	Ser	Thr 30	Thr	Lys
Val	Ala	Gln 35	Gln	Met	Arg	Arg	Ala 40	Ala	Ala	Val	Val	Gly 45	Glu	Ser	Thr
Glu	Glu 50	Thr	Arg	Leu	Gly	Arg 55	Ala	Leu	Gly	Ala	Ala 60	Gly	Phe	Thr	Asn

Lys	Gln	Leu	Ser	Glu	Asn	Thr	Ala	Gln	Gly	Glu	Glu	Lys	Arg	Val	Met
65					70					75					80

Cys Leu Gln Asn

<210> 364

<211> 127

<212> PRT

<213> homo sapiens

<400> 364

Cys	Ala	Tyr	Arg	Thr	Glu	Lys	Trp	Lys	Ser	His	Thr	Val	Pro	Cys	Ser
1				5					10					15	
Pro	Glu	Val	Lys	Leu	Val	Leu	Thr	Leu	Ala	Leu	Arg	Ala	Phe	Ser	Ser
			20					25					30		
Met	Glu	Pro	Leu	Gly	Leu	Gly	Arg	Lys	Ala	Arg	Val	Ser	Ala	His	Arg
		35					40					45			
His	Thr	Ser	Tyr	Leu	Gln	Asp	Ile	Asp	Cys	Leu	Cys	Arg	Gly	Ser	Thr
	50					55					60				
Gly	Gln	Pro	Thr	Ala	Asn	Thr	Ala	Ala	Ser	Leu	Val	Ser	Ala	Ser	Leu
65					70					75					80
Leu	Pro	Val	His	Pro	Gly	Asp	Tyr	Ser	Trp	Ile	Asn	Leu	Pro	Lys	Asn
				85					90					95	
Ser	Ala	Phe	Ile	Met	Ser	Leu	Phe	Cys	Ser	Lys	Thr	Gln	Asn	Gly	Ser
			100					105					110		
Leu	Pro	Pro	Arg	Gly	Arg	Pro	Ser	His	His	Cys	Ile	Pro	Asn	Arg	
		115					120					125			

<210> 365

<211> 114

<212> PRT

<213> homo sapiens

<400> 365

Pro	Tyr	Val	His	Ser	Pro	Ala	Trp	Ser	Pro	Trp	Gly	Leu	Val	Gly	Arg
1				5					10					15	
Leu	Val	Ser	Val	His	Thr	Asp	Ile	Pro	Ala	Thr	Phe	Arg	Thr	Leu	Ile
			20					25					30		
Val	Ser	Ala	Glu	Val	Ala	Leu	Gly	Ser	Gln	Leu	Gln	Thr	Gln	Gln	Pro
		35					40					45			
Pro	Trp	Phe	Gln	Leu	Leu	Ser	Phe	Gln	Tyr	Ile	Leu	Glu	Thr	Thr	Pro
	50					55					60				
Gly	Leu	Ile	Phe	Leu	Arg	Thr	Gln	His	Ser	Leu	Cys	His	Phe	Ser	Val
65					70					75					80
Arg	Lys	Pro	Lys	Met	Ala	Pro	Cys	His	Leu	Glu	Ala	Asp	Gln	Val	Ile
				85					90				95		
Thr	Val	Ser	Pro	Thr	Ala	Ser	Thr	Val	Cys	Ile	Trp	Tyr	Ile	Val	Gln
			100					105					110		

Ala Pro

<210> 366

<211> 30

<212> PRT

<213> homo sapiens

<400> 366

Asn	Leu	His	Ser	Asn	Ile	Lys	Val	Phe	Phe	Tyr	Asn	Val	Pro	Lys	Ile
1				5					10					15	
Ser	Gly	Pro	Gln	Gln	Ala	Val	Phe	Val	Pro	Val	Phe	Phe	Asn		
			20					25					30		

<210> 367

<211> 44

<212> PRT

<213> homo sapiens

<400> 367

Lys	Glu	Cys	Met	Ser	Glu	Ala	Gln	Phe	Leu	Ala	Thr	Thr	Leu	Thr	Lys
1				5					10					15	
Gly	Asn	Asn	Cys	Arg	Gly	Ile	Leu	Gln	Leu	Ile	His	Thr	Gln	His	Leu
			20					25					30		
Leu	His	Thr	Val	Phe	Thr	Asp	Ser	Asn	Leu	Val	Gly				
		35					40								

<210> 368

<211> 34

<212> PRT

<213> homo sapiens

<400> 368

Asn	Val	Asp	Phe	Arg	Cys	Lys	Asn	Met	Leu	Glu	Ile	Arg	Phe	Ser	Ala
1				5					10					15	
Ile	Lys	Pro	Asn	Thr	Lys	Lys	Ile	Lys	Lys	Asn	Val	Cys	Gln	Lys	Pro
			20					25					30		
Asn	Ser														

<210> 369

<211> 147

<212> PRT

<213> homo sapiens

<400> 369

Gln	Pro	Ser	Ser	Leu	Leu	His	His	Cys	Pro	Tyr	Pro	Tyr	Pro	Pro	Arg
1				5					10					15	
His	Leu	Leu	Ala	Thr	Pro	Leu	Leu	Lys	Pro	Gln	Leu	Leu	Ala	Gly	Ser
			20					25					30		
Pro	Ala	His	Ala	Ser	Leu	Ile	Ser	Phe	Leu	Ala	Ser	Pro	Gln	Arg	Ala
		35					40					45			

Ser	Met	Pro	Ser	His	Pro	Asp	Arg	Ala	Tyr	Asn	Ser	Cys	Tyr	Ser	Ala
		195					200					205			
Gly	Val	Phe	His	Leu	His	Gln	Gly	Asp	Ile	Leu	Ser	Val	Ile	Ile	Pro
	210					215					220				
Arg	Ala	Arg	Ala	Lys	Leu	Asn	Leu	Ser	Pro	His	Gly	Thr	Phe	Leu	Gly
	225				230					235					240
Phe	Val	Lys	Leu												

<210> 371
 <211> 185
 <212> PRT
 <213> homo sapiens

<400> 371

Thr	Pro	Ala	Ser	Trp	Ile	Arg	Thr	Pro	Tyr	Pro	Trp	Ala	Cys	Arg	Pro
1				5					10					15	
Leu	Pro	Arg	Leu	Arg	Ala	Gly	Cys	His	Ile	Thr	Ser	Val	Thr	Ser	Glu
			20					25					30		
Ser	Phe	Phe	Cys	Phe	Trp	Val	Ser	Thr	Ala	Leu	Leu	Phe	Arg	Asp	Leu
		35					40					45			
Ser	Pro	Leu	Ser	Gln	Ala	Ser	Arg	Ala	Ser	Glu	Leu	Cys	Ser	Gly	Arg
	50					55					60				
Leu	Cys	Gln	Gly	Tyr	Pro	Ser	Pro	Phe	Trp	Glu	Gly	Pro	Pro	Val	Pro
	65				70					75					80
Cys	Ser	Arg	Leu	Thr	Ser	Leu	Leu	Arg	Leu	Cys	Ser	Ser	Val	Cys	Trp
				85					90					95	
Val	Ser	Arg	Ala	Met	Ala	Gln	Ala	Thr	Ala	Pro	Arg	Ala	Ala	Pro	Gln
			100					105					110		
Leu	Asn	Gln	Arg	Ala	Thr	Glu	Ser	Ala	Gly	Ser	Leu	Thr	Gly	Pro	Pro
		115					120					125			
Met	Leu	Pro	Gly	Gly	Pro	Leu	Gly	Ala	Ser	Lys	Lys	Gly	Asp	Glu	Ala
	130					135					140				
Gly	Met	Ser	Trp	Gly	Pro	Cys	Gln	Gln	Leu	Trp	Phe	Gln	Glu	Trp	Gly
	145				150					155					160
Ser	Lys	Glu	Val	Ala	Gly	Arg	Val	Arg	Val	Arg	Ala	Val	Val	Gln	Lys
				165					170					175	
Gly	Arg	Arg	Leu	Leu	Arg	Lys	Glu	Lys							
			180					185							

<210> 372
 <211> 148
 <212> PRT
 <213> homo sapiens

<400> 372

Val	Leu	Tyr	His	Cys	Ala	Ser	Arg	Tyr	Arg	Arg	Arg	Ala	Arg	Gln	Thr
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1				5				10				15			
Cys	Ala	Pro	Ser	Tyr	Thr	Arg	Ser	Ala	Asp	Leu	Pro	Ser	Arg	Thr	Pro
			20					25					30		
Pro	Val	Glu	Asp	Leu	Leu	Glu	Leu	Ser	Arg	Ala	Phe	Trp	Val	Gly	Ala
		35					40					45			
Asp	Gly	Gly	Gly	Arg	Val	Arg	Val	Leu	Gly	Gly	Thr	Glu	Ala	His	Glu
	50					55					60				
Asp	Gly	Ile	Pro	Pro	Glu	Ser	Met	Asp	His	Tyr	Ala	Asp	Gly	His	Arg
	65				70					75					80
Pro	Gln	His	Cys	His	Leu	Gly	Tyr	Arg	Cys	His	Gly	Arg	Pro	Gln	Arg
				85					90					95	
Glu	Gly	Leu	Pro	Arg	Cys	Leu	Lys	Val	Pro	Pro	Val	Asn	Leu	Ser	Ser
			100					105					110		
Val	Ser	Val	Pro	Phe	Pro	Val	Thr	His	Arg	Ala	Gly	Met	Glu	Phe	Asn
		115					120					125			
Gly	Cys	Ser	Gly	Gln	Thr	Leu	Val	His	Gly	Gln	Thr	Ser	Leu	Leu	Trp
	130					135					140				
Ile	Leu	Gln	Asp												
	145														
<210> 373															
<211> 135															
<212> PRT															
<213> homo sapiens															
<400> 373															
Cys	Leu	Pro	Val	Arg	Arg	Leu	Arg	Gln	Phe	Glu	Pro	Lys	Thr	Pro	Lys
	1			5					10					15	
Val	Glu	Ala	Glu	Phe	Gln	Ser	Met	Gly	Ser	Arg	Leu	Ser	Gln	Pro	Phe
			20					25					30		
Glu	Ser	Tyr	Ile	Thr	Ala	Pro	Pro	Gly	Thr	Ala	Ala	Ala	Pro	Ala	Lys
		35					40					45			
Pro	Ala	Pro	Pro	Ala	Thr	Pro	Gly	Ala	Pro	Thr	Ser	Pro	Ala	Glu	His
	50					55					60				
Arg	Leu	Leu	Lys	Thr	Cys	Trp	Ser	Cys	Arg	Val	Leu	Ser	Gly	Leu	Gly
	65				70					75					80
Leu	Met	Gly	Ala	Gly	Gly	Tyr	Val	Tyr	Trp	Val	Ala	Arg	Lys	Pro	Met
				85					90					95	
Lys	Met	Gly	Tyr	Pro	Pro	Ser	Pro	Trp	Thr	Ile	Thr	Gln	Met	Val	Ile
			100					105					110		
Gly	Leu	Ser	Ile	Ala	Thr	Trp	Gly	Ile	Val	Val	Met	Ala	Asp	Pro	Lys
		115					120					125			
Gly	Lys	Ala	Tyr	Arg	Val	Val									
	130						135								

<210> 374
 <211> 152
 <212> PRT
 <213> homo sapiens

<400> 374

Ile	Pro	Cys	Leu	Leu	Cys	Val	Ser	Arg	Gly	Lys	Gly	Gln	Arg	Gln	Lys
1				5					10					15	
Thr	Asp	Ser	Leu	Val	Val	Leu	Ser	Asn	Asn	Ala	Val	Gly	Leu	Pro	Phe
			20					25					30		
Gly	Val	Cys	His	Asp	Asn	Asp	Thr	Pro	Gly	Gly	Asn	Ala	Glu	Ala	Asp
		35					40					45			
Asp	His	Leu	Arg	Asn	Gly	Pro	Trp	Thr	Arg	Gly	Val	Ser	His	Leu	His
	50					55					60				
Gly	Leu	Pro	Cys	His	Pro	Val	His	Val	Pro	Ala	Arg	Pro	His	Gln	Pro
	65				70					75					80
Gln	Pro	Arg	Lys	His	Ala	Thr	Ala	Pro	Ala	Gly	Leu	Gln	Gln	Ala	Val
				85					90					95	
Phe	Cys	Trp	Gly	Gly	Arg	Arg	Ser	Gly	Cys	Ser	Trp	Gly	Arg	Arg	Phe
			100					105					110		
Gly	Gly	Arg	Gly	Gly	Gly	Thr	Gly	Arg	Ser	Asp	Ile	Gly	Leu	Lys	
		115					120				125				
Arg	Leu	Gly	Gln	Pro	Arg	Pro	His	Ala	Leu	Glu	Leu	Gly	Leu	Asn	Leu
	130					135					140				
Gly	Arg	Leu	Trp	Phe	Lys	Leu	Ala								
145					150										

<210> 375
 <211> 107
 <212> PRT
 <213> homo sapiens

<400> 375

Gly	Ala	Glu	Leu	Gln	Leu	Arg	Ser	Cys	Ala	Met	Ala	Val	Ser	Gln	Glu
1				5					10					15	
Gly	Leu	Asp	Gly	Glu	Val	Lys	Ala	Pro	Asp	Ala	Arg	Ile	Phe	Ile	Pro
			20					25					30		
Cys	Ala	Asn	Thr	Ala	Phe	Thr	Pro	Asp	Leu	Gln	Val	Leu	Gln	Gln	Val
		35					40					45			
Leu	Ser	Ser	Phe	Thr	Val	Ser	Ser	Pro	Leu	Phe	His	Ser	Gly	Phe	Ile
	50					55					60				
Cys	Tyr	Thr	Pro	Asn	Leu	Phe	Ser	Gln	Ser	Thr	Pro	Gln	Ser	Leu	Pro
	65				70					75					80
Cys	Trp	Gly	Gln	His	Arg	Lys	Arg	Gln	Asn	Leu	Arg	Lys	Glu	Lys	Gly
				85					90					95	
Asn	Leu	Gln	Pro	Ala	Met	Asp	Leu	Met	Ile	Pro					

<210> 376
 <211> 113
 <212> PRT
 <213> homo sapiens

<400> 376

Ile	Pro	Lys	Asn	Phe	Tyr	His	Asn	Ile	His	Arg	Ser	Leu	Tyr	Gln	Leu
1				5					10					15	
Tyr	Leu	Glu	Val	Lys	Gln	Ala	Trp	Glu	Ser	Ile	Asp	Cys	Ser	Ala	Cys
			20					25				30			
Pro	Arg	Val	Glu	Ala	Leu	Asn	Lys	Ala	Thr	Lys	Thr	Pro	Glu	Ile	Thr
		35					40					45			
Asp	Leu	Thr	Phe	Gln	Trp	Pro	Thr	Gly	Pro	Gly	Ser	Gly	Gln	Val	Gly
	50					55					60				
His	Gln	Ala	Asn	His	Leu	Phe	Pro	Cys	Ala	Ser	Leu	Cys	Lys	Ser	Trp
	65				70					75					80
Ser	Val	Pro	Leu	Ala	Arg	Pro	Ser	Leu	Val	Gln	Asp	Leu	Gly	Pro	Gln
				85					90					95	
Thr	Lys	Glu	Ser	Arg	Gly	Leu	Gly	Phe	Pro	Asp	Pro	Arg	Met	Val	Ser
			100					105					110		
Leu															

<210> 377
 <211> 124
 <212> PRT
 <213> homo sapiens

<400> 377

Phe	Gly	Gly	Pro	Gln	Ala	Gln	Pro	His	Ser	Ala	Val	Gly	Ser	Ser	Leu
1				5					10					15	
Ser	Ser	Gln	Ile	Gln	Val	Asn	Leu	Ser	Phe	Lys	Asn	Lys	Gly	Glu	Pro
			20					25					30		
Gln	Thr	Cys	Ser	Thr	Thr	Arg	Asp	Asn	Asn	Thr	Pro	Trp	Gln	Glu	Asp
		35					40					45			
His	Val	Leu	Asp	Cys	Leu	Arg	Thr	Ala	Thr	Val	Arg	Gln	Glu	Ala	Cys
	50					55				60					
Cys	Asp	Pro	Leu	Cys	Ser	Met	Pro	Ile	Ala	Gln	Ala	Ser	Ser	Ile	Pro
	65				70					75				80	
Tyr	His	Leu	Pro	Pro	Met	Leu	Phe	Phe	Gly	Thr	Thr	Thr	Leu	Ala	Lys
				85					90					95	
Arg	Glu	Tyr	Gly	Lys	Gln	Arg	Pro	Arg	Ala	Leu	Leu	Gln	Tyr	Arg	His
			100					105					110		
Phe	Glu	Val	Gly	Arg	Gln	His	Met	Leu	His	Ser	Lys				
		115					120								

<210> 378
 <211> 66
 <212> PRT
 <213> homo sapiens

<400> 378

His	Lys	Ile	Ile	Leu	Ile	Ser	Arg	Tyr	Arg	Arg	Asn	Ser	Val	Val	Thr
1				5					10					15	
Cys	Gln	Ala	Ile	Leu	Tyr	Thr	Pro	Met	Ile	Leu	Gln	Arg	Lys	His	Pro
			20					25					30		
Ser	Leu	Leu	Leu	Pro	Leu	Leu	Trp	Gln	Leu	Lys	Cys	Ile	Cys	Ser	Ser
			35				40					45			
Thr	Leu	Lys	Arg	Arg	Lys	Arg	Asn	Asn	Leu	Ser	Leu	Ile	Pro	Lys	Leu
	50					55					60				
Pro	His														
65															

<210> 379
 <211> 67
 <212> PRT
 <213> homo sapiens

<400> 379

Pro	Glu	Lys	Ser	Pro	Gly	Ala	Gly	Pro	Leu	Leu	Gly	Gly	Ser	Pro	Phe
1				5					10					15	
Phe	Phe	Phe	Phe	Tyr	Val	Ser	Lys	Ser	Thr	Glu	Phe	Ile	Leu	Lys	His
			20					25					30		
Ser	Ile	Lys	Phe	Glu	Ser	His	Glu	Thr	Lys	Ala	Ser	Leu	His	Tyr	Met
		35					40					45			
Leu	Ile	Leu	Ala	Lys	Ser	Lys	Asp	Gln	His	Thr	Ile	Asp	Ile	His	Asp
	50					55					60				
Asn	Val	Val													
65															

<210> 380
 <211> 71
 <212> PRT
 <213> homo sapiens

<400> 380

Phe	Cys	Ile	His	Phe	Glu	Cys	Leu	His	Val	Lys	Thr	Gln	Leu	Ile	Tyr
1				5					10					15	
Tyr	Phe	Asn	Ile	Lys	Pro	Ile	Ser	Phe	Glu	Ala	Lys	Leu	Ile	Leu	Leu
			20					25					30		
Phe	Tyr	Lys	Ser	Asn	Gly	Asp	Ser	Phe	Phe	Arg	Met	Leu	Lys	Ala	Gln
		35				40						45			
Cys	Leu	Arg	Phe	Met	Leu	Ala	Ala	Leu	Leu	Ala	Leu	Leu	Leu	Pro	Glu
	50					55					60				

Met Lys Thr Lys Gln Asn Arg
65 70

<210> 381
<211> 107
<212> PRT
<213> homo sapiens

<400> 381

Met	Asp	Gly	Ala	Gln	Gly	Arg	Leu	Leu	Pro	Val	Ser	Ser	Arg	His	Ser
1				5					10					15	
Asn	Leu	Ala	Leu	Leu	Lys	Pro	Thr	Ser	Arg	Asp	Leu	Thr	Ala	Pro	Pro
			20					25					30		
Glu	Gly	Ala	Ser	Leu	Met	Thr	Val	Gly	Gly	Ile	Thr	Ala	Pro	Arg	Asp
		35					40					45			
Val	Gln	Val	Trp	Asn	Pro	Arg	Thr	Trp	Glu	Ser	Val	Thr	Leu	Arg	Gly
	50					55					60				
Lys	Arg	Asp	Pro	Ala	Pro	Val	Leu	Gln	Phe	Arg	Ile	Ser	Trp	Trp	Gly
65					70					75					80
Asp	Asp	Arg	Gly	Trp	Leu	Arg	Trp	Ala	Leu	Ser	Asn	His	Gly	Gly	Pro
				85					90					95	
Tyr	Lys	Gly	Arg	Gly	Val	Thr	Arg	Val	Cys	Ala					
			100					105							

<210> 382
<211> 143
<212> PRT
<213> homo sapiens

<400> 382

Glu	Val	Glu	Asn	His	Thr	Asn	Leu	Leu	Ser	Tyr	Ser	Ser	Arg	Gly	Gln
1				5					10					15	
Glu	Ser	Lys	Met	Val	Phe	Thr	Arg	Leu	Lys	Ser	Cys	Gln	Cys	Gly	Phe
			20					25					30		
Val	Ser	Pro	Arg	Arg	Leu	Trp	Gly	Arg	Ile	Gln	Cys	Leu	Phe	Gln	Leu
		35					40					45			
Leu	Gln	Gly	Pro	Pro	His	Arg	Leu	Ala	Pro	Gly	Leu	Leu	Ala	Ile	Phe
	50					55					60				
Thr	Ala	Arg	Ser	Phe	Leu	Ala	Ser	Cys	Ala	Asp	Pro	Arg	Asp	Ser	Pro
65					70					75					80
Ser	Leu	Ile	Arg	Ala	Pro	Met	Ile	Thr	Gln	Gly	Pro	Pro	Gln	Pro	Ser
				85					90					95	
Thr	Val	Ile	Ser	Pro	Pro	Arg	Asn	Pro	Glu	Leu	Lys	His	Arg	Arg	Arg
			100					105					110		
Val	Pro	Phe	Ala	Thr	Gln	Gly	Asn	Thr	Phe	Pro	Arg	Pro	Gly	Val	Pro
		115					120					125			
Asn	Leu	Asp	Ile	Ser	Gly	Gly	Cys	Tyr	Ser	Thr	His	Arg	His	Gln	

130

135

140

<210> 383
 <211> 86
 <212> PRT
 <213> homo sapiens

<400> 383

Ser 1	His	Thr	His	Ala 5	Gln	Leu	Ser	Asn	His 10	Gly	Gly	Val	Gln	Glu 15	Pro
Pro	Leu	Pro	Leu 20	Gly	Val	Pro	Lys	Pro 25	Trp	Gly	Ser	Asp	Ser 30	Gly	Ala
Leu	Ser	Arg 35	Pro	Gly	Cys	Lys	Leu 40	Lys	Thr	Pro	Gly	Gly 45	Phe	Gln	Asn
Ala	Gln	Cys 50	Leu	Gly	His	Asn 55	Leu	Asp	Gln	Leu	Asn 60	Leu	Asn	Leu	Gln
Arg 65	Asp	Ile	Thr	Ala	Pro 70	Gln	Glu	Thr	Pro	Arg 75	Gly	Ser	Gln	Ser	Ala 80
Lys	Pro	Glu	Glu	Thr 85	Ile										

<210> 384
 <211> 123
 <212> PRT
 <213> homo sapiens

<400> 384

Leu 1	Glu	Pro	Ile	Arg 5	Phe	Gln	Gln	Lys	Val 10	Met	Glu	Lys	Glu	Thr 15	Glu
Lys	Arg	Ile	Ser 20	Glu	Ile	Glu	Asp	Ala 25	Ala	Phe	Leu	Ala	Arg 30	Glu	Lys
Ala	Lys	Gln 35	Asp	Ala	Glu	Tyr	Tyr 40	Ala	Ala	His	Lys	Tyr 45	Ala	Thr	Ser
Asn	Lys 50	His	Lys	Leu	Thr	Pro 55	Glu	Tyr	Leu	Glu	Leu 60	Lys	Lys	Tyr	Gln
Ala 65	Ile	Ala	Ser	Asn	Ser 70	Lys	Ile	Tyr	Phe	Gly 75	Ser	Asn	Ile	Pro	Asn 80
Met	Phe	Val	Asp	Ser 85	Ser	Cys	Ala	Leu	Lys 90	Tyr	Ser	Asp	Ile	Arg 95	Thr
Gly	Arg	Glu	Ser 100	Ser	Leu	Pro	Ser	Lys 105	Glu	Ala	Leu	Glu	Pro 110	Ser	Gly
Glu	Asn	Val 115	Ile	Gln	Asn	Lys	Glu 120	Ser	Thr	Gly					

<210> 385
 <211> 83
 <212> PRT
 <213> homo sapiens

<400> 385

Asp	Asn	Ser	Cys	Val	Arg	Tyr	Val	Glu	Ala	Gln	Gln	Lys	Ser	His	Gly
1				5					10					15	
Thr	Thr	Ser	Arg	Asn	Leu	Ser	Ala	Val	Arg	Pro	Val	Ser	Leu	Met	Thr
			20					25					30		
Val	Cys	Trp	Leu	Cys	Gln	Thr	Leu	Tyr	Leu	Gly	Lys	Glu	Ser	Pro	Asp
		35					40					45			
Leu	Asn	Gly	Ser	Phe	Pro	Trp	Ala	Leu	Ser	Tyr	Arg	Gly	Ile	Cys	Asn
	50					55					60				
Met	Glu	Lys	Ile	Ile	Phe	His	Phe	Cys	Ser	Phe	Asn	Ser	Ile	Asn	Ser
65					70					75					80
Leu	Tyr	Lys													

<210> 386

<211> 88

<212> PRT

<213> homo sapiens

<400> 386

Cys	Leu	Thr	Phe	Gln	Cys	Arg	Gln	Tyr	Leu	Ser	Ile	Arg	Leu	Ser	Ser
1				5					10					15	
Phe	Met	Ser	Ser	Ser	Leu	Glu	Arg	Asn	Thr	Tyr	Arg	Ile	Leu	Asp	Lys
			20					25					30		
Thr	Val	Ala	Glu	Lys	Thr	Ile	Cys	Val	Ser	Asp	Ser	Trp	Leu	Tyr	Pro
		35					40					45			
Pro	Ile	Ser	Gly	Ala	Pro	Arg	Thr	Ile	Ala	Gly	Glu	Val	Glu	Gln	Met
	50					55					60				
Lys	Cys	Lys	Phe	Ser	Val	Asn	Leu	Lys	Ser	Pro	Tyr	Asn	Asp	Cys	Ser
65					70					75					80
His	Leu	Thr	Pro	Trp	Ala	Thr	Ser								
				85											

<210> 387

<211> 105

<212> PRT

<213> homo sapiens

<400> 387

Thr	Cys	Glu	Pro	Phe	Arg	Asn	Pro	Gln	Val	Gly	Lys	Asp	Pro	Thr	Pro
1				5					10					15	
Ser	Leu	Arg	Ile	Ile	Cys	Leu	Ala	Ile	Thr	Gly	Ser	Trp	Lys	Cys	Phe
			20					25					30		
Leu	Gly	Cys	Val	Lys	Ile	Asn	Gln	Gly	Gly	Met	Lys	His	Ile	Phe	Leu
		35					40					45			
Ala	Thr	Lys	Leu	Glu	Phe	Leu	Arg	Glu	Gln	Met	Gln	Arg	Asp	Leu	Leu
	50					55					60				

Leu 65	Leu	Ala	Arg	Leu	Gln 70	Gly	Pro	Leu	Trp	Ser 75	His	Thr	Glu	Ala	Val 80
Thr	Gly	His	Lys	Pro 85	Arg	Arg	Ala	Arg	Gly 90	Ser	Cys	Ala	Glu	Ala 95	Pro
Gly	Pro	Leu	Ser 100	Gly	Ser	Phe	Pro	Ser 105							

<210> 388
 <211> 173
 <212> PRT
 <213> homo sapiens

<400> 388

Ala 1	Gln	Glu	Ser	Pro 5	Trp	Gln	Leu	Cys	Arg 10	Gly	Ala	Arg	Thr	Ser 15	Lys
Arg	Lys	Leu	Pro 20	Lys	Leu	Gly	Met	Glu 25	Gln	His	Cys	Asn	Glu 30	Met	Cys
Pro	Pro	Ser 35	Ser	Leu	Phe	Leu	Pro 40	Gly	Ala	Tyr	Lys	Ala 45	Gln	Met	Tyr
Ser	Asp 50	Val	Trp	Thr	Asn	Thr 55	Lys	Lys	Lys	Lys	Lys 60	Lys	Lys	Lys	Lys
Lys 65	Ala	Phe	Leu	Ser	His 70	Arg	His	Lys	Thr	Gln 75	Ile	Ile	Tyr	Cys	Tyr 80
Glu	Ala	Leu	Phe	Thr 85	Asn	Gly	Gln	Phe	Leu 90	His	Phe	Ile	Ala	Ala 95	Cys
Glu	Arg	Leu	Pro 100	Asp	Gly	Arg	Pro	Ile 105	Ser	Leu	Val	Leu	Gln 110	Thr	Ser
Ser	Gln	Ala 115	Ala	Phe	Tyr	Gln	Lys 120	Gly	Glu	Asn	Ser	Cys 125	Leu	Ser	Phe
Leu	Lys 130	Asn	Ala	Phe	Leu	Tyr 135	Leu	Ser	Ile	Arg	His 140	Tyr	Thr	Ser	Glu
Leu 145	Tyr	Lys	Arg	Pro	Gly 150	Gly	Thr	Met	Ser	Leu 155	Val	Asp	Thr	Phe	His 160
Cys	Ser	Val	Ala	Pro 165	Phe	Leu	Ala	Trp	Glu 170	Ala	Ser	Ala			

<210> 389
 <211> 105
 <212> PRT
 <213> homo sapiens

<400> 389

Thr 1	Cys	Glu	Pro	Phe 5	Arg	Asn	Pro	Gln	Val 10	Gly	Lys	Asp	Pro	Thr 15	Pro
Ser	Leu	Arg	Ile 20	Ile	Cys	Leu	Ala	Ile 25	Thr	Gly	Ser	Trp	Lys 30	Cys	Phe
Leu	Gly	Cys	Val	Lys	Ile	Asn	Gln	Gly	Gly	Met	Lys	His	Ile	Phe	Leu

35					40					45					
Ala	Thr	Lys	Leu	Glu	Phe	Leu	Arg	Glu	Gln	Met	Gln	Arg	Asp	Leu	Leu
	50					55					60				
Leu	Leu	Ala	Arg	Leu	Gln	Gly	Pro	Leu	Trp	Ser	His	Thr	Glu	Ala	Val
65					70					75					80
Thr	Gly	His	Lys	Pro	Arg	Arg	Ala	Arg	Gly	Ser	Cys	Ala	Glu	Ala	Pro
				85					90					95	
Gly	Pro	Leu	Ser	Gly	Ser	Phe	Pro	Ser							
			100					105							

<210> 390

<211> 262

<212> PRT

<213> homo sapiens

<400> 390

Arg	Cys	Pro	Arg	Arg	Gly	Arg	Glu	Met	Asp	Ser	Gly	Cys	Trp	Leu	Phe
1				5					10					15	
Gly	Gly	Glu	Phe	Glu	Asp	Ser	Val	Phe	Glu	Glu	Arg	Pro	Glu	Arg	Arg
			20					25					30		
Ser	Gly	Pro	Pro	Ala	Ser	Tyr	Cys	Ala	Lys	Leu	Cys	Glu	Pro	Gln	Trp
		35					40					45			
Phe	Tyr	Glu	Glu	Thr	Glu	Ser	Ser	Asp	Asp	Val	Glu	Val	Leu	Thr	Leu
	50					55					60				
Lys	Lys	Phe	Lys	Gly	Asp	Leu	Ala	Tyr	Arg	Arg	Gln	Glu	Tyr	Gln	Lys
65					70					75					80
Ala	Leu	Gln	Glu	Tyr	Ser	Ser	Ile	Ser	Glu	Lys	Leu	Ser	Ser	Thr	Asn
				85					90					95	
Phe	Ala	Met	Lys	Arg	Asp	Val	Gln	Glu	Gly	Gln	Ala	Arg	Cys	Leu	Ala
			100					105					110		
His	Leu	Gly	Arg	His	Met	Glu	Ala	Leu	Glu	Ile	Ala	Ala	Asn	Leu	Glu
		115					120					125			
Asn	Lys	Ala	Thr	Asn	Thr	Asp	His	Leu	Thr	Thr	Val	Leu	Tyr	Leu	Gln
	130					135					140				
Leu	Ala	Ile	Cys	Ser	Ser	Leu	Gln	Asn	Leu	Glu	Lys	Thr	Ile	Phe	Cys
145					150					155					160
Leu	Gln	Lys	Leu	Ile	Ser	Leu	His	Pro	Phe	Asn	Pro	Trp	Asn	Trp	Gly
				165					170					175	
Lys	Leu	Ala	Glu	Ala	Tyr	Leu	Asn	Leu	Gly	Pro	Ala	Leu	Ser	Ala	Ala
			180					185					190		
Leu	Ala	Ser	Ser	Gln	Lys	Gln	His	Ser	Phe	Thr	Ser	Ser	Asp	Lys	Thr
		195					200					205			
Ile	Lys	Ser	Phe	Phe	Pro	His	Ser	Gly	Lys	Asp	Cys	Leu	Leu	Cys	Phe
	210					215					220				

Pro	Glu	Thr	Leu	Pro	Glu	Ser	Ser	Leu	Ile	Phe	Cys	Gly	Arg	Asp	Thr
225					230					235					240
Arg	Asn	Gly	Arg	Lys	Ile	Gly	Lys	Phe	Cys	Lys	Cys	Ala	Asn	Leu	Val
				245					250					255	
Gly	Glu	Arg	Gly	Thr	Gly										
			260												

<210> 391
 <211> 66
 <212> PRT
 <213> homo sapiens

<400> 391

Lys	Pro	Val	Pro	Leu	Ser	Pro	Thr	Arg	Leu	Ala	His	Leu	Gln	Asn	Phe
1				5					10					15	
Pro	Ile	Phe	Leu	Pro	Phe	Leu	Val	Ser	Leu	Pro	Gln	Lys	Ile	Lys	Glu
			20					25					30		
Leu	Ser	Gly	Lys	Val	Ser	Gly	Lys	His	Lys	Arg	Gln	Ser	Phe	Pro	Glu
		35					40					45			
Cys	Gly	Lys	Lys	Asp	Leu	Ile	Val	Leu	Ser	Leu	Glu	Val	Lys	Leu	Cys
	50					55					60				
Cys	Phe														
65															

<210> 392
 <211> 78
 <212> PRT
 <213> homo sapiens

<400> 392

Gln	Ala	Gly	Gly	Arg	Val	Pro	Trp	Leu	Asn	Gly	Leu	Cys	Trp	Leu	Leu
1				5					10					15	
Tyr	Phe	Pro	Ser	Leu	Gln	Gln	Ser	Pro	Ala	Pro	Pro	Tyr	Ala	Tyr	Pro
			20					25					30		
Gly	Glu	Pro	Asp	Thr	Glu	Pro	Asp	Leu	Pro	Gly	His	Pro	Phe	Ser	Trp
		35					40					45			
Gln	Asn	Trp	Leu	Met	Thr	Ile	Phe	Gln	Arg	Tyr	Trp	Asn	Thr	Pro	Ala
	50					55					60				
Val	Leu	Ser	Asp	Thr	Leu	Val	Val	Cys	Arg	Pro	Gly	Leu	Leu		
65					70					75					

<210> 393
 <211> 79
 <212> PRT
 <213> homo sapiens

<400> 393

Thr	Ser	Leu	Glu	Gly	Ile	Asp	Leu	Gln	Pro	Ser	His	Leu	Thr	Ile	Tyr
1				5					10					15	

Thr	Ala	Ala	Leu 20	Lys	Glu	Lys	Thr	Pro 25	Asp	Phe	Arg	Arg	Leu 30	Ser	Pro
Arg	Val	Ser 35	Glu	Thr	Ala	Asp	Ser 40	Arg	Lys	Val	Ala	Arg 45	Gly	Pro	Arg
Phe	Val 50	Met	Arg	Asp	Asn	Pro 55	Gly	Arg	Gly	Gly	Asp 60	His	Arg	Gly	Leu
Gln 65	Ala	Pro	Gly	Trp	Met 70	Lys	Glu	Gly	Arg	Gly 75	Trp	Gly	Val	Leu	

<210> 394

<211> 72

<212> PRT

<213> homo sapiens

<400> 394

Val 1	Thr	Pro	Pro	Pro 5	Pro	Ser	Gln	Ile	Ser 10	Ser	Phe	Leu	Pro	Pro 15	Ser
Thr	Ala	Pro	Phe 20	Thr	Lys	Pro	Pro	Ile 25	Pro	Asp	Pro	Pro	Ser 30	Ser	Thr
Pro	Ala	Pro 35	Gly	Asp	Pro	Tyr	Asp 40	His	Pro	Arg	Ala	Arg 45	Gly	Cys	Pro
Ala	Leu 50	Gln	Ile	Gly	Ala	His 55	Gly	Arg	Pro	Tyr	Gly 60	Ser	Pro	Arg	Ser
Pro 65	Arg	Arg	Glu	Glu	Arg 70	Asp	Val								

<210> 395

<211> 98

<212> PRT

<213> homo sapiens

<400> 395

Pro 1	Pro	Pro	Pro	Pro 5	Pro	Lys	Phe	His	Pro 10	Ser	Phe	Arg	Leu	Leu 15	Gln
Pro	Pro	Leu	Gln 20	Asn	Pro	Pro	Ser	Pro 25	Thr	Leu	Leu	His	Pro 30	Pro	Arg
Arg	Leu	Glu 35	Thr	Pro	Met	Ile	Thr 40	Pro	Ala	Pro	Gly	Val 45	Val	Pro	His
Tyr	Lys 50	Ser	Gly	Pro	Thr	Gly 55	Asp	Leu	Thr	Gly	Val 60	Arg	Gly	Leu	Arg
Asp 65	Ala	Arg	Arg	Glu	Thr 70	Ser	Glu	Val	Trp	Arg 75	Leu	Phe	Leu	Gln 80	Gly
Cys	Cys	Val	Asp	Cys 85	Glu	Val	Gly	Gly	Leu 90	Lys	Ile	Asn	Ser	Leu 95	Glu

Gly Gly

<210> 396

<211> 80

<212> PRT
 <213> homo sapiens

<400> 396

Asn	Trp	Arg	Gln	Thr	Val	Trp	Gln	Arg	Val	Arg	Glu	Gly	Ala	Cys	Ala
1				5					10					15	
Gln	Glu	Ser	Ser	Arg	Pro	Ala	Ser	Gly	Cys	Arg	Phe	Leu	Arg	Cys	Ala
			20					25					30		
Ile	Gly	Ala	Ser	Ala	Phe	Ser	Gly	Asp	Arg	Gly	Ser	Ala	Val	Ala	Thr
		35					40					45			
Asn	Thr	Gln	Pro	His	Thr	His	Asn	His	Thr	His	Lys	Trp	Gly	Gln	Pro
	50					55					60				
His	Pro	Val	Gln	Ala	Phe	Thr	Asn	Val	Ile	Ser	Val	Leu	Phe	Tyr	Phe
65					70					75					80

<210> 397
 <211> 309
 <212> PRT
 <213> homo sapiens

<400> 397

Tyr	Asp	Asn	Ser	Ser	Thr	Cys	Lys	Lys	Gly	Lys	Val	Phe	Pro	Gly	Lys
1				5					10					15	
Ile	Ser	Val	Thr	Val	Ser	Glu	Thr	Phe	Asp	Pro	Glu	Glu	Lys	His	Ser
			20					25					30		
Met	Ala	Tyr	Gln	Asp	Leu	His	Ser	Glu	Ile	Thr	Ser	Leu	Phe	Lys	Asp
		35					40					45			
Val	Phe	Gly	Thr	Ser	Val	Tyr	Gly	Gln	Thr	Val	Ile	Leu	Thr	Val	Ser
	50					55					60				
Thr	Ser	Leu	Ser	Pro	Arg	Ser	Glu	Met	Arg	Ala	Asp	Asp	Lys	Phe	Val
65					70					75					80
Asn	Val	Thr	Ile	Val	Thr	Ile	Leu	Ala	Glu	Thr	Thr	Ser	Asp	Asn	Glu
				85					90					95	
Lys	Thr	Val	Thr	Glu	Lys	Ile	Asn	Lys	Ala	Ile	Arg	Ser	Ser	Ser	Ser
			100					105					110		
Asn	Phe	Leu	Asn	Tyr	Asp	Leu	Thr	Leu	Arg	Cys	Asp	Tyr	Tyr	Gly	Cys
		115					120					125			
Asn	Gln	Thr	Ala	Asp	Asp	Cys	Leu	Asn	Gly	Leu	Ala	Cys	Asp	Cys	Lys
	130					135					140				
Ser	Asp	Leu	Gln	Arg	Pro	Asn	Pro	Gln	Ser	Pro	Phe	Cys	Val	Ala	Ser
145					150					155					160
Ser	Leu	Lys	Cys	Pro	Asp	Ala	Cys	Asn	Ala	Gln	His	Lys	Gln	Cys	Leu
				165					170					175	
Ile	Lys	Lys	Ser	Gly	Gly	Ala	Pro	Glu	Cys	Ala	Cys	Val	Pro	Gly	Tyr
			180					185					190		

[illegible]

			20						25					30			
Thr	Ser	Thr	Phe	Asp	Phe	Ser	Gln	Pro	Gln	Pro	Arg	Lys	Asn	Gly	Ser		
		35					40					45					
Trp	Asp	Lys	Gln	Leu	Val	Phe	Val	Ser	Lys	Thr	Gln	Ile	Gly	His	Ile		
	50					55					60						
Asn	Ala	Thr	Ala	Phe	Arg	Ser	Phe	Asp	Phe	Asp							
65					70					75							

<210> 400
 <211> 70
 <212> PRT
 <213> homo sapiens

Arg	Lys	Lys	Ala	Val	Cys	Phe	Met	Asn	Asp	Leu	Ile	Cys	Phe	Leu	Asp		
1				5					10					15			
Asn	Thr	Phe	Lys	Asn	Asn	Val	Leu	Ser	Gln	Ala	Trp	Trp	Cys	Val	His		
			20					25					30				
Leu	Val	Pro	Thr	Ile	Trp	Glu	Ala	Glu	Ala	Gly	Gly	Ser	Leu	Glu	Pro		
		35					40					45					
Arg	Ser	Leu	Lys	Leu	Gln	Cys	Pro	Val	Val	Ala	Pro	Val	Asn	Asn	Cys		
	50					55					60						
Thr	Pro	Ala	Trp	Ala	Thr												
65					70												

<210> 401
 <211> 69
 <212> PRT
 <213> homo sapiens

Leu	Val	Pro	Gln	Gly	Ser	Leu	Leu	Gln	Thr	His	Pro	Phe	Val	Phe	Phe		
1				5					10					15			
Ser	Phe	Leu	Glu	Met	Arg	Ser	Arg	Tyr	Val	Ala	Gln	Ala	Gly	Val	Gln		
			20					25					30				
Leu	Phe	Thr	Gly	Ala	Thr	Thr	Gly	His	Cys	Ser	Phe	Lys	Leu	Leu	Gly		
		35					40					45					
Ser	Ser	Asp	Pro	Pro	Ala	Ser	Ala	Ser	Gln	Ile	Val	Gly	Thr	Arg	Cys		
	50					55					60						
Thr	His	His	His	Ala													
65																	

<210> 402
 <211> 80
 <212> PRT
 <213> homo sapiens

Pro	Pro	Leu	Trp	Val	Ala	Thr	Val	Arg	Asn	Gly	Cys	Cys	His	Val	Phe		

1					5					10					15	
Trp	Thr	Leu	Pro 20	Ala	Asn	Arg	Ser	Leu 25	Pro	Gly	Phe	Gly	Asn 30	Thr	Ser	
Ile	Thr	Ser 35	Leu	Leu	Leu	Phe	Cys 40	Arg	Asp	Lys	Thr	Phe 45	Glu	Val	Ala	
Arg	Pro 50	Arg	Thr	Ser	Lys	Asp 55	Ser	Cys	Tyr	Ser	Ala 60	Thr	Val	Tyr	Thr	
Ala 65	His	Leu	Ser	Tyr	Ser 70	His	Val	Leu	Ser	Ser 75	Leu	Val	Arg	Leu	Phe 80	

<210> 403

<211> 81

<212> PRT

<213> homo sapiens

<400> 403

Leu 1	Thr	Asn	Met	Ser 5	Asp	His	Leu	Phe	Gly 10	Trp	Leu	Leu	Leu	Glu 15	Met
Ala	Val	Val	Met 20	Phe	Ser	Gly	Leu	Cys 25	Gln	Pro	Thr	Asp	Pro 30	Cys	Gln
Val	Leu	Glu 35	Ile	Leu	Leu	Leu	Pro 40	Arg	Cys	Tyr	Phe	Ser 45	Ala	Gly	Ile
Lys	Leu 50	Leu	Arg	Trp	Pro	Asp 55	Pro	Glu	His	Pro	Arg 60	Ile	Pro	Val	Thr
Val 65	Leu	Gln	Tyr	Thr	Leu 70	Leu	Ile	Tyr	Pro	Ile 75	Leu	Met	Cys	Phe	Leu 80

Leu

<210> 404

<211> 75

<212> PRT

<213> homo sapiens

<400> 404

Val 1	Ser	His	Tyr	Pro 5	His	Ser	Val	Ser	Lys 10	Pro	Pro	Lys	His	Gln 15	Thr
Lys	Gln	Met	Val 20	Val	Ala	Leu	Thr	His 25	Ser	Arg	Leu	Thr	Ser 30	Glu	Phe
Lys	Trp	Glu 35	Asn	Thr	Pro	Tyr	Thr 40	Thr	Val	Ile	Ile	Pro 45	Leu	Trp	Thr
Leu	Asn 50	Ile	Thr	Tyr	Phe	Leu 55	Lys	Ile	Ile	Leu	Leu 60	Lys	Lys	Lys	Ala
His 65	Glu	Asn	Arg	Ile	Asn 70	Glu	Gln	Cys	Ile	Leu 75					

<210> 405

<211> 328

<212> PRT

<213> homo sapiens

<400> 405

Arg 1	Tyr	Leu	Asn	Met 5	Gly	Asn	Leu	Leu	Lys 10	Val	Leu	Thr	Cys	Thr 15	Asp
Leu	Glu	Gln	Gly 20	Pro	Asn	Phe	Phe	Leu 25	Asp	Phe	Glu	Asn	Ala 30	Gln	Pro
Thr	Glu	Ser 35	Glu	Lys	Glu	Ile	Tyr 40	Asn	Gln	Val	Asn	Val 45	Val	Leu	Lys
Asp	Ala 50	Glu	Gly	Ile	Leu	Glu 55	Asp	Leu	Gln	Ser	Tyr 60	Arg	Gly	Ala	Gly
His 65	Glu	Ile	Arg	Glu	Ala 70	Ile	Gln	His	Pro	Ala 75	Asp	Glu	Lys	Leu	Gln 80
Glu	Lys	Ala	Trp	Gly 85	Ala	Val	Val	Pro	Leu 90	Val	Gly	Lys	Leu	Lys 95	Lys
Phe	Tyr	Glu	Phe 100	Ser	Gln	Arg	Leu	Glu 105	Ala	Ala	Leu	Arg	Gly 110	Leu	Leu
Gly	Ala	Leu 115	Thr	Ser	Thr	Pro	Tyr 120	Ser	Pro	Thr	Gln	His 125	Leu	Glu	Arg
Glu	Gln 130	Ala	Leu	Ala	Lys	Gln 135	Phe	Ala	Glu	Ile	Leu 140	His	Phe	Thr	Leu
Arg 145	Phe	Asp	Glu	Leu	Lys 150	Met	Thr	Asn	Pro	Ala 155	Ile	Gln	Asn	Asp	Phe 160
Ser	Tyr	Tyr	Arg	Arg 165	Thr	Leu	Ser	Arg	Met 170	Arg	Ile	Asn	Asn	Val 175	Pro
Ala	Glu	Gly	Glu 180	Asn	Glu	Val	Asn	Asn 185	Glu	Leu	Ala	Asn	Arg 190	Met	Ser
Leu	Phe	Tyr 195	Ala	Glu	Ala	Thr	Pro 200	Met	Leu	Lys	Thr	Leu 205	Ser	Asp	Ala
Thr	Thr 210	Lys	Phe	Val	Ser	Glu 215	Asn	Lys	Asn	Leu	Pro 220	Ile	Glu	Asn	Thr
Thr 225	Asp	Cys	Leu	Ser	Thr 230	Met	Ala	Ser	Val	Cys 235	Arg	Val	Met	Leu	Glu 240
Thr	Pro	Glu	Tyr	Arg 245	Ser	Arg	Phe	Thr	Asn 250	Glu	Glu	Thr	Val	Ser 255	Phe
Cys	Leu	Arg	Val 260	Met	Val	Gly	Val	Ile 265	Ile	Leu	Tyr	Asp	His 270	Val	His
Pro	Val	Gly 275	Ala	Phe	Ala	Lys	Thr 280	Ser	Lys	Ile	Asp	Met 285	Lys	Gly	Cys
Ile	Lys 290	Val	Leu	Lys	Asp	Gln 295	Pro	Pro	Asn	Ser	Val 300	Glu	Gly	Leu	Leu
Asn 305	Ala	Leu	Arg	Tyr	Thr 310	Thr	Lys	His	Leu	Asn 315	Asp	Glu	Thr	Thr	Ser 320

130

<210> 410
 <211> 142
 <212> PRT
 <213> homo sapiens

<400> 410

Trp 1	Lys	Gln	Arg	Arg 5	Pro	Ala	Val	Ala	Leu 10	Asp	Thr	Pro	Met	Pro 15	Gln
Ala	Val	Gly	Lys 20	Gln	Ser	Leu	Gly	Glu 25	Val	Ala	Pro	Leu	Gly 30	Ser	Leu
Thr	Leu	Cys 35	Val	Glu	Arg	Gln	Gly 40	Arg	His	Glu	Glu	Gly 45	Arg	Cys	Glu
Trp 50	Ser	Thr	Val	His	Pro	Gly 55	Ile	Ser	Gln	Pro	Glu 60	Ser	Pro	Pro	Ser
Leu 65	Ala	Ala	Pro	Glu	His 70	Ser	Leu	Trp	Pro	Thr 75	Ala	Thr	Glu	Met	Ser 80
Ala	Cys	Gln	Asp	Thr 85	Trp	Arg	Arg	Lys	Lys 90	Thr	Arg	His	Gln	Lys 95	Lys
Leu	Pro	Pro	Gln 100	Glu	Gln	Ile	Glu	Leu 105	Leu	Asp	Gln	Gly	His 110	Thr	Arg
Ser	Gly	Arg 115	His	Pro	Ala	Pro	Cys 120	Ala	Gln	Gly	Lys	Glu 125	Thr	Gln	Phe
Asn 130	Val	Trp	Leu	Leu	Cys	Ser 135	Arg	Glu	Thr	Ala	Thr 140	Leu	Pro		

<210> 411
 <211> 244
 <212> PRT
 <213> homo sapiens

<400> 411

Lys 1	Arg	Arg	Gly	Val 5	Arg	Gln	Phe	Arg	Trp 10	Leu	Val	Cys	Thr	Arg 15	Arg
Ala	Ser	Pro	Gly 20	Ala	Ala	Arg	Ser	Ala 25	Pro	Ile	Ala	Pro	Ala 30	Thr	Gly
Ser	Gly	Arg 35	Arg	Pro	Asn	Met	Asp 40	Ser	Ala	Gly	Gln	Asp 45	Ile	Asn	Leu
Asn 50	Ser	Pro	Asn	Lys	Gly	Leu 55	Leu	Ser	Asp	Ser	Met 60	Thr	Asp	Val	Pro
Val 65	Asp	Thr	Gly	Val	Ala 70	Ala	Arg	Thr	Pro	Ala 75	Val	Glu	Gly	Leu	Thr 80
Glu	Ala	Glu	Glu	Glu 85	Glu	Leu	Arg	Ala	Glu 90	Leu	Thr	Lys	Val	Glu 95	Glu
Glu	Ile	Val	Thr 100	Leu	Arg	Gln	Val	Leu 105	Ala	Ala	Lys	Glu	Arg 110	His	Cys

<210> 413
 <211> 143
 <212> PRT
 <213> homo sapiens

<400> 413

Ala	Leu	Glu	Thr	Cys	Thr	Ser	Cys	Gln	Leu	Leu	Asp	Arg	Phe	Cys	Phe
1				5					10					15	
Ser	Ser	Pro	Arg	Val	Glu	Arg	Pro	Ser	Leu	Leu	Leu	Ser	Ser	Pro	Gln
			20					25					30		
Cys	Leu	Ser	Leu	Ala	Ala	Arg	Thr	Trp	Arg	Arg	Val	Thr	Ile	Ser	Ser
		35					40					45			
Ser	Thr	Leu	Val	Ser	Ser	Ala	Leu	Ser	Ser	Ser	Ser	Ser	Ala	Ser	Val
	50					55						60			
Arg	Pro	Ser	Thr	Ala	Gly	Val	Arg	Ala	Ala	Thr	Pro	Val	Ser	Thr	Gly
	65				70					75					80
Thr	Ser	Val	Met	Glu	Ser	Asp	Ser	Arg	Pro	Leu	Leu	Gly	Glu	Phe	Arg
				85					90					95	
Leu	Ile	Ser	Trp	Pro	Ala	Glu	Ser	Met	Phe	Gly	Arg	Arg	Pro	Asp	Pro
			100					105					110		
Val	Ala	Gly	Ala	Met	Gly	Ala	Glu	Arg	Ala	Ala	Pro	Gly	Glu	Ala	Arg
		115					120					125			
Arg	Val	His	Thr	Ser	Gln	Arg	Asn	Cys	Leu	Thr	Pro	Arg	Arg	Phe	
	130					135					140				

<210> 414
 <211> 105
 <212> PRT
 <213> homo sapiens

<400> 414

Arg	Gly	Arg	Gly	Ala	Leu	Trp	Trp	Ala	Ala	Lys	Glu	Leu	Arg	Arg	Thr
1				5					10					15	
Lys	Lys	Leu	Ser	Asp	Tyr	Val	Gly	Lys	Asn	Glu	Lys	Thr	Lys	Ile	Ile
			20					25					30		
Ala	Lys	Ile	Gln	Gln	Arg	Gly	Gln	Gly	Ala	Pro	Ala	Arg	Glu	Pro	Ile
		35					40					45			
Ile	Ser	Ser	Glu	Glu	Gln	Lys	Gln	Leu	Met	Leu	Tyr	Tyr	His	Arg	Arg
	50					55					60				
Gln	Glu	Glu	Leu	Lys	Arg	Leu	Glu	Glu	Asn	Asp	Asp	Asp	Ala	Tyr	Leu
	65				70					75					80
Asn	Ser	Pro	Trp	Ala	Asp	Asn	Thr	Ala	Leu	Lys	Arg	His	Phe	His	Gly
				85					90					95	
Val	Lys	Asp	Ile	Lys	Trp	Arg	Pro	Arg							
			100					105							

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Ala 1	Ala	Glu	Leu	Arg 5	Asp	Cys	Gly	Ser	Arg 10	Arg	Ile	Ser	Arg	Ser 15	Pro
Ser	Ser	Asn	Ser 20	His	Leu	Ser	Pro	Arg 25	Ile	Ser	Leu	Ser	Gly 30	Asn	Leu
Gly	Pro	Gln 35	Thr	Ser	Arg	Leu	Gly 40	Gly	Pro	Pro	Ser	Pro	Ser 45	Ala	Thr
Trp	Ser 50	Val	Phe	Trp	Gln	Leu 55	Pro	Arg	Gln	Gln	Ser 60	Leu	Pro	Gly	Arg
Gly 65	Ser	Ala	Asn	Leu	Leu 70	Pro	Ser	Val	Arg	Ser 75	Glu	Ser	Ala	Val	Leu 80
Ser	Asp	Cys	Val	Gly 85	Gly	Phe	Pro	Gly	Arg 90	Ser	Ser	Val	Arg	Ala 95	Trp
Ile	Ala	Gly	Pro 100	Arg	Cys	Thr	Pro	Ala 105	Ser	Pro	Thr	Arg	Val 110	Leu	Ser
Leu	Ser	Trp 115	Arg	Leu	Phe	Asn	Ser 120	Ala	Ser	Leu	Leu 125	Leu	Ala	Thr	
Ser	Thr 130	Ser	Gly	Ser	Glu	Cys 135	Arg	Phe	Pro	Arg	Ser 140	Pro	Arg	Ala	Arg
Glu 145	Arg	Gly	Ile	Pro	Asp 150	Cys	Glu	Arg	Leu	Leu 155	Val	Arg	Arg	Ser	Cys 160
Trp	Arg	Ser	Gly	Asp 165	Pro	Arg	Pro	Ala	Gly 170	Pro	Ala	Gly	His	Ala 175	Ala
Gly	Ala	Phe	Ser 180	Thr	Pro	Gln	Tyr	Leu 185	Gly	Gly	Thr	Ala	Met 190	Val	Leu
Leu	His	Val 195	Lys	Arg	Gly	Asp	Glu 200	Ser	Gln	Phe	Leu	Leu 205	Gln	Ala	Pro
Gly	Ser 210	Thr	Glu	Leu	Glu	Glu 215	Leu	Thr	Val	Gln	Val 220	Ala	Arg	Val	Tyr
Asn 225	Gly	Arg	Leu	Lys	Val 230	Gln	Arg	Leu	Cys	Ser 235	Glu	Met	Glu	Glu	Leu 240
Ala	Glu	His	Gly	Ile 245	Phe	Leu	Pro	Pro	Asn 250	Met	Gln	Gly	Leu	Thr 255	Asp
Asp	Gln	Ile	Glu 260	Glu	Leu	Lys	Leu	Lys 265	Asp	Glu	Trp	Gly	Glu 270	Lys	Cys
Val	Pro	Ser 275	Gly	Gly	Ala	Val	Phe 280	Lys	Lys	Asp	Asp	Ile 285	Gly	Arg	Arg
Asn	Gly 290	Gln	Ala	Pro	Asn	Glu 295	Lys	Met	Lys	Gln	Val 300	Leu	Lys	Lys	Thr

Ile 305	Glu	Glu	Ala	Lys	Ala 310	Ile	Ile	Ser	Lys	Lys 315	Gln	Val	Glu	Ala	Gly 320
Val	Cys	Val	Thr	Met 325	Glu	Met	Val	Lys	Asp 330	Ala	Leu	Asp	Gln	Leu 335	Arg
Gly	Ala	Val	Met 340	Ile	Val	Tyr	Pro	Met 345	Gly	Leu	Pro	Pro	Tyr 350	Asp	Pro
Ile	Arg	Met 355	Glu	Phe	Glu	Asn	Lys 360	Glu	Asp	Leu	Ser	Gly 365	Thr	Gln	Ala
Gly	Leu 370	Asn	Val	Ile	Lys	Glu 375	Ala	Glu	Ala	His	Cys 380	Gly	Gly	Gln	Pro
Arg 385	Ser														

<210> 416
 <211> 182
 <212> PRT
 <213> homo sapiens

<400> 416

Gly 1	Val	Glu	Lys	Ala 5	Pro	Ala	Ala	Trp	Pro 10	Ala	Gly	Pro	Ala	Gly 15	Arg
Gly	Ser	Pro	Asp 20	Arg	Gln	Gln	Leu	Arg 25	Arg	Thr	Asn	Ser	Arg 30	Ser	Gln
Ser	Gly	Ile 35	Pro	Arg	Ser	Leu	Ala 40	Arg	Gly	Glu	Arg	Gly 45	Lys	Arg	His
Ser	Leu 50	Pro	Glu	Val	Asp	Val 55	Ala	Lys	Ser	Asn	Ser 60	Glu	Ala	Glu	Leu
Lys 65	Ser	Arg	Gln	Leu	Lys 70	Leu	Arg	Thr	Arg	Val 75	Gly	Glu	Ala	Gly 80	Val
His	Arg	Gly	Pro	Ala 85	Ile	Gln	Ala	Arg	Thr 90	Glu	Leu	Arg	Pro	Gly 95	Lys
Pro	Pro	Thr	Gln 100	Ser	Glu	Arg	Thr	Ala 105	Asp	Ser	Glu	Arg	Thr 110	Asp	Gly
Arg	Arg	Phe 115	Ala	Asp	Pro	Leu	Pro 120	Gly	Ser	Asp	Cys	Cys 125	Arg	Gly	Asn
Cys	Gln 130	Asn	Thr	Asp	Gln	Val 135	Ala	Glu	Gly	Glu	Gly 140	Gly	Pro	Pro	Asn
Arg 145	Leu	Val	Trp	Gly	Pro 150	Arg	Phe	Pro	Leu	Arg 155	Glu	Ile	Arg	Gly	Leu 160
Arg	Trp	Glu	Leu	Leu 165	Asp	Gly	Glu	Arg	Glu 170	Ile	Arg	Arg	Glu	Pro 175	Gln
Ser	Arg	Ser	Ser 180	Ala	Ala										

<210> 417

<211> 467
 <212> PRT
 <213> homo sapiens

<400> 417

His 1	Thr	Leu	Ser	Arg 5	Trp	Thr	Lys	His	Ser 10	Ile	Pro	Arg	Trp	Asn 15	Asp
Ala	Arg	Thr	Asp 20	Asp	Thr	Trp	His	Ser 25	Glu	Leu	Asp	Met	Arg 30	Lys	Ile
Gly	Gln	Ala 35	Arg	Asn	Thr	Leu	Met 40	Asp	Met	Arg	Leu	Ser 45	Gln	Val	Ser
Asp	Ser 50	Val	Ser	Gly	Gln	Thr 55	Val	Val	Asp	Pro	Lys 60	Gly	Tyr	Leu	Thr
Asp 65	Leu	Asn	Ser	Met	Ile 70	Pro	Thr	His	Gly	Gly 75	Asp	Ile	Asn	Asp	Ile 80
Lys	Lys	Ala	Arg	Leu 85	Leu	Leu	Lys	Ser	Val 90	Arg	Glu	Thr	Asn 95	Pro	His
His	Pro	Pro	Ala 100	Trp	Ile	Ala	Ser	Ala 105	Arg	Leu	Glu	Glu	Val 110	Thr	Gly
Lys	Leu	Gln 115	Val	Ala	Arg	Asn	Leu 120	Ile	Met	Lys	Gly	Thr 125	Glu	Met	Cys
Pro	Lys 130	Ser	Glu	Asp	Val	Trp 135	Leu	Glu	Ala	Ala	Arg 140	Leu	Gln	Pro	Gly
Asp 145	Thr	Ala	Lys	Ala	Val 150	Val	Ala	Gln	Ala	Val 155	Arg	His	Leu	Pro	Gln 160
Ser	Val	Arg	Ile	Tyr 165	Ile	Arg	Ala	Ala	Glu 170	Leu	Glu	Thr	Asp	Ile 175	Arg
Ala	Lys	Lys	Arg 180	Val	Leu	Arg	Lys	Ala 185	Leu	Glu	His	Val	Pro 190	Asn	Ser
Val	Arg	Leu 195	Trp	Lys	Ala	Ala	Val 200	Glu	Leu	Glu	Glu	Pro 205	Glu	Asp	Ala
Arg	Ile 210	Met	Leu	Ser	Arg	Ala 215	Val	Glu	Cys	Cys	Pro 220	Thr	Ser	Val	Glu
Leu 225	Trp	Leu	Ala	Leu	Ala 230	Arg	Leu	Glu	Thr	Tyr 235	Glu	Asn	Ala	Arg	Lys 240
Val	Leu	Asn	Lys	Ala 245	Arg	Glu	Asn	Ile	Pro 250	Thr	Asp	Arg	His	Ile 255	Trp
Ile	Thr	Ala	Ala 260	Lys	Leu	Glu	Glu	Ala 265	Asn	Gly	Asn	Thr	Gln 270	Met	Val
Glu	Lys	Ile 275	Ile	Asp	Arg	Ala	Ile 280	Thr	Ser	Leu	Arg	Ala 285	Asn	Gly	Val
Glu	Ile 290	Asn	Arg	Glu	Gln	Trp 295	Ile	Gln	Asp	Ala	Glu 300	Glu	Cys	Asp	Arg

Ala 305	Gly	Ser	Val	Ala	Thr 310	Cys	Gln	Ala	Val	Met 315	Arg	Ala	Val	Ile	Gly 320
Ile	Gly	Ile	Glu	Glu 325	Glu	Asp	Arg	Lys	His 330	Thr	Trp	Met	Glu	Asp 335	Ala
Asp	Ser	Cys	Val 340	Ala	His	Asn	Ala	Leu 345	Glu	Cys	Ala	Arg	Ala 350	Ile	Tyr
Ala	Tyr	Ala 355	Leu	Gln	Val	Phe	Pro 360	Ser	Lys	Lys	Ser	Val 365	Trp	Leu	Arg
Ala	Ala 370	Tyr	Phe	Glu	Lys	Asn 375	His	Gly	Thr	Arg	Glu 380	Ser	Leu	Glu	Ala
Leu 385	Leu	Gln	Arg	Ala	Val 390	Ala	His	Cys	Pro	Lys 395	Ala	Glu	Val	Leu	Trp 400
Leu	Met	Gly	Ala	Lys 405	Ser	Lys	Trp	Leu	Ala 410	Gly	Asp	Val	Pro	Ala 415	Ala
Arg	Ser	Ile	Leu 420	Ala	Leu	Ala	Phe	Gln 425	Ala	Asn	Pro	Asn	Ser	Glu 430	Glu
Ile	Trp	Leu 435	Ala	Ala	Val	Lys	Leu 440	Glu	Ser	Glu	Asn	Asp 445	Glu	Tyr	Glu
Arg	Ala 450	Arg	Arg	Leu	Leu	Ala 455	Lys	Ala	Arg	Thr	Val 460	Pro	Pro	Pro	Pro
Gly 465	Cys	Ser													

<210> 418
 <211> 352
 <212> PRT
 <213> homo sapiens

<400> 418

Thr 1	Pro	Gly	Arg	Trp 5	Gly	His	Cys	Pro	Arg 10	Leu	Gly	Gln	Gln	Pro 15	Pro
Gly	Pro	Leu	Val 20	Leu	Ile	Ile	Leu	Gly 25	Leu	Gln	Leu	His	Gly 30	Cys	Gln
Pro	Asp	Leu 35	Leu	Thr	Val	Gly	Val 40	Gly	Leu	Glu	Gly	Gln 45	Gly	Gln	Asp
Ala 50	Pro	Cys	Cys	Arg	His	Ile 55	Pro	Cys	Gln	Pro	Leu 60	Gly	Leu	Gly	Ala
His 65	Glu	Pro	Gln	His	Leu 70	Cys	Phe	Gly	Ala	Val 75	Gly	His	Ser	Pro	Leu 80
Gln	Glu	Cys	Phe	Gln 85	Gly	Leu	Pro	Ser	Ala 90	Met	Val	Leu	Leu	Glu 95	Val
Arg	Gly	Ala	Gln 100	Pro	His	Thr	Leu	Leu 105	Ala	Gly	Glu	His	Leu 110	Gln	Gly
Val	Gly	Val 115	Asp	Gly	Ser	Cys	Thr 120	Leu	Gln	Gly	Ile	Val 125	Gly	Tyr	Thr

65				70				75				80			
Pro	Met	Pro	Arg	Leu 85	Cys	Thr	Leu	Thr	Ala 90	Leu	Pro	His	Leu	Leu 95	Leu
Leu	Leu	Leu	Ser 100	Ala	Met	Leu	Gln	Leu 105	Lys	Leu	Val	Glu	Glu 110	Gly	Pro
Gly	Ile	Pro 115	Gln	Val	Arg	Val	Asn 120	Leu	His	Ser	Ala	Val 125	Glu	Pro	Leu
Pro	Gly 130	Leu	Gly	Asp	Leu	Pro 135	Leu	Thr	Pro	Lys	Gln 140	Leu	Gly	His	Gly
Gln 145	Glu	His	Met	Gly	Val 150	Met	Leu	Thr	Leu	Leu 155	Gln	Gly	Ile	His	Ala 160
Leu	Gly	Pro	Pro	Leu 165	Gly	Pro	Cys	Leu	Glu 170	Glu	Asp	Gly	Leu	Arg 175	Pro
Gln	Asp	Thr	Gly 180	Val	Gly	Ala	Leu	Leu 185	Gln	Arg	Leu	Gly	His 190	Glu	Cys
Ile	Cys	Asp 195	Val	Leu	Gln	Pro	Arg 200	Thr	Val	Leu	Gln	Pro 205	His	Gly	Leu
Gln	Pro 210	Gln	Pro	Arg	Val	Leu 215	Trp	Val	Leu	Gln	Thr 220	Arg	Leu	Phe	Gln
Asn 225	Gly	Pro	Cys	Ser	Ser 230	Lys	Leu	Pro	Asn	Leu 235	Leu	Leu	Gln	Pro	Arg 240
Glu	Gln	Lys	Pro	Gln 245	Gly	Cys	Gly	Val	Gly 250	Thr	Leu	Leu	Gln	Pro 255	Leu
Val	Ile	Gly	Phe 260	Pro	Arg	Leu	Leu	His 265	His	Leu	Leu	Leu	Leu 270	Leu	Asp
Leu	Pro	Leu 275	His	His	Pro	Gln	Leu 280	Gly	Glu	Val	Leu	Ile 285	Val	Pro	Gln
Gly	Leu 290	Leu	Ala	Gln	Ile	Leu 295	Gly	Cys	Pro	Asp	Val 300	Val	Leu	His	Pro
Leu 305	Gln	Leu	His	Arg	Leu 310	His	Glu	His	Pro	Gly 315	Gly	Gly	Gly	Thr	Val 320
Arg	Ala	Leu	Ala	Ser 325	Ser	Leu	Arg	Ala	Arg 330	Ser	Tyr	Ser	Ser	Phe 335	Ser
Asp	Ser	Ser	Phe 340	Thr	Ala	Ala	Ser	Gln 345	Ile	Ser	Ser	Leu	Leu 350	Gly	Leu
Ala	Trp	Lys 355	Ala	Arg	Ala	Arg	Met 360	Leu	Leu	Ala	Ala	Gly 365	Thr	Ser	Pro
Ala	Ser 370	His	Leu	Asp	Leu	Ala 375	Pro	Met	Ser	His	Ser 380	Thr	Ser	Ala	Leu
Gly 385	Gln	Trp	Ala	Thr	Ala 390	Leu	Cys	Arg	Ser	Ala 395	Ser	Arg	Asp	Ser	Arg 400
Val	Pro	Trp	Phe	Phe	Ser	Lys	Tyr	Ala	Ala	Arg	Ser	His	Thr	Leu	Phe

405

410

415

Leu Leu Gly Asn Thr Cys Arg Ala
420

<210> 420

<211> 109

<212> PRT

<213> homo sapiens

<400> 420

Gly 1	Arg	Thr	Leu	Pro 5	Arg	Gly	Gly	Gly	Thr 10	Val	Trp	Val	Gln	Gly 15	His
Gly	Leu	Glu	Gly 20	Trp	Trp	Ala	Ala	Leu 25	Ser	Gly	Ser	Gly	Phe 30	Pro	Ala
Val	Gly	Phe 35	Leu	Phe	Trp	Leu	Leu 40	Arg	Leu	Val	Tyr	Phe 45	Leu	Ser	Leu
Leu	Pro 50	Val	Thr	Pro	Gly	Ala 55	Pro	Glu	Tyr	Arg	Leu 60	Phe	Ser	Pro	Trp
Ala 65	Val	Ser	Leu	Ser	Cys 70	Phe	Leu	Thr	Leu	Leu 75	Pro	Gly	Leu	Leu	Cys 80
Val	His	Leu	Arg	Leu 85	Ala	Trp	Ser	Lys	Gln 90	Val	Arg	Pro	Leu	Leu 95	Leu
Tyr	Ser	Leu	Val 100	Leu	Phe	Trp	His	Leu 105	Val	Lys	Leu	Ala			

<210> 421

<211> 177

<212> PRT

<213> homo sapiens

<400> 421

Val 1	Ser	Val	Pro	Ser 5	Ser	Ser	Ala	Ala	Gly 10	Thr	Leu	Phe	Gln	Gly 15	Leu
Cys	Gly	Ala	Pro 20	Asp	Ala	Pro	His	Pro 25	Leu	Ser	Lys	Ile	Pro 30	Gly	Gly
Arg	Gly	Gly 35	Gly	Arg	Asp	Pro	Ser 40	Leu	Ser	Ala	Leu	Ile 45	Tyr	Lys	Asp
Glu	Lys 50	Leu	Thr	Val	Thr	Gln 55	Asp	Leu	Pro	Val	Asn 60	Asp	Gly	Lys	Pro
His 65	Ile	Val	His	Phe	Gln 70	Tyr	Glu	Val	Thr	Glu 75	Val	Lys	Val	Ser	Ser 80
Trp	Asp	Ala	Val	Leu 85	Ser	Ser	Gln	Ser	Leu 90	Phe	Val	Glu	Ile	Pro 95	Asp
Gly	Leu	Leu	Ala 100	Asp	Gly	Ser	Lys	Glu 105	Gly	Leu	Leu	Ala	Leu 110	Leu	Glu
Phe	Ala	Glu 115	Glu	Lys	Met	Lys	Val	Asn 120	Tyr	Val	Phe	Ile 125	Cys	Phe	Arg

Lys	Gly	Arg	Glu	Asp	Arg	Ala	Pro	Leu	Leu	Lys	Thr	Phe	Ser	Phe	Leu
	130					135					140				
Gly	Phe	Glu	Ile	Val	Arg	Pro	Gly	His	Pro	Cys	Val	Pro	Ser	Arg	Pro
145					150					155					160
Asp	Val	Met	Phe	Met	Val	Tyr	Pro	Leu	Asp	Gln	Asn	Leu	Ser	Asp	Glu
				165					170					175	

Asp

<210> 422
 <211> 114
 <212> PRT
 <213> homo sapiens

<400> 422

Ala	Ser	Arg	Pro	Tyr	Ile	Leu	Glu	Leu	Arg	Glu	Lys	Asp	Pro	Cys	Arg
1				5					10					15	
Pro	Leu	Ala	His	Arg	Gly	Ser	Ser	Thr	Val	Gly	Glu	Gly	His	Gln	Glu
			20					25					30		
His	His	Arg	Gly	Pro	Gly	Thr	Met	Cys	Leu	Gln	His	Trp	Ser	Trp	Gly
		35					40					45			
His	Leu	Leu	Asn	Gly	Lys	Ile	Leu	Leu	Ser	Trp	Val	Phe	Ile	Ile	Leu
	50					55					60				
Gly	Gly	Ser	Ala	Gln	Gly	Gly	Arg	Arg	Arg	Arg	Gly	Glu	Trp	Val	Gly
65					70					75					80
Gly	Arg	Val	Gly	Gly	Cys	Gly	Val	Ala	Arg	Ala	Gly	Arg	Ser	Leu	Trp
				85					90					95	
Ala	Lys	Ser	Leu	Ser	Gly	Arg	Gly	Arg	Val	Pro	Ser	Ser	Cys	Leu	Ser
			100					105					110		

Glu Arg

<210> 423
 <400> 423
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<210> 424
 <400> 424
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<210> 425
 <400> 425
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<210> 426
 <211> 50
 <212> PRT
 <213> homo sapiens

<400> 426

Pro	Phe	Cys	Ser	Ser	Leu	Ala	Lys	Leu	Gln	Gly	Ile	Trp	Gly	Met	Trp
1				5					10					15	

Asp	Leu	Gln	Phe 20	Pro	Ala	Pro	Ala	Ser 25	Ala	Leu	Ser	Gln	Val 30	Leu	Thr
Pro	Ala	Pro 35	Ala	Ser	Ala	Pro	Ala 40	Pro	Gly	Arg	Ala	Pro 45	Ala	Pro	Ala
Ala	Ala 50														

<210> 427
 <211> 114
 <212> PRT
 <213> homo sapiens

<400> 427

Glu 1	Asp	Lys	Met	Arg 5	Pro	Gly	Leu	Ser	Phe 10	Leu	Leu	Ala	Leu	Leu 15	Phe
Phe	Leu	Gly	Gln 20	Ala	Ala	Gly	Asp	Leu 25	Gly	Asp	Val	Gly	Pro 30	Pro	Ile
Pro	Ser	Pro 35	Gly	Phe	Ser	Ser	Phe 40	Pro	Gly	Val	Asp	Ser 45	Ser	Ser	Ser
Phe	Ser 50	Ser	Ser	Ser	Arg	Ser 55	Gly	Ser	Ser	Ser	Ser 60	Arg	Ser	Leu	Gly
Ser 65	Gly	Gly	Ser	Val	Ser 70	Gln	Leu	Phe	Ser	Asn 75	Phe	Thr	Gly	Ser	Val 80
Asp	Asp	Arg	Gly	Thr 85	Cys	Gln	Cys	Ser	Val 90	Ser	Leu	Pro	Asp	Asn 95	Asn
Phe	Pro	Val	Asp 100	Arg	Val	Glu	Arg	Trp 105	Asn	Ser	Gln	Leu	Ile 110	Val	Ile
Ser	Gln														

<210> 428
 <211> 113
 <212> PRT
 <213> homo sapiens

<400> 428

Glu 1	Ile	Thr	Met	Ser 5	Cys	Glu	Phe	Gln	Arg 10	Ser	Thr	Leu	Ser	Thr 15	Gly
Lys	Leu	Leu	Ser 20	Gly	Arg	Glu	Thr	Glu 25	His	Trp	Gln	Val	Pro 30	Arg	Ser
Ser	Thr	Glu 35	Pro	Val	Lys	Leu	Glu 40	Asn	Asn	Trp	Asp	Thr 45	Glu	Pro	Pro
Leu	Pro 50	Lys	Leu	Arg	Leu	Glu 55	Leu	Glu	Pro	Asp	Leu 60	Glu	Leu	Glu	Leu
Lys 65	Leu	Glu	Leu	Glu	Ser 70	Thr	Pro	Gly	Lys	Glu 75	Leu	Lys	Pro	Gly	Leu 80
Gly	Ile	Gly	Gly	Pro	Thr	Ser	Pro	Lys	Ser	Pro	Ala	Ala	Trp	Pro	Arg

85

90

95

Lys Asn Arg Arg Ala Arg Arg Asn Glu Arg Pro Gly Leu Ile Leu Ser
100 105 110

Ser

<210> 429

<211> 50

<212> PRT

<213> homo sapiens

<400> 429

Ala Ala Ala Gly Ala Gly Ala Arg Pro Gly Ala Gly Ala Glu Ala Gly
1 5 10 15
Ala Gly Val Asn Thr Trp Glu Arg Ala Gly Ala Gly Asn Trp
20 25 30
Arg Ser His Ile Pro Gln Ile Pro Cys Ser Leu Ala Lys Glu Glu Gln
35 40 45
Lys Gly
50

<210> 430

<211> 224

<212> PRT

<213> homo sapiens

<400> 430

Gln Thr Gln Lys Val Val Thr Ser Pro Pro Arg Ile Thr Leu His Trp
1 5 10 15
Leu Leu Pro Cys Ala Ala His Pro Pro Asp Leu His Lys Lys Gly Gln
20 25 30
Glu Asn Ser Gly Cys Ala Pro Ala Thr Ala His Ser Ala Pro Pro Gly
35 40 45
Arg Ser Pro Pro Glu Leu Arg Ala Gly Leu Gln Arg Leu Ala Arg Ala
50 55 60
Val Leu Pro Val Ser Arg Phe Ser Ala Pro Gln Pro Pro Ala Ala Ser
65 70 75 80
Phe Ser Gly Pro Arg Val Ala Pro Ser Glu Glu Ser Gly Pro Gly Thr
85 90 95
Ser Ser Asn Ser Gly Arg Leu Ala Leu Pro Arg Leu Arg Ser Leu Cys
100 105 110
Pro Leu Gly Val Ala Arg Pro Arg Cys Cys Arg Ala Leu Ala Arg Cys
115 120 125
Cys Cys Ser Ser Ser Pro Arg Thr Ala Ala Trp Ala Arg Arg Ala Gly
130 135 140
Ser Ser Ser Leu Ala Ser Pro Thr Ser Pro Thr Ser Ala Glu Leu Gln
145 150 155 160

Ala	His	Pro	Gly	Gln 165	Pro	Ala	Ala	Val	Pro 170	Arg	His	Arg	Ile	Pro 175	Glu
His	Ala	Ala	Ala 180	Gln	Pro	Ala	Gly	Pro 185	Arg	Asp	His	Glu	Gly 190	Gly	Ala
Gly	Ala	Gly 195	Arg	Arg	Leu	Asp	Pro 200	Ala	Gly	His	Glu	Ala 205	Val	Pro	Pro
Gly	His 210	Gln	Glu	Val	Pro	Val 215	Leu	Ala	Leu	Arg	Pro 220	Arg	Leu	Pro	Arg

<210> 431

<211> 408

<212> PRT

<213> homo sapiens

<400> 431

Pro 1	Ala	Leu	Leu	Gly 5	Leu	Pro	Phe	Ile	Gly 10	Ser	Ser	Leu	Ala	Pro 15	Pro
Thr	Leu	Gln	Ile 20	Cys	Ile	Lys	Lys	Ala 25	Lys	Lys	Thr	Leu	Ala 30	Val	Pro
Gln	Gln	Arg 35	Leu	Ile	Leu	Leu	Pro 40	Arg	Val	Gly	Ala	Pro 45	Arg	Ser	Cys
Ala	Arg 50	Ala	Cys	Ser	Ala	Ser 55	Pro	Ala	Leu	Ser	Ser 60	Arg	Cys	Pro	Ala
Ser 65	Pro	Arg	Pro	Ser	Arg 70	Arg	Leu	Pro	Ala	Phe 75	Arg	Gly	Pro	Glu	Ser 80
His	Pro	Ala	Lys	Arg 85	Ala	Gly	Pro	Gly	Gln 90	Ala	Arg	Thr	Pro	Ala 95	Ala
Ser	Pro	Phe	Pro 100	Gly	Ser	Ala	Pro	Ser 105	Ala	Pro	Ser	Gly	Ser 110	Arg	Ala
His	Asp	Ala 115	Ala	Gly	Pro	Trp	Leu 120	Ala	Ala	Ala	Ala	Leu 125	Pro	Arg	Leu
Ala	Leu 130	Leu	Pro	Gly	Leu	Gly 135	Ala	Arg	Ala	Leu	Pro 140	Leu	Trp	Pro	Ala
Arg 145	Leu	Leu	Leu	Gln	Ala 150	Gln	Asn	Cys	Lys	Pro 155	Ile	Pro	Ala	Asn	Leu 160
Gln	Leu	Cys	His	Gly 165	Ile	Glu	Tyr	Gln	Asn 170	Met	Arg	Leu	Pro	Asn 175	Leu
Leu	Gly	His	Glu 180	Thr	Met	Lys	Glu	Val 185	Leu	Glu	Gln	Ala	Gly 190	Ala	Trp
Ile	Pro	Leu 195	Val	Met	Lys	Gln	Cys 200	His	Pro	Asp	Thr	Lys 205	Lys	Phe	Leu
Cys	Ser 210	Leu	Phe	Ala	Pro	Val 215	Cys	Leu	Asp	Asp	Leu 220	Asp	Glu	Thr	Ile
Gln 225	Pro	Cys	His	Ser	Leu 230	Cys	Val	Gln	Val	Lys 235	Asp	Arg	Cys	Ala	Pro 240

Val	Met	Ser	Ala	Phe 245	Gly	Phe	Pro	Trp	Pro 250	Asp	Met	Leu	Glu	Cys 255	Asp
Arg	Phe	Pro	Gln 260	Asp	Asn	Asp	Leu	Cys 265	Ile	Pro	Leu	Ala	Ser 270	Ser	Asp
His	Leu	Leu 275	Pro	Ala	Thr	Glu	Glu 280	Ala	Pro	Lys	Val	Cys 285	Glu	Ala	Cys
Lys	Asn 290	Lys	Asn	Asp	Asp	Asp 295	Asn	Asp	Ile	Met	Glu 300	Thr	Leu	Cys	Lys
Asn 305	Asp	Phe	Ala	Leu	Lys 310	Ile	Lys	Val	Lys	Glu 315	Ile	Thr	Tyr	Ile	Asn 320
Arg	Asp	Thr	Lys	Ile 325	Ile	Leu	Glu	Thr	Lys 330	Ser	Lys	Thr	Ile	Tyr 335	Lys
Leu	Asn	Gly	Val 340	Ser	Glu	Arg	Asp	Leu 345	Lys	Lys	Ser	Val	Leu 350	Trp	Leu
Lys	Asp	Ser	Leu	Gln	Cys	Thr	Cys 360	Glu	Glu	Met	Asn	Asp 365	Ile	Asn	Ala
Pro	Tyr 370	Leu	Val	Met	Gly	Gln 375	Lys	Gln	Gly	Gly	Glu 380	Leu	Val	Ile	Thr
Ser 385	Val	Lys	Arg	Trp	Gln 390	Lys	Gly	Gln	Arg	Glu 395	Phe	Lys	Arg	Ile	Ser 400
Arg	Ser	Ile	Arg	Lys 405	Leu	Gln	Cys								

<210> 432

<211> 323

<212> PRT

<213> homo sapiens

<400> 432

Val 1	Ile	Ser	Phe	Thr 5	Phe	Ile	Phe	Ser	Ala 10	Lys	Ser	Phe	Leu	Gln 15	Ser
Val	Ser	Ile	Met 20	Ser	Leu	Ser	Ser	Ser 25	Phe	Leu	Phe	Leu	Gln 30	Ala	Ser
His	Thr	Phe 35	Gly	Ala	Ser	Ser	Val 40	Ala	Gly	Arg	Arg	Trp 45	Ser	Leu	Leu
Ala	Arg 50	Gly	Met	Gln	Arg	Ser 55	Leu	Ser	Trp	Gly	Lys 60	Arg	Ser	His	Ser
Ser 65	Met	Ser	Gly	Gln	Gly 70	Lys	Pro	Lys	Ala	Asp 75	Met	Thr	Gly	Ala	Gln 80
Arg	Ser	Phe	Thr	Cys 85	Thr	Gln	Ser	Glu	Trp 90	His	Gly	Trp	Met	Val 95	Ser
Ser	Arg	Ser	Ser 100	Arg	Gln	Thr	Gly	Ala 105	Lys	Ser	Glu	His	Arg 110	Asn	Phe
Leu	Val	Ser	Gly	Trp	His	Cys	Phe	Met	Thr	Ser	Gly	Ile	Gln	Ala	Pro

115						120						125					
Ala	Cys	Ser	Ser	Thr	Ser	Phe	Met	Val	Ser	Trp	Pro	Ser	Arg	Leu	Gly		
	130					135					140						
Ser	Arg	Met	Phe	Trp	Tyr	Ser	Met	Pro	Trp	His	Ser	Cys	Arg	Leu	Ala		
145					150					155					160		
Gly	Met	Gly	Leu	Gln	Phe	Cys	Ala	Cys	Arg	Arg	Ser	Arg	Ala	Gly	Gln		
				165					170					175			
Arg	Gly	Arg	Ala	Arg	Ala	Pro	Ser	Pro	Gly	Ser	Ser	Ala	Arg	Arg	Gly		
			180					185					190				
Arg	Ala	Ala	Ala	Ala	Ser	Gln	Gly	Pro	Ala	Ala	Ser	Trp	Ala	Arg	Asp		
		195					200					205					
Pro	Glu	Gly	Ala	Glu	Gly	Ala	Glu	Pro	Gly	Lys	Gly	Glu	Ala	Ala	Gly		
	210					215					220						
Val	Arg	Ala	Cys	Pro	Gly	Pro	Ala	Leu	Phe	Ala	Gly	Cys	Asp	Ser	Gly		
225					230					235					240		
Pro	Arg	Lys	Ala	Gly	Ser	Arg	Arg	Leu	Gly	Arg	Gly	Glu	Ala	Gly	His		
				245					250					255			
Arg	Glu	Asp	Ser	Ala	Gly	Glu	Ala	Leu	Gln	Ala	Arg	Ala	Gln	Leu	Arg		
			260					265					270				
Gly	Ala	Pro	Thr	Arg	Gly	Ser	Arg	Met	Ser	Arg	Cys	Trp	Gly	Thr	Ala		
		275					280					285					
Arg	Val	Phe	Leu	Ala	Phe	Phe	Met	Gln	Ile	Trp	Arg	Val	Gly	Gly	Ala		
	290					295					300						
Arg	Glu	Glu	Pro	Met	Lys	Gly	Asn	Pro	Arg	Arg	Ala	Gly	His	Tyr	Phe		
305					310					315					320		
Leu	Gly	Leu															

<210> 433
 <211> 333
 <212> PRT
 <213> homo sapiens

<400> 433

Arg	Gly	Arg	Thr	Trp	Glu	Leu	Phe	Leu	Ala	Gly	Arg	Arg	Val	Leu	Val
1				5					10					15	
Thr	Gly	Ala	Gly	Lys	Gly	Ile	Gly	Arg	Gly	Thr	Val	Gln	Ala	Leu	His
			20					25					30		
Ala	Thr	Gly	Ala	Arg	Val	Val	Ala	Val	Ser	Arg	Thr	Gln	Ala	Asp	Leu
		35					40					45			
Asp	Ser	Leu	Val	Arg	Glu	Cys	Pro	Gly	Ile	Glu	Pro	Val	Cys	Val	Asp
	50					55				60					
Leu	Gly	Asp	Trp	Glu	Ala	Thr	Glu	Arg	Ala	Leu	Gly	Ser	Val	Gly	Pro
65					70					75					80
Val	Asp	Leu	Arg	Gly	Asp	Cys	Ala	Asp	Met	Glu	Leu	Phe	Leu	Ala	Gly

85								90					95				
Arg	Arg	Val	Leu	Val	Thr	Gly	Ala	Gly	Lys	Gly	Ile	Gly	Arg	Gly	Thr		
			100					105					110				
Val	Gln	Ala	Leu	His	Ala	Thr	Gly	Ala	Arg	Val	Val	Ala	Val	Ser	Arg		
		115					120					125					
Thr	Gln	Ala	Asp	Leu	Asp	Ser	Leu	Val	Arg	Glu	Cys	Pro	Gly	Ile	Glu		
	130					135					140						
Pro	Val	Cys	Val	Asp	Leu	Gly	Asp	Trp	Glu	Ala	Thr	Glu	Arg	Ala	Leu		
	145				150					155					160		
Gly	Ser	Val	Gly	Pro	Val	Asp	Leu	Leu	Val	Asn	Asn	Ala	Ala	Val	Ala		
				165					170					175			
Leu	Leu	Gln	Pro	Phe	Leu	Glu	Val	Thr	Lys	Glu	Ala	Phe	Asp	Arg	Ser		
			180					185					190				
Phe	Glu	Val	Asn	Leu	Arg	Ala	Val	Ile	Gln	Val	Ser	Gln	Ile	Val	Ala		
		195					200					205					
Arg	Gly	Leu	Ile	Ala	Arg	Gly	Val	Pro	Gly	Ala	Ile	Val	Asn	Val	Ser		
	210					215					220						
Ser	Gln	Cys	Ser	Gln	Arg	Ala	Val	Thr	Asn	His	Ser	Val	Tyr	Cys	Ser		
	225				230					235					240		
Thr	Lys	Gly	Ala	Leu	Asp	Met	Leu	Thr	Lys	Val	Met	Ala	Leu	Glu	Leu		
				245					250				255				
Gly	Pro	His	Lys	Ile	Arg	Val	Asn	Ala	Val	Asn	Pro	Thr	Val	Val	Met		
			260					265					270				
Thr	Ser	Met	Gly	Gln	Ala	Thr	Trp	Ser	Asp	Pro	His	Lys	Ala	Lys	Thr		
		275					280					285					
Met	Leu	Asn	Arg	Ile	Pro	Leu	Gly	Lys	Phe	Ala	Glu	Val	Glu	His	Val		
	290					295					300						
Val	Asn	Ala	Ile	Leu	Phe	Leu	Leu	Ser	Asp	Arg	Ser	Gly	Met	Thr	Thr		
	305				310					315					320		
Gly	Ser	Thr	Leu	Pro	Val	Glu	Gly	Gly	Phe	Trp	Ala	Cys					
				325					330								

<210> 434

<211> 210

<212> PRT

<213> homo sapiens

<400> 434

Ala	Pro	Gly	His	Asn	Leu	Arg	His	Leu	Asp	Asp	Arg	Thr	Gln	Val	His
1				5					10					15	
Leu	Lys	Gly	Ser	Val	Lys	Gly	Leu	Leu	Gly	Asp	Leu	Gln	Glu	Gly	Leu
			20					25					30		
Gln	Gln	Gly	Asp	Ser	Gly	Val	Val	His	Gln	Gln	Val	His	Gly	Ala	His
		35					40					45			

Ala	Ala	Gln	Arg	Pro	Leu	Gly	Gly	Leu	Pro	Val	Thr	Gln	Val	His	Ala
	50					55					60				
His	Gly	Phe	Tyr	Pro	Arg	Ala	Leu	Ala	Asp	Lys	Ala	Val	Lys	Ile	Arg
65					70					75					80
Leu	Ser	Pro	Ala	His	Ser	His	His	Pro	Arg	Ala	Arg	Arg	Val	Gln	Arg
				85					90					95	
Leu	Asp	Arg	Ala	Ala	Pro	Tyr	Thr	Phe	Ala	Cys	Pro	Gly	Asp	Gln	His
			100					105					110		
Pro	Ala	Ala	Arg	Glu	Glu	Gln	Leu	His	Val	Gly	Ala	Val	Ser	Ala	Gln
		115					120					125			
Val	His	Gly	Ala	His	Ala	Ala	Gln	Arg	Pro	Leu	Gly	Gly	Leu	Pro	Val
	130					135					140				
Thr	Gln	Val	His	Ala	His	Gly	Phe	Tyr	Pro	Arg	Ala	Leu	Ala	Asp	Lys
145					150					155					160
Ala	Val	Lys	Ile	Arg	Leu	Ser	Pro	Ala	His	Ser	His	His	Pro	Arg	Ala
				165					170					175	
Arg	Arg	Val	Gln	Arg	Leu	Asp	Arg	Ala	Ala	Pro	Tyr	Thr	Phe	Ala	Cys
			180					185					190		
Pro	Gly	Asp	Gln	His	Pro	Ala	Ala	Arg	Glu	Glu	Gln	Leu	Pro	Cys	Ser
		195					200					205			
Pro	Thr														
	210														

<210> 435
 <211> 132
 <212> PRT
 <213> homo sapiens

<400> 435

Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Leu	Gly	Ser	Arg	Ile	Arg	Phe
1				5					10					15	
Ile	Gly	Gly	Ile	Gly	Gly	Arg	Met	Ser	Thr	Ala	Trp	Gly	Leu	Arg	Cys
			20					25					30		
Val	Glu	Gly	Ala	Gln	Gln	Ala	Gln	Lys	Pro	Pro	Ser	Thr	Gly	Lys	Val
		35					40					45			
Glu	Pro	Val	Val	Met	Pro	Leu	Arg	Ser	Leu	Ser	Arg	Lys	Arg	Met	Ala
	50					55					60				
Phe	Thr	Thr	Cys	Ser	Thr	Ser	Ala	Asn	Leu	Pro	Ser	Gly	Ile	Arg	Phe
65					70					75					80
Ser	Ile	Val	Leu	Ala	Leu	Trp	Gly	Ser	Leu	Gln	Val	Ala	Trp	Pro	Met
				85					90					95	
Asp	Val	Ile	Thr	Thr	Val	Gly	Phe	Thr	Ala	Phe	Thr	Arg	Ile	Leu	Trp
			100					105					110		
Gly	Pro	Ser	Ser	Arg	Ala	Ile	Thr	Leu	Val	Ser	Met	Ser	Arg	Ala	Pro
		115					120					125			

Leu Val Glu Gln
130

<210> 436
<211> 94
<212> PRT
<213> homo sapiens

<400> 436

Lys	Ala	Lys	Ser	Trp	Val	Pro	Ser	Asp	Phe	Arg	Phe	Gln	Glu	Leu	Pro
1				5					10					15	
Glu	Asn	Thr	Arg	Ser	Gln	Arg	Val	Ile	Phe	Trp	Ser	Leu	Phe	Cys	Arg
			20					25					30		
Asp	Ser	Trp	Glu	Tyr	Gly	His	Pro	Ala	Pro	Arg	Cys	Gly	Asn	Glu	Ser
		35					40					45			
Ser	Arg	Ser	Gly	Glu	Ala	Ala	Leu	Ala	Asp	Val	Gln	Leu	Ala	Ala	Pro
		50				55					60				
Val	Ser	Asn	Gln	Leu	His	Pro	Asp	Gly	Val	Glu	Asp	Arg	Gly	Val	Gly
65					70					75					80
Gly	Leu	Leu	Pro	Glu	Leu	His	His	Ala	Glu	Pro	Tyr	Leu	Val		
				85					90						

<210> 437
<211> 70
<212> PRT
<213> homo sapiens

<400> 437

Phe	Ser	Gly	Val	Cys	Phe	Ala	Gly	Ile	Ala	Gly	Ser	Met	Ala	Thr	Leu
1				5					10					15	
Leu	His	Asp	Ala	Val	Met	Asn	Pro	Ala	Glu	Val	Val	Lys	Gln	Arg	Leu
			20					25					30		
Gln	Met	Tyr	Asn	Ser	Gln	His	Arg	Ser	Ala	Ile	Ser	Cys	Ile	Arg	Thr
		35					40					45			
Val	Trp	Arg	Thr	Glu	Gly	Leu	Gly	Ala	Phe	Tyr	Arg	Ser	Tyr	Thr	Thr
	50					55					60				
Pro	Ser	Pro	Ile	Ser	Cys										
65					70										

<210> 438
<211> 98
<212> PRT
<213> homo sapiens

<400> 438

Lys	Ala	Pro	Asn	Pro	Ser	Val	Leu	His	Thr	Val	Arg	Met	Gln	Leu	Ile
1				5					10					15	
Ala	Asp	Arg	Cys	Cys	Glu	Leu	Tyr	Ile	Cys	Lys	Arg	Cys	Phe	Thr	Thr
			20					25					30		

Ser	Ala	Gly	Phe	Ile	Thr	Ala	Ser	Trp	Ser	Arg	Val	Ala	Ile	Leu	Pro
		35					40					45			
Ala	Ile	Pro	Ala	Lys	Gln	Thr	Pro	Glu	Asn	Tyr	Pro	Leu	Arg	Ser	Gly
	50					55					60				
Val	Leu	Arg	Lys	Phe	Leu	Glu	Pro	Lys	Ile	Arg	Arg	Asn	Pro	Gly	Leu
	65				70					75					80
Ser	Phe	Leu	Arg	Ser	Lys	Met	Tyr	Tyr	Gln	Ser	Ala	Gln	Val	Ser	Thr
				85					90					95	

Asp Ser

<210> 439
 <211> 270
 <212> PRT
 <213> homo sapiens

<400> 439

Arg	Ser	Val	Val	Arg	Arg	Cys	Leu	Lys	Met	Ala	Ala	Glu	Glu	Pro	Gln
1				5					10					15	
Gln	Gln	Lys	Gln	Glu	Pro	Leu	Gly	Ser	Asp	Ser	Glu	Gly	Val	Asn	Cys
			20					25					30		
Leu	Ala	Tyr	Asp	Glu	Ala	Ile	Met	Ala	Gln	Gln	Asp	Arg	Ile	Gln	Gln
		35					40					45			
Glu	Ile	Ala	Val	Gln	Asn	Pro	Leu	Val	Ser	Glu	Arg	Leu	Glu	Leu	Ser
	50				55						60				
Val	Leu	Tyr	Lys	Glu	Tyr	Ala	Glu	Asp	Asp	Asn	Ile	Tyr	Gln	Gln	Lys
	65				70					75					80
Ile	Lys	Asp	Leu	His	Lys	Lys	Tyr	Ser	Tyr	Ile	Arg	Lys	Thr	Arg	Pro
				85					90					95	
Asp	Gly	Asn	Cys	Phe	Tyr	Arg	Ala	Phe	Gly	Phe	Ser	His	Leu	Glu	Ala
			100					105					110		
Leu	Leu	Asp	Asp	Ser	Lys	Glu	Leu	Gln	Arg	Phe	Lys	Ala	Val	Ser	Ala
		115					120					125			
Lys	Ser	Lys	Glu	Asp	Leu	Val	Ser	Gln	Gly	Phe	Thr	Glu	Phe	Thr	Ile
	130					135					140				
Glu	Asp	Phe	His	Asn	Thr	Phe	Met	Asp	Leu	Ile	Glu	Gln	Val	Glu	Lys
	145				150					155					160
Gln	Thr	Ser	Val	Ala	Asp	Leu	Leu	Ala	Ser	Phe	Asn	Asp	Gln	Ser	Thr
				165					170					175	
Ser	Asp	Tyr	Leu	Val	Val	Tyr	Leu	Arg	Leu	Leu	Thr	Ser	Gly	Tyr	Leu
			180					185					190		
Gln	Arg	Glu	Ser	Lys	Phe	Phe	Glu	His	Phe	Ile	Glu	Gly	Gly	Arg	Thr
		195					200					205			
Val	Lys	Glu	Phe	Cys	Gln	Gln	Glu	Val	Glu	Pro	Met	Cys	Lys	Glu	Ser
	210					215					220				

Asp 225	His	Ile	His	Ile	Ile 230	Ala	Leu	Ala	Gln	Ala 235	Leu	Ser	Val	Ser	Ile 240
Gln	Val	Glu	Tyr	Met 245	Asp	Arg	Gly	Glu	Gly 250	Gly	Thr	Thr	Asn	Pro 255	His
Ile	Phe	Pro	Glu 260	Gly	Phe	Arg	Ala	Gln 265	Gly	Leu	Thr	Leu	Phe 270		

<210> 440

<211> 145

<212> PRT

<213> homo sapiens

<400> 440

Arg 1	Trp	Arg	Arg	Arg 5	Asn	Leu	Ser	Ser	Arg 10	Ser	Arg	Ser	Arg	Trp 15	Ala
Ala	Thr	Pro	Lys 20	Val	Leu	Thr	Val	Trp 25	Pro	Met	Met	Lys	Pro 30	Ser	Trp
Leu	Ser	Arg 35	Thr	Glu	Phe	Ser	Lys 40	Arg	Leu	Leu	Cys	Arg 45	Thr	Leu	Trp
Cys	Gln 50	Ser	Gly	Trp	Ser	Ser 55	Arg	Ser	Tyr	Thr	Arg 60	Ser	Met	Leu	Lys
Met 65	Thr	Thr	Ser	Ile	Asn 70	Arg	Arg	Ser	Arg	Thr 75	Ser	Thr	Lys	Ser	Thr 80
Arg	Thr	Ser	Ala	Arg 85	Pro	Gly	Leu	Thr	Ala 90	Thr	Val	Ser	Ile	Gly 95	Leu
Ser	Asp	Ser	Pro 100	Thr	Trp	Arg	His	Cys 105	Trp	Met	Thr	Ala	Arg 110	Ser	Cys
Ser	Gly	Ser 115	Arg	Leu	Cys	Leu	Pro 120	Arg	Ala	Arg	Lys	Thr 125	Trp	Cys	Pro
Arg	Ala 130	Ser	Leu	Asn	Ser	Gln 135	Leu	Arg	Ile	Ser	Thr 140	Thr	Arg	Ser	Trp
Thr 145															

<210> 441

<211> 210

<212> PRT

<213> homo sapiens

<400> 441

Ile 1	Ala	Pro	Ser	Arg 5	Leu	Lys	Gln	Gly	Lys 10	Thr	Leu	Gly	Ser	Glu 15	Ala
Leu	Arg	Glu	Asp 20	Val	Arg	Ile	Gly	Gly 25	Ala	Ala	Leu	Ala	Ala 30	Val	His
Val	Leu	His 35	Leu	Asp	Gly	His	Ala 40	Glu	Gly	Leu	Gly	Gln 45	Arg	Asn	Asp

Val	Asp 50	Val	Val	Ala	Leu	Leu 55	Ala	His	Gly	Leu	His 60	Leu	Leu	Leu	Ala
Glu 65	Leu	Leu	Asp	Ser	Pro 70	Ser	Thr	Leu	Asp	Glu 75	Val	Leu	Glu	Glu	Leu 80
Ala	Leu	Ala	Leu	Gln 85	Val	Ala	Arg	Gly	Glu 90	Gln	Pro	Gln	Val	Asp 95	His
Lys	Val	Val	Gly 100	Gly	Ala	Leu	Val	Ile 105	Glu	Gly	Gly	Gln	Gln 110	Val	Gly
Asp	Arg	Gly 115	Leu	Leu	Leu	His	Leu 120	Leu	Asn	Gln	Val	His 125	Glu	Arg	Val
Val	Glu 130	Ile	Leu	Asn	Cys	Glu 135	Phe	Ser	Glu	Ala	Leu 140	Gly	His	Gln	Val
Phe 145	Leu	Ala	Leu	Gly	Arg 150	His	Ser	Leu	Glu	Pro 155	Leu	Gln	Leu	Leu	Ala 160
Val	Ile	Gln	Gln	Cys 165	Leu	Gln	Val	Gly	Glu 170	Ser	Glu	Ser	Pro	Ile 175	Glu
Thr	Val	Ala	Val 180	Arg	Pro	Gly	Leu	Ala 185	Asp	Val	Arg	Val	Leu 190	Phe	Val
Glu	Val	Leu 195	Asp	Leu	Leu	Leu	Ile 200	Asp	Val	Val	Ile	Phe 205	Ser	Ile	Leu
Leu	Val 210														

<210> 442
 <211> 322
 <212> PRT
 <213> homo sapiens

<400> 442

Asn 1	Ser	Glu	Arg	Gly 5	Arg	Leu	Gln	Ala	Met 10	Met	Thr	His	Leu	His 15	Val
Lys	Ser	Thr	Glu 20	Pro	Lys	Ala	Ala	Pro 25	Gln	Pro	Leu	Asn	Leu 30	Val	Ser
Ser	Val	Thr 35	Leu	Ser	Lys	Ser	Ala 40	Ser	Glu	Ala	Ser	Pro 45	Gln	Ser	Leu
Pro	His 50	Thr	Pro	Thr	Thr	Pro 55	Thr	Ala	Pro	Leu	Thr 60	Pro	Val	Thr	Gln
Gly 65	Pro	Ser	Val	Ile	Thr 70	Thr	Thr	Ser	Met	His 75	Thr	Val	Gly	Pro	Ile 80
Arg	Arg	Arg	Tyr	Ser 85	Asp	Lys	Tyr	Asn	Val 90	Pro	Ile	Ser	Ser	Ala 95	Asp
Ile	Ala	Gln	Asn 100	Gln	Glu	Phe	Tyr	Lys 105	Asn	Ala	Glu	Val	Arg 110	Pro	Pro
Phe	Thr	Tyr 115	Ala	Ser	Leu	Ile	Arg 120	Gln	Ala	Ile	Leu	Glu 125	Ser	Pro	Glu

Lys	Gln	Leu	Thr	Leu	Asn	Glu	Ile	Tyr	Asn	Trp	Phe	Thr	Arg	Met	Phe
	130					135					140				
Ala	Tyr	Phe	Arg	Arg	Asn	Ala	Ala	Thr	Trp	Lys	Asn	Ala	Val	Arg	His
145					150					155					160
Asn	Leu	Ser	Leu	His	Lys	Cys	Phe	Val	Arg	Val	Glu	Asn	Val	Lys	Gly
				165					170					175	
Ala	Val	Trp	Thr	Val	Asp	Glu	Val	Glu	Phe	Gln	Lys	Arg	Arg	Pro	Gln
			180					185					190		
Lys	Ile	Ser	Gly	Asn	Pro	Ser	Leu	Ile	Lys	Asn	Met	Gln	Ser	Ser	His
		195					200					205			
Ala	Tyr	Cys	Thr	Pro	Leu	Asn	Ala	Ala	Leu	Gln	Ala	Ser	Met	Ala	Glu
	210					215					220				
Asn	Ser	Ile	Pro	Leu	Tyr	Thr	Thr	Ala	Ser	Met	Gly	Asn	Pro	Thr	Leu
					230					235					240
Gly	Asn	Leu	Ala	Ser	Ala	Ile	Arg	Glu	Glu	Leu	Asn	Gly	Ala	Met	Glu
				245					250					255	
His	Thr	Asn	Ser	Asn	Glu	Ser	Asp	Ser	Ser	Pro	Gly	Arg	Ser	Pro	Met
			260					265					270		
Gln	Ala	Val	His	Pro	Val	His	Val	Lys	Glu	Glu	Pro	Leu	Asp	Pro	Glu
		275					280					285			
Glu	Ala	Glu	Gly	Pro	Leu	Ser	Leu	Val	Thr	Thr	Ala	Asn	His	Ser	Pro
	290					295					300				
Asp	Phe	Asp	His	Asp	Arg	Asp	Tyr	Glu	Asp	Glu	Pro	Val	Asn	Glu	Asp
305					310					315					320
Met	Glu														

<210> 443
 <211> 103
 <212> PRT
 <213> homo sapiens

<400> 443

Phe	Gly	Thr	Arg	Ala	Pro	Ala	Ser	His	Asp	Asp	Pro	Pro	Ala	Cys	Glu
1				5					10					15	
Val	Tyr	Arg	Thr	Gln	Ser	Cys	Pro	Ser	Ala	Pro	Glu	Ser	Gly	Ile	Lys
			20					25					30		
Cys	His	Pro	Leu	Gln	Val	Arg	Ile	Gly	Gly	Phe	Ser	Thr	Glu	Leu	Thr
		35					40					45			
Ser	Tyr	Ser	Asn	Asp	Pro	Asn	Arg	Pro	Pro	Asp	Ser	Arg	His	Pro	Arg
	50					55					60				
Pro	Leu	Cys	His	His	Asn	His	Gln	His	Ala	His	Gly	Gly	Thr	His	Pro
65					70					75					80
Gln	Ala	Val	Leu	Arg	Gln	Ile	Gln	Arg	Ala	His	Phe	Val	Ser	Arg	Tyr
				85					90					95	

Cys Ala Glu Pro Arg Ile Leu
100

<210> 444
<211> 101
<212> PRT
<213> homo sapiens

<400> 444

Ser	Leu	Ser	Trp	Ser	Lys	Ser	Gly	Leu	Trp	Leu	Ala	Val	Val	Thr	Lys
1				5					10					15	
Asp	Arg	Gly	Pro	Ser	Ala	Ser	Ser	Gly	Ser	Arg	Gly	Ser	Ser	Leu	Thr
			20					25					30		
Cys	Thr	Gly	Cys	Thr	Ala	Cys	Ile	Gly	Asp	Leu	Pro	Gly	Leu	Leu	Ser
		35					40					45			
Leu	Ser	Leu	Leu	Leu	Val	Cys	Ser	Ile	Ala	Pro	Phe	Ser	Ser	Ser	Arg
	50					55					60				
Ile	Ala	Leu	Ala	Lys	Leu	Pro	Arg	Val	Gly	Phe	Pro	Met	Glu	Ala	Val
65					70					75					80
Val	Tyr	Arg	Gly	Ile	Leu	Phe	Ser	Ala	Ile	Glu	Ala	Cys	Lys	Ala	Ala
				85					90					95	
Leu	Arg	Gly	Val	Gln											
			100												

<210> 445
<211> 539
<212> PRT
<213> homo sapiens

<400> 445

Leu	Asp	Val	Gln	Val	Lys	Asp	Asp	Ser	Arg	Ala	Leu	Thr	Leu	Gly	Ala
1				5					10					15	
Leu	Thr	Leu	Pro	Leu	Ala	Arg	Leu	Leu	Thr	Ala	Pro	Glu	Leu	Ile	Leu
			20					25					30		
Asp	Gln	Trp	Phe	Gln	Leu	Ser	Ser	Ser	Gly	Pro	Asn	Ser	Arg	Leu	Tyr
		35					40					45			
Met	Lys	Leu	Val	Met	Arg	Ile	Leu	Tyr	Leu	Asp	Ser	Ser	Glu	Ile	Cys
	50					55					60				
Phe	Pro	Thr	Val	Pro	Gly	Cys	Pro	Gly	Ala	Trp	Asp	Val	Asp	Ser	Glu
65					70				75						80
Asn	Pro	Gln	Arg	Gly	Ser	Ser	Val	Asp	Ala	Pro	Pro	Arg	Pro	Cys	His
				85					90					95	
Thr	Thr	Pro	Asp	Ser	Gln	Phe	Gly	Thr	Glu	His	Val	Leu	Arg	Ile	His
			100					105					110		
Val	Leu	Glu	Ala	Gln	Asp	Leu	Ile	Ala	Lys	Asp	Arg	Phe	Leu	Gly	Gly
		115					120					125			

Leu	Val	Lys	Gly	Lys	Ser	Asp	Pro	Tyr	Val	Lys	Leu	Lys	Leu	Ala	Gly
	130					135					140				
Arg	Ser	Phe	Arg	Ser	His	Val	Val	Arg	Glu	Asp	Leu	Asn	Pro	Arg	Trp
145					150					155					160
Asn	Glu	Val	Phe	Glu	Val	Ile	Val	Thr	Ser	Val	Pro	Gly	Gln	Glu	Leu
				165					170					175	
Glu	Val	Glu	Val	Phe	Asp	Lys	Asp	Leu	Asp	Lys	Asp	Asp	Phe	Leu	Gly
			180					185					190		
Arg	Cys	Lys	Val	Arg	Leu	Thr	Thr	Val	Leu	Asn	Ser	Gly	Phe	Leu	Asp
		195					200					205			
Glu	Trp	Leu	Thr	Leu	Glu	Asp	Val	Pro	Ser	Gly	Arg	Leu	His	Leu	Arg
	210					215					220				
Leu	Glu	Arg	Leu	Thr	Pro	Arg	Pro	Thr	Ala	Ala	Glu	Leu	Glu	Glu	Val
225					230					235					240
Leu	Gln	Val	Asn	Ser	Leu	Ile	Gln	Thr	Gln	Lys	Ser	Ala	Glu	Leu	Ala
				245					250					255	
Ala	Ala	Leu	Leu	Ser	Ile	Tyr	Met	Glu	Arg	Ala	Glu	Asp	Leu	Pro	Leu
			260					265					270		
Arg	Lys	Gly	Thr	Lys	His	Leu	Ser	Pro	Tyr	Ala	Thr	Leu	Thr	Val	Gly
		275					280					285			
Asp	Ser	Ser	His	Lys	Thr	Lys	Thr	Ile	Ser	Gln	Thr	Ser	Ala	Pro	Val
		290				295					300				
Trp	Asp	Glu	Ser	Ala	Ser	Phe	Leu	Ile	Arg	Lys	Pro	His	Thr	Glu	Ser
305					310					315					320
Leu	Glu	Leu	Gln	Val	Arg	Gly	Glu	Gly	Thr	Gly	Val	Leu	Gly	Ser	Leu
				325					330					335	
Ser	Leu	Pro	Leu	Ser	Glu	Leu	Leu	Val	Ala	Asp	Gln	Leu	Cys	Leu	Asp
			340					345					350		
Arg	Trp	Phe	Thr	Leu	Ser	Ser	Gly	Gln	Gly	Gln	Val	Leu	Leu	Arg	Ala
		355					360					365			
Gln	Leu	Gly	Ile	Leu	Val	Ser	Gln	His	Ser	Gly	Val	Glu	Ala	His	Ser
	370					375					380				
His	Ser	Tyr	Ser	His	Ser	Ser	Ser	Ser	Leu	Ser	Glu	Glu	Pro	Glu	Leu
385					390					395					400
Ser	Gly	Gly	Pro	Pro	His	Ile	Thr	Ser	Ser	Ala	Pro	Glu	Leu	Arg	Gln
				405					410					415	
Arg	Leu	Thr	His	Val	Asp	Ser	Pro	Leu	Glu	Ala	Pro	Ala	Gly	Pro	Leu
			420					425					430		
Gly	Gln	Val	Lys	Leu	Thr	Leu	Trp	Tyr	Tyr	Ser	Glu	Glu	Arg	Lys	Leu
		435					440					445			
Val	Ser	Ile	Val	His	Gly	Cys	Arg	Ser	Leu	Arg	Gln	Asn	Gly	Arg	Asp
	450					455					460				

Pro 465	Pro	Asp	Pro	Tyr 470	Val	Ser	Leu	Leu	Leu	Leu 475	Pro	Asp	Lys	Asn	Arg 480
Gly	Thr	Lys	Arg 485	Thr	Ser	Gln	Lys	Lys 490	Arg	Thr	Leu	Ser	Pro 495	Glu	
Phe	Asn	Glu	Arg 500	Phe	Glu	Trp	Glu	Leu 505	Pro	Leu	Asp	Glu	Ala 510	Gln	Arg
Arg	Lys	Leu 515	Asp	Val	Ser	Val	Lys 520	Ser	Asn	Ser	Ser	Phe 525	Met	Ser	Arg
Glu	Arg 530	Asp	Cys	Trp	Gly	Arg 535	Cys	Ser	Trp	Thr					

<210> 446
 <211> 99
 <212> PRT
 <213> homo sapiens

<400> 446

Leu 1	Leu	Cys	Leu	Pro 5	Ala	Phe	Val	Ser	Leu 10	His	His	Arg	Leu	Asn 15	Val
Met	Ser	Leu	Lys 20	Leu	Gly	Ser	Lys	Gly 25	Arg	Ala	Cys	Ala	Leu 30	Gln	Pro
Phe	His	Leu 35	Thr	Gly	Pro	Tyr	Ser 40	Gly	Leu	Cys	Leu	Thr 45	Lys	Glu	Lys
Asn 50	Arg	Met	Phe	Pro	Leu	Leu 55	His	Gly	Leu	Tyr	Pro 60	Ser	Gly	Pro	Leu
Gly 65	Arg	Gly	Pro	Glu	Leu 70	Ala	Val	Ser	Cys	Phe 75	Ala	Cys	Thr	Leu	Phe 80
Ser	Leu	Pro	Pro	Asn 85	Ser	Ser	Gly	Pro	Ser 90	Val	Ser	Val	Pro	Gly 95	Gln
Trp	Gln	His													

<210> 447
 <211> 112
 <212> PRT
 <213> homo sapiens

<400> 447

Val 1	Trp	Ile	Lys	Leu 5	Phe	Thr	Cys	Ser	Thr 10	Ser	Ser	Asn	Ser	Ala 15	Ala
Val	Gly	Arg	Gly 20	Val	Arg	Arg	Ser	Arg 25	Arg	Lys	Cys	Arg	Arg 30	Pro	Asp
Gly	Thr	Ser 35	Ser	Arg	Val	Ser	His 40	Ser	Ser	Arg	Lys	Pro 45	Leu	Phe	Lys
Thr	Val 50	Val	Arg	Arg	Thr	Leu 55	His	Leu	Pro	Arg	Lys 60	Ser	Ser	Leu	Ser
Lys 65	Ser	Leu	Ser	Lys	Thr 70	Ser	Thr	Ser	Ser	Ser 75	Trp	Pro	Gly	Thr	Asp 80

Val	Thr	Ile	Thr	Ser 85	Lys	Thr	Ser	Phe	Gln 90	Arg	Gly	Leu	Arg	Ser 95	Ser
Arg	Thr	Thr	Trp 100	Leu	Arg	Lys	Leu	Arg 105	Pro	Ala	Asn	Phe	Ser 110	Leu	Thr

<210> 448
<400> 448
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<210> 449
<400> 449
000

<210> 450
<400> 450
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<210> 451
<211> 56
<212> PRT
<213> homo sapiens

<400> 451

Phe 1	Phe	Phe	Phe	Phe 5	Val	Glu	Thr	Gly	Phe 10	Arg	His	Val	Asp	Glu 15	Thr
Gly	Leu	Glu	Leu 20	Leu	Ala	Ser	Ser	Asp 25	Leu	Pro	Pro	Gln	Leu 30	Leu	Lys
Val	Leu	Gly 35	Leu	Tyr	Arg	His	Glu 40	Pro	Leu	Ser	Leu	Ala 45	Leu	Lys	Arg
Phe	Ser 50	Gln	Arg	Pro	Ser	Val 55	Arg								

<210> 452
<211> 56
<212> PRT
<213> homo sapiens

<400> 452

Ile 1	Arg	Phe	Gly	Ile 5	Ser	Cys	Pro	Gly	Pro 10	Gly	Ile	Ser	Leu	Gln 15	Glu
Pro	Leu	Pro	Leu 20	Cys	Trp	Arg	His	Ser 25	Phe	Arg	Ile	Arg	Arg 30	Arg	Arg
Glu	Lys	Arg 35	Lys	Cys	Lys	Gly	Gly 40	Arg	Ser	Phe	Pro	Gly 45	Arg	Thr	Ile
Ser	Val 50	Thr	His	Met	Asp	Pro 55	Arg								

<210> 453
<211> 57
<212> PRT
<213> homo sapiens

<400> 453

Val 1	Thr	Glu	Met	Val 5	Arg	Pro	Gly	Lys	Asp 10	Leu	Pro	Pro	Leu	His 15	Phe
Leu	Phe	Ser	Leu 20	Leu	Leu	Leu	Ile	Leu 25	Lys	Leu	Cys	Leu	Gln 30	Gln	Arg
Gly	Arg	Gly 35	Ser	Cys	Arg	Glu	Ile 40	Pro	Gly	Pro	Gly	Gln 45	Glu	Met	Pro
Asn	Leu 50	Ile	Tyr	Leu	Thr	Glu 55	Gly	Leu							

<210> 454
 <211> 80
 <212> PRT
 <213> homo sapiens

<400> 454

Ile 1	Leu	Ala	Phe	Trp 5	Arg	Ala	Ala	Pro	Leu 10	Trp	His	His	Gln	Thr 15	Leu
Leu	Cys	Phe	Pro 20	Ser	Thr	Trp	Asn	Ser 25	Ser	Asn	Ile	Arg	Gly 30	Cys	Glu
Gly	Leu	Ala 35	Ile	Leu	Leu	Ser	Trp 40	Val	His	Val	Ser	Asp 45	Arg	Asn	Gly
Ala	Ala 50	Trp	Glu	Arg	Ser	Pro 55	Ser	Phe	Thr	Phe	Ser 60	Leu	Leu	Pro	Pro
Pro 65	Pro	Tyr	Ser	Lys	Thr 70	Val	Pro	Pro	Thr	Glu 75	Gly	Gln	Gly	Leu	Leu 80

<210> 455
 <211> 182
 <212> PRT
 <213> homo sapiens

<400> 455

Ala 1	Arg	Leu	Pro	Leu 5	Leu	Ala	Ala	Glu	Asp 10	Arg	Gly	Gln	Pro	Gly 15	Ser
Val	Lys	Asp	Pro 20	Lys	Met	Ala	Gly	Arg 25	Lys	Leu	Ala	Leu	Lys 30	Thr	Ile
Asp	Trp	Val 35	Ala	Phe	Ala	Glu	Ile 40	Ile	Pro	Gln	Asn	Gln 45	Lys	Ala	Ile
Ala	Ser 50	Ser	Leu	Lys	Ser	Trp 55	Asn	Glu	Thr	Leu	Thr 60	Ser	Arg	Leu	Ala
Ala 65	Leu	Pro	Glu	Asn	Pro 70	Pro	Ala	Ile	Asp	Trp 75	Ala	Tyr	Tyr	Lys	Ala 80
Asn	Val	Ala	Lys 85	Gly	Leu	Val	Asp	Asp 90	Phe	Glu	Lys	Lys	Phe 95	Asn	
Ala	Leu	Lys	Val 100	Pro	Val	Pro	Glu	Asp 105	Lys	Tyr	Thr	Ala	Gln 110	Val	Asp

Ala	Glu	Glu	Lys	Glu	Asp	Val	Lys	Ser	Cys	Ala	Glu	Trp	Val	Ser	Leu
		115					120					125			
Ser	Lys	Ala	Arg	Ile	Val	Glu	Tyr	Glu	Lys	Glu	Met	Glu	Lys	Met	Lys
	130					135					140				
Asn	Leu	Ile	Pro	Phe	Asp	Gln	Met	Thr	Ile	Glu	Asp	Leu	Asn	Glu	Ala
	145				150					155					160
Phe	Pro	Glu	Thr	Lys	Leu	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr	Trp	Pro	His
				165					170					175	
Gln	Pro	Ile	Glu	Asn	Leu										
			180												

<210> 456
 <211> 76
 <212> PRT
 <213> homo sapiens

<400> 456

Ala	Gln	Ser	Ile	Ala	Gly	Gly	Phe	Ser	Gly	Lys	Ala	Ala	Asn	Leu	Glu
1				5					10					15	
Val	Arg	Val	Ser	Phe	Gln	Asp	Phe	Arg	Glu	Leu	Ala	Met	Ala	Phe	Trp
			20					25					30		
Phe	Trp	Gly	Met	Ile	Ser	Ala	Lys	Ala	Thr	Gln	Ser	Met	Val	Phe	Arg
		35					40					45			
Ala	Ser	Phe	Arg	Pro	Ala	Ile	Leu	Gly	Ser	Phe	Thr	Asp	Pro	Gly	Cys
	50					55					60				
Pro	Arg	Ser	Ser	Ala	Ala	Ser	Asn	Gly	Ser	Arg	Ala				
65					70					75					

<210> 457
 <211> 104
 <212> PRT
 <213> homo sapiens

<400> 457

Cys	Pro	Glu	Cys	Val	Ile	Gln	Gly	Pro	Glu	Leu	Pro	Pro	Gly	Leu	Asn
1				5					10					15	
Phe	Ile	Asn	Ser	Gln	Leu	Val	Gly	Glu	Ala	Asn	Arg	Asp	Thr	Phe	Ser
			20					25					30		
Cys	Leu	Ile	Trp	Phe	Leu	Gly	Lys	Leu	His	Ser	Ser	Pro	Gln	Trp	Ser
		35					40					45			
Ser	Asp	Gln	Met	Glu	Leu	Ser	Ser	Ser	Ser	Pro	Ser	Leu	Ser	His	
	50					55				60					
Ile	Leu	Gln	Ser	Trp	Pro	Leu	Arg	Glu	Thr	Pro	Thr	Gln	His	Lys	Ile
65					70					75				80	
Ser	His	Leu	Leu	Phe	Leu	Arg	His	Pro	Pro	Gly	Gln	Tyr	Ile	Tyr	Pro
				85					90					95	
Leu	Ala	Arg	Glu	Pro	Ser	Ala	His								

<210> 458
 <211> 223
 <212> PRT
 <213> homo sapiens

<400> 458

Arg 1	Gly	Ala	Gly	Gly 5	His	Gln	Gly	Glu	Ser 10	Gly	Arg	Pro	Glu	Gly 15	Trp
Pro	Pro	Pro	Phe 20	Leu	His	Pro	Arg	Gly 25	Arg	Phe	Gln	Val	Pro 30	Trp	Leu
Glu	Ser	Val 35	Leu	Ile	Val	Val	Ser 40	Asn	Asn	Ile	Asp	Glu 45	Glu	Ala	Leu
Ala	Arg 50	Leu	Ala	Gln	Glu	Gly 55	Ser	Glu	Val	Asn	Val 60	Ile	Gly	Ile	Gly
Thr 65	Ser	Val	Val	Thr	Cys 70	Pro	Gln	Gln	Pro	Ser 75	Leu	Gly	Gly	Val	Tyr 80
Lys	Leu	Val	Ala	Val 85	Gly	Gly	Gln	Pro	Arg 90	Met	Lys	Leu	Thr	Glu 95	Asp
Pro	Glu	Lys	Gln 100	Thr	Leu	Pro	Gly	Ser 105	Lys	Ala	Ala	Phe	Arg 110	Leu	Leu
Gly	Ser	Asp 115	Gly	Ser	Pro	Leu	Met 120	Asp	Met	Leu	Gln	Leu 125	Ala	Glu	Glu
Pro	Val 130	Pro	Gln	Ala	Gly	Gln 135	Glu	Leu	Arg	Val	Trp 140	Pro	Pro	Gly	Ala
Gln 145	Glu	Pro	Cys	Thr	Val 150	Arg	Pro	Ala	Gln	Val 155	Glu	Pro	Leu	Leu	Arg 160
Leu	Cys	Leu	Gln 165	Gln	Gly	Gln	Leu	Cys	Glu 170	Pro	Leu	Pro	Ser	Leu 175	Ala
Glu	Ser	Arg	Ala 180	Leu	Ala	Gln	Leu	Ser 185	Leu	Ser	Arg	Leu	Ser 190	Pro	Glu
His	Arg	Arg 195	Leu	Arg	Ser	Pro	Ala 200	Gln	Tyr	Gln	Val	Val 205	Leu	Ser	Glu
Arg	Leu 210	Gln	Ala	Leu	Val	Asn 215	Ser	Leu	Cys	Ala	Gly 220	Gln	Ser	Pro	

<210> 459
 <211> 157
 <212> PRT
 <213> homo sapiens

<400> 459

Val 1	Ile	Arg	Val	Val 5	Ser	Ser	Gln	Pro	Arg 10	Ser	Glu	Ser	Gln	Gly 15	Asp
Cys	Pro	Ala	His 20	Arg	Leu	Phe	Thr	Arg 25	Ala	Cys	Ser	Leu	Ser 30	Asp	Ser

Thr	Thr	Trp	Tyr	Cys	Ala	Gly	Leu	Arg	Ser	Arg	Leu	Cys	Ser	Gly	Leu
		35					40					45			
Ser	Arg	Leu	Arg	Asp	Ser	Trp	Ala	Lys	Ala	Leu	Asp	Ser	Ala	Arg	Asp
	50					55					60				
Gly	Ser	Gly	Ser	His	Ser	Cys	Pro	Cys	Trp	Arg	Gln	Ser	Arg	Ser	Ser
	65				70					75					80
Gly	Ser	Thr	Trp	Ala	Gly	Leu	Thr	Val	Gln	Gly	Ser	Trp	Ala	Pro	Gly
				85					90					95	
Gly	His	Thr	Leu	Ser	Ser	Cys	Pro	Ala	Cys	Gly	Thr	Gly	Ser	Ser	Ala
			100					105					110		
Asn	Cys	Ser	Met	Ser	Met	Ser	Gly	Asp	Pro	Ser	Glu	Pro	Arg	Ser	Arg
		115					120					125			
Lys	Ala	Ala	Leu	Leu	Pro	Gly	Asn	Val	Cys	Phe	Ser	Gly	Ser	Ser	Val
	130					135					140				
Ser	Phe	Ile	Arg	Gly	Trp	Pro	Pro	Thr	Ala	Thr	Ser	Leu			
	145				150					155					

<210> 460
 <211> 93
 <212> PRT
 <213> homo sapiens

Pro	Pro	Leu	Phe	Pro	His	Leu	Leu	Phe	Leu	Trp	Gly	Lys	Val	Ser	Asp
1				5					10					15	
Ser	Cys	Cys	Phe	Gln	Ser	Ala	Pro	Leu	Arg	Val	Ser	Gly	Gly	Leu	Pro
			20					25					30		
Arg	Thr	Gln	Thr	Val	His	Gln	Gly	Leu	Gln	Pro	Leu	Gly	Gln	His	His
		35					40					45			
Leu	Val	Leu	Cys	Arg	Ala	Pro	Gln	Pro	Pro	Val	Leu	Arg	Ala	Glu	Ser
	50					55					60				
Ala	Gln	Gly	Gln	Leu	Gly	Gln	Gly	Ser	Arg	Leu	Cys	Gln	Gly	Trp	Glu
	65				70					75					80
Arg	Leu	Thr	Gln	Leu	Ser	Leu	Leu	Glu	Ala	Glu	Pro	Gln			
				85					90						

<210> 461
 <211> 328
 <212> PRT
 <213> homo sapiens

Phe	Ser	Leu	Ile	Leu	Cys	Lys	His	Ser	Ile	Gly	Asp	Arg	Lys	Asn	Tyr
1				5					10					15	
Ala	Ser	Ala	Lys	Leu	Ser	Glu	Leu	Leu	Pro	Glu	Glu	Val	Glu	Ala	Glu
			20					25					30		

Val	Lys	Ala	Ala	Ala	Glu	Ile	Ser	Met	Gly	Thr	Glu	Val	Ser	Glu	Glu
		35					40					45			
Asp	Ile	Cys	Asn	Ile	Leu	His	Leu	Cys	Thr	Gln	Val	Ile	Glu	Ile	Ser
	50					55					60				
Glu	Tyr	Arg	Thr	Gln	Leu	Tyr	Glu	Tyr	Leu	Gln	Asn	Arg	Met	Met	Ala
	65				70					75					80
Ile	Ala	Pro	Asn	Val	Thr	Val	Met	Val	Gly	Glu	Leu	Val	Gly	Ala	Arg
				85					90					95	
Leu	Ile	Ala	His	Ala	Gly	Ser	Leu	Leu	Asn	Leu	Ala	Lys	His	Ala	Ala
			100					105					110		
Ser	Thr	Val	Gln	Ile	Leu	Gly	Ala	Glu	Lys	Ala	Leu	Phe	Arg	Ala	Leu
		115					120					125			
Lys	Ser	Arg	Arg	Asp	Thr	Pro	Lys	Tyr	Gly	Leu	Ile	Tyr	His	Ala	Ser
	130					135					140				
Leu	Val	Gly	Gln	Thr	Ser	Pro	Lys	His	Lys	Gly	Lys	Ile	Ser	Arg	Met
	145				150					155					160
Leu	Ala	Ala	Lys	Thr	Val	Leu	Ala	Ile	Arg	Tyr	Asp	Ala	Phe	Gly	Glu
				165					170					175	
Asp	Ser	Ser	Ser	Ala	Met	Gly	Val	Glu	Asn	Arg	Ala	Lys	Leu	Glu	Ala
			180					185					190		
Arg	Leu	Arg	Thr	Leu	Glu	Asp	Arg	Gly	Ile	Arg	Lys	Ile	Ser	Gly	Thr
		195					200					205			
Gly	Lys	Ala	Leu	Ala	Lys	Thr	Glu	Lys	Tyr	Glu	His	Lys	Ser	Glu	Val
	210					215					220				
Lys	Thr	Tyr	Asp	Pro	Ser	Gly	Asp	Ser	Thr	Leu	Pro	Thr	Cys	Ser	Lys
	225				230					235					240
Lys	Arg	Lys	Ile	Glu	Gln	Val	Asp	Lys	Glu	Asp	Glu	Ile	Thr	Glu	Lys
				245					250					255	
Lys	Ala	Lys	Lys	Ala	Lys	Ile	Lys	Val	Lys	Val	Glu	Glu	Glu	Glu	Glu
			260					265					270		
Glu	Lys	Val	Ala	Glu	Glu	Glu	Glu	Thr	Ser	Val	Lys	Lys	Lys	Lys	Lys
		275					280					285			
Arg	Gly	Lys	Lys	Lys	His	Ile	Lys	Glu	Glu	Pro	Leu	Ser	Glu	Glu	Glu
	290					295					300				
Pro	Cys	Thr	Ser	Thr	Ala	Ile	Ala	Ser	Pro	Glu	Lys	Lys	Lys	Lys	Lys
	305				310					315					320
Lys	Lys	Lys	Arg	Glu	Asn	Glu	Asp								
				325											

<210> 462

<211> 124

<212> PRT

<213> homo sapiens

<400> 462

Tyr 1	Asn	Arg	Asn	Ser 5	Phe	Leu	Leu	Ile	Leu 10	Val	Leu	Ser	Leu	Phe 15	Phe
Leu	Phe	Leu	Leu 20	Phe	Leu	Trp	Thr	Ser 25	Asn	Cys	Cys	Ala	Gly 30	Thr	Trp
Phe	Phe	Leu 35	Arg	Lys	Trp	Phe	Phe 40	Leu	Asn	Val	Phe	Leu 45	Phe	Thr	Pro
Phe	Leu 50	Leu	Leu	Leu	His	Arg 55	Cys	Phe	Phe	Phe	Phe 60	Cys	His	Phe	Phe
Phe 65	Phe	Leu	Phe	Phe	Asn 70	Phe	Asn	Phe	Asn	Leu 75	Gly	Phe	Phe	Gly	Phe 80
Leu	Phe	Ser	Asn	Phe 85	Ile	Leu	Phe	Ile	Tyr 90	Leu	Phe	Tyr	Phe	Ala 95	Phe
Phe	Arg	Thr	Gly 100	Trp	Lys	Cys	Gly	Val 105	Thr	Arg	Arg	Ile	Val 110	Ser	Leu
His	Phe	Thr 115	Phe	Val	Phe	Ile	Phe 120	Phe	Cys	Phe	Cys				

<210> 463
 <211> 101
 <212> PRT
 <213> homo sapiens

<400> 463

Ser 1	Ser	Phe	Ser	Leu 5	Phe	Phe	Phe	Phe	Phe 10	Phe	Phe	Phe	Ser	Gly 15	Leu
Ala	Ile	Ala	Val 20	Leu	Val	His	Gly	Ser 25	Ser	Ser	Glu	Ser	Gly 30	Ser	Ser
Leu	Met	Cys 35	Phe	Phe	Leu	Pro	Leu 40	Phe	Phe	Phe	Phe	Phe 45	Thr	Asp	Val
Ser	Ser 50	Ser	Ser	Ala	Thr	Phe 55	Ser	Ser	Ser	Ser	Ser 60	Ser	Thr	Leu	Thr
Leu 65	Ile	Leu	Ala	Phe	Leu 70	Ala	Phe	Phe	Ser	Val 75	Ile	Ser	Ser	Ser	Leu 80
Ser	Thr	Cys	Ser	Ile 85	Leu	Arg	Phe	Leu	Glu 90	Gln	Val	Gly	Ser	Val 95	Glu
Ser	Pro	Glu	Gly 100	Ser											

<210> 464
 <211> 427
 <212> PRT
 <213> homo sapiens

<400> 464

Gly 1	Gly	Ser	Ser	Arg 5	Arg	His	Gly	Gly	Gly 10	Tyr	Ala	Ala	Val	Ala 15	Leu
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Leu	Val	Leu	Leu 20	Leu	Leu	Gly	Pro	Gly 25	Gly	Trp	Cys	Leu	Ala 30	Glu	Pro
Pro	Arg	Asp 35	Ser	Leu	Arg	Glu	Glu 40	Leu	Val	Ile	Thr	Pro 45	Leu	Pro	Ser
Gly	Asp 50	Val	Ala	Ala	Thr	Phe 55	Gln	Phe	Arg	Thr	Arg 60	Trp	Asp	Ser	Glu
Leu 65	Gln	Arg	Glu	Gly	Val 70	Ser	His	Tyr	Arg	Leu 75	Phe	Pro	Lys	Ala	Leu 80
Gly	Gln	Leu	Ile	Ser 85	Lys	Tyr	Ser	Leu	Arg 90	Glu	Leu	His	Leu	Ser 95	Phe
Thr	Gln	Gly	Phe 100	Trp	Arg	Thr	Arg	Tyr 105	Trp	Gly	Pro	Pro	Phe 110	Leu	Gln
Ala	Pro	Ser 115	Gly	Ala	Glu	Leu	Trp 120	Val	Trp	Phe	Gln	Asp 125	Thr	Val	Thr
Asp	Val 130	Asp	Lys	Ser	Trp	Lys 135	Glu	Leu	Ser	Asn	Val 140	Leu	Ser	Gly	Ile
Phe 145	Cys	Ala	Ser	Leu	Asn 150	Phe	Ile	Asp	Ser	Thr 155	Asn	Thr	Val	Thr	Pro 160
Thr	Ala	Ser	Phe	Lys 165	Pro	Leu	Gly	Leu	Ala 170	Asn	Asp	Thr	Asp	His 175	Tyr
Phe	Leu	Arg	Tyr 180	Ala	Val	Leu	Pro	Arg 185	Glu	Val	Val	Cys	Thr 190	Glu	Asn
Leu	Thr	Pro 195	Trp	Lys	Lys	Leu	Leu 200	Pro	Cys	Ser	Ser	Lys 205	Ala	Gly	Leu
Ser	Val 210	Leu	Leu	Lys	Ala	Asp 215	Arg	Leu	Phe	His	Thr 220	Ser	Tyr	His	Ser
Gln 225	Ala	Val	His	Ile	Arg 230	Pro	Val	Cys	Arg	Asn 235	Ala	Arg	Cys	Thr	Ser 240
Ile	Ser	Trp	Glu	Leu 245	Arg	Gln	Thr	Leu	Ser 250	Val	Val	Phe	Asp	Ala 255	Phe
Ile	Thr	Gly	Gln 260	Gly	Lys	Lys	Asp	Trp 265	Ser	Leu	Phe	Arg	Met 270	Phe	Ser
Arg	Thr	Leu 275	Thr	Glu	Pro	Cys	Pro 280	Leu	Ala	Ser	Glu	Ser 285	Arg	Val	Tyr
Val	Asp 290	Ile	Thr	Thr	Tyr	Asn 295	Gln	Asp	Asn	Glu	Thr 300	Leu	Glu	Val	His
Pro 305	Pro	Pro	Thr	Thr	Thr 310	Tyr	Gln	Asp	Val	Ile 315	Leu	Gly	Thr	Arg	Lys 320
Thr	Tyr	Ala	Ile	Tyr 325	Asp	Leu	Leu	Asp	Thr 330	Ala	Met	Ile	Asn	Asn 335	Ser
Arg	Asn	Leu	Asn 340	Ile	Gln	Leu	Lys	Trp 345	Lys	Arg	Pro	Pro	Glu 350	Asn	Glu

Ala	Pro	Pro	Val	Pro	Phe	Leu	His	Ala	Gln	Arg	Tyr	Val	Ser	Gly	Tyr
		355					360					365			
Gly	Leu	Gln	Lys	Gly	Glu	Leu	Ser	Thr	Leu	Leu	Tyr	Asn	Thr	His	Pro
	370					375					380				
Tyr	Arg	Ala	Phe	Pro	Val	Leu	Leu	Leu	Asp	Thr	Val	Pro	Trp	Tyr	Leu
	385				390					395					400
Arg	Leu	Leu	His	Pro	Leu	Pro	Ala	Cys	Pro	Gly	Pro	Ala	Ala	Thr	Pro
				405					410					415	
Pro	Pro	Gly	Asp	Ala	Asp	Ser	Ala	Ala	Gly	Gln					
			420					425							

<210> 465
 <211> 128
 <212> PRT
 <213> homo sapiens

<400> 465

Ser	Pro	Ser	Ile	Leu	Tyr	Gly	Ser	Cys	Thr	Cys	His	Ser	His	Lys	Ala
1				5					10					15	
Phe	Gly	Gly	Pro	Asp	Thr	Gly	Gly	His	Pro	Ser	Cys	Arg	Pro	His	Gln
			20					25					30		
Val	Gln	Ser	Cys	Gly	Ser	Gly	Ser	Lys	Thr	Leu	Ser	Leu	Met	Trp	Ile
		35					40					45			
Asn	Leu	Gly	Arg	Ser	Ser	Val	Met	Ser	Ser	Gln	Gly	Ser	Ser	Ala	Pro
	50					55					60				
Leu	Ser	Thr	Ser	Ser	Thr	Pro	Pro	Thr	Gln	Ser	Leu	Pro	Leu	Pro	Pro
	65				70					75					80
Ser	Asn	Pro	Trp	Val	Trp	Pro	Met	Thr	Leu	Thr	Thr	Thr	Phe	Cys	Ala
				85					90					95	
Met	Leu	Cys	Cys	Arg	Gly	Arg	Trp	Ser	Ala	Pro	Lys	Thr	Ser	Pro	Pro
			100					105					110		
Gly	Arg	Ser	Ser	Cys	Pro	Val	Val	Pro	Arg	Gln	Ala	Ser	Leu	Cys	Cys
		115					120					125			

<210> 466
 <211> 124
 <212> PRT
 <213> homo sapiens

<400> 466

Pro	Gln	Ala	Trp	Arg	Arg	Leu	Cys	Arg	Cys	Cys	Ser	Ala	Arg	Pro	Val
1				5					10					15	
Ala	Pro	Gly	Ala	Arg	Arg	Leu	Val	Pro	Cys	Arg	Thr	Pro	Thr	Arg	Gln
			20					25					30		
Pro	Ala	Gly	Gly	Thr	Cys	His	His	Pro	Ala	Ala	Phe	Arg	Gly	Arg	Ser
		35					40					45			
Arg	His	Ile	Pro	Val	Pro	His	Ala	Leu	Gly	Phe	Gly	Ala	Ser	Ala	Gly

50					55					60					
Arg 65	Ser	Val	Pro	Leu	Gln 70	Ala	Leu	Ser	Gln	Ser 75	Pro	Gly	Ala	Ala	Asp 80
Leu	Gln	Val	Phe	Ser 85	Thr	Gly	Ala	Ala	Pro 90	Val	Ile	His	Thr	Arg 95	Leu
Leu	Glu	Asp	Pro 100	Ile	Leu	Gly	Ala	Thr 105	Leu	Pro	Ala	Gly	Pro 110	Ile	Arg
Cys	Arg	Ala 115	Val	Gly	Leu	Val	Pro 120	Arg	His	Cys	His				

<210> 467

<211> 106

<212> PRT

<213> homo sapiens

<400> 467

Phe 1	Leu	His	Lys	Thr 5	His	Asn	Arg	Ala	Val 10	Glu	Glu	Ala	Lys	Glu 15	Pro
Phe	Leu	Cys	Leu 20	Cys	Ser	Arg	Thr	Glu 25	Arg	Gly	Pro	Leu	Ala 30	Ser	Val
Ser	Leu	Leu 35	Val	Leu	Pro	Gly	Leu 40	Tyr	Gln	Ala	Leu	Arg 45	Arg	Gly	Met
Glu	Thr 50	Pro	His	Ser	Gly	Ala 55	Trp	Leu	Gly	Glu	Gly 60	Glu	Ala	Ala	Gly
Val 65	Leu	Trp	Ala	Ser	Arg 70	Gly	Tyr	Asn	Leu	Ser 75	Ser	Leu	Gly	Asn	Val 80
Cys	Pro	Phe	Val	Gly 85	Ser	Ser	Pro	Thr	Arg 90	Arg	Gly	Thr	Gln	Leu 95	Tyr
Thr	Gly	Thr	Ile 100	Cys	Val	Trp	Ser	Val 105	Leu						

<210> 468

<211> 164

<212> PRT

<213> homo sapiens

<400> 468

Ile 1	Ser	Thr	Lys	Gln 5	Thr	Thr	His	Arg	Leu 10	Ser	Gln	Cys	Lys	Val 15	Glu
Ser	Pro	Asp	Val 20	Ser	Asp	Tyr	Cys	Leu 25	Gln	Met	Asp	Thr	Arg 30	Ser	Pro
Glu	Ser	Ser 35	Asp	Tyr	Thr	Leu	Glu 40	Lys	Pro	Lys	Glu	Pro 45	Leu	Pro	Pro
Pro	Leu 50	Pro	Gln	Ala	Arg	Pro 55	Gln	Ser	Gly	Ala	Phe 60	Pro	Tyr	Pro	Ala
Ser 65	Arg	Pro	Gly	Thr	Val 70	Arg	Glu	Glu	Pro	Ala 75	Gly	Ser	Arg	Trp	Pro 80

Glu	Gly	Leu	Ser	Gln 85	Ser	Tyr	Tyr	Arg	Gly 90	Ile	Lys	Arg	Ala	Pro 95	Leu	
Leu	Pro	Pro	Gln 100	Pro	Cys	Cys	Glu	Ser 105	Cys	Ala	Gly	Ile	Asn 110	Leu	Arg	
Asn	Ser	Pro 115	Glu	Ala	Glu	Thr	Gly 120	Leu	Met	Pro	Trp	Glu 125	Arg	Ser	Glu	
Cys	Glu 130	Pro	Met	Ala	Pro	Ser 135	Leu	Leu	Gly	Thr	Asn 140	Leu	Pro	Lys	Tyr	
Val 145	Lys	Ala	Glu	Gly	Asp 150	Arg	Asp	Leu	Ala	Glu 155	Gly	Arg	Lys	Ser	Phe 160	
Ser	Ser	Arg	Asn													

<210> 469
 <211> 108
 <212> PRT
 <213> homo sapiens

<400> 469

Glu 1	Ile	Arg	Gly	Arg 5	Pro	Pro	Leu	Phe	Met 10	Pro	Pro	Leu	Ser	Cys 15	Val	
Asp	Glu	Phe	Leu 20	Gln	Asn	Arg	Pro	His 25	Thr	Asp	Cys	Pro	Ser 30	Val	Lys	
Leu	Ser	Pro 35	Pro	Thr	Cys	Arg	Thr 40	Thr	Ala	Tyr	Lys	Trp 45	Thr	His	Val	
Pro	Gln 50	Arg	Ala	Gln	Ile	Ile 55	Pro	Ser	Arg	Ser	Pro 60	Lys	Asn	Pro	Cys	
Arg 65	Leu	Pro	Phe	Pro	Lys 70	Pro	Gly	Pro	Arg	Val 75	Gly	Arg	Phe	His	Thr 80	
Pro	Pro	Gln	Gly	Leu 85	Val	Gln	Ser	Gly	Lys 90	Asn	Gln	Gln	Ala	His 95	Ala	
Gly	Gln	Arg	Ala 100	Ser	Leu	Ser	Pro	Thr 105	Thr	Glu	Ala					

<210> 470
 <211> 317
 <212> PRT
 <213> homo sapiens

<400> 470

Asn 1	Met	Val	Asp	Tyr 5	Tyr	Glu	Val	Leu	Gly 10	Val	Gln	Arg	His	Ala 15	Ser	
Pro	Glu	Asp	Ile 20	Lys	Lys	Ala	Tyr	Arg 25	Lys	Leu	Ala	Leu	Lys 30	Trp	His	
Pro	Asp	Lys 35	Asn	Pro	Glu	Asn	Lys 40	Glu	Glu	Ala	Glu	Arg 45	Lys	Phe	Lys	
Gln	Val	Ala	Glu	Ala	Tyr	Glu	Val	Leu	Ser	Asp	Ala	Lys	Lys	Arg	Asp	

50				55				60							
Ile 65	Tyr	Asp	Lys	Tyr	Gly 70	Lys	Glu	Gly	Leu	Asn 75	Gly	Gly	Gly	Gly	Gly 80
Gly	Ser	His	Phe	Asp 85	Ser	Pro	Phe	Glu	Phe 90	Gly	Phe	Thr	Phe	Arg 95	Asn
Pro	Asp	Asp	Val 100	Phe	Arg	Glu	Phe	Phe 105	Gly	Gly	Arg	Asp	Pro 110	Phe	Ser
Phe	Asp	Phe 115	Phe	Glu	Asp	Pro	Phe 120	Glu	Asp	Phe	Phe	Gly 125	Asn	Arg	Arg
Gly	Pro 130	Arg	Gly	Ser	Arg	Ser 135	Arg	Gly	Thr	Gly	Ser 140	Phe	Phe	Ser	Ala
Phe 145	Ser	Gly	Phe	Pro	Ser 150	Phe	Gly	Ser	Gly	Phe 155	Ser	Ser	Phe	Asp	Thr 160
Gly	Phe	Thr	Ser	Phe 165	Gly	Ser	Leu	Gly	His 170	Gly	Gly	Leu	Thr	Ser 175	Phe
Ser	Ser	Thr	Ser 180	Phe	Gly	Gly	Ser	Gly 185	Met	Gly	Asn	Phe	Lys 190	Ser	Ile
Ser	Thr	Ser 195	Thr	Lys	Met	Val	Asn 200	Gly	Arg	Lys	Ile	Thr 205	Thr	Lys	Arg
Ile 210	Val	Glu	Asn	Gly	Gln	Glu 215	Arg	Val	Glu	Val	Glu 220	Glu	Asp	Gly	Gln
Leu 225	Lys	Ser	Leu	Thr 230	Ile	Asn	Gly	Val	Ala	Asp 235	Asp	Asp	Ala	Leu	Ala 240
Glu	Glu	Arg	Met	Arg 245	Arg	Gly	Gln	Asn	Ala 250	Leu	Pro	Ala	Gln	Pro 255	Ala
Gly	Leu	Arg	Pro 260	Pro	Lys	Pro	Pro	Arg 265	Pro	Ala	Ser	Leu	Leu 270	Arg	His
Ala	Pro	His 275	Cys	Leu	Ser	Glu	Glu 280	Glu	Gly	Glu	Gln	Asp 285	Arg	Pro	Gly
Ala	Pro 290	Gly	Pro	Trp	Asp	Pro 295	Leu	Gly	Val	Arg	Ser 300	Arg	Ile	Glu	Arg
Arg 305	Trp	Gln	Glu	Glu	Glu 310	Ala	Glu	Ala	Glu	Arg 315	Gly	Val			

<210> 471

<211> 123

<212> PRT

<213> homo sapiens

<400> 471

Ser 1	Met	Pro	Leu	Val 5	Gln	Leu	Pro	Ser	Ser 10	Phe	Lys	Leu	Leu	Ser 15	Leu
Leu	Leu	Leu	Leu 20	Pro	Leu	Ala	Thr	Phe 25	Phe	Gln	Ser	Cys	Cys 30	Gly	Arg

Arg	Gly	Gly	Pro	Arg	Ala	Arg	Val	Pro	Gln	Val	Gly	Pro	Ala	Arg	Pro
		35					40					45			
Pro	Pro	Gln	Arg	Asp	Ser	Glu	Ala	Arg	Val	Ser	Ala	Ala	Arg	Gln	Ala
	50					55					60				
Gly	Ala	Ala	Ser	Ala	Gly	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Ala	Gly	Arg
	65				70					75					80
Ser	Gly	Leu	Ser	Ala	Cys	Ala	Pro	Gln	Arg	Gly	His	Arg	Arg	Arg	Pro
				85					90					95	
His	His	Leu	Leu	Leu	Arg	Thr	Leu	Thr	Gly	His	Leu	Leu	Gln	Leu	Leu
			100					105					110		
Leu	Phe	Leu	Asp	Arg	Ser	Arg	Gln	Phe	Ser	Leu					
		115					120								

<210> 472
 <211> 105
 <212> PRT
 <213> homo sapiens

<400> 472

Lys	Ile	Arg	Ser	Asn	Gln	Cys	Leu	Trp	Ser	Asn	Phe	Leu	Pro	Pro	Ser
1				5					10					15	
Asn	Ser	Ser	Leu	Cys	Phe	Cys	Phe	Phe	Leu	Leu	Pro	Pro	Ser	Phe	Asn
			20					25					30		
Pro	Ala	Ala	Asp	Ala	Glu	Gly	Val	Pro	Gly	Pro	Gly	Cys	Pro	Arg	Ser
		35					40					45			
Val	Leu	Leu	Ala	Leu	Leu	Leu	Arg	Glu	Thr	Val	Arg	Arg	Val	Ser	Gln
	50					55					60				
Gln	Arg	Gly	Arg	Pro	Gly	Arg	Leu	Arg	Arg	Ala	Glu	Ala	Gly	Arg	Leu
	65				70					75					80
Gly	Trp	Gln	Gly	Val	Leu	Ala	Ser	Pro	His	Ala	Leu	Leu	Ser	Glu	Gly
				85					90					95	
Ile	Val	Val	Gly	His	Thr	Ile	Tyr	Cys							
			100					105							

<210> 473
 <211> 159
 <212> PRT
 <213> homo sapiens

<400> 473

Ile	Val	Ser	Glu	Arg	Ser	Leu	Arg	Ser	Leu	Trp	Thr	Ala	His	Trp	Ala
1				5					10					15	
Leu	Pro	Glu	Met	Asp	Ser	Arg	Ile	Pro	Tyr	Asp	Asp	Tyr	Pro	Val	Val
			20					25					30		
Phe	Leu	Pro	Ala	Tyr	Glu	Asn	Pro	Pro	Ala	Trp	Ile	Pro	Pro	His	Glu
		35					40					45			
Arg	Val	His	His	Pro	Asp	Tyr	Asn	Asn	Glu	Leu	Thr	Gln	Phe	Leu	Pro

50

55

60

Arg Thr Ile Thr Leu Lys Lys Pro Pro Gly Ala Gln Leu Gly Phe Asn
65 70 75 80

Ile Arg Gly Gly Lys Ala Ser Gln Leu Gly Ile Phe Ile Ser Lys Val
85 90 95

Ile	Pro	Asp	Ser	Asp	Ala	His	Arg	Ala	Gly	Leu	Gln	Glu	Gly	Asp	Gln
			100					105					110		

Val	Leu	Ala	Val	Asn	Asp	Val	Asp	Phe	Gln	Asp	Ile	Glu	His	Ser	Lys
		115					120					125			

Ala Val Glu Ile Leu Lys Thr Ala Arg Glu Ile Ser Met Arg Val Arg
130 135 140

Phe Phe Pro Tyr Asn Tyr His Arg Gln Lys Glu Arg Thr Val His
145 150 155

<210> 474

<211> 75

<212> PRT

<213> homo sapiens

<400> 474

Pro 1 Pro Thr Gly Arg 5 Pro Pro Pro Phe Phe 10 Phe Phe Phe Phe Phe 15 Phe

Phe Ser Ile Val Phe Tyr Phe Leu Gly Glu Arg Leu Gly Gly Gly Arg
20 25 30

Gly Glu Asn Ser Val Ser Leu Glu Ser Gln Lys Cys Met Asn Leu Leu
35 40 45

Val	Val	Gln	Gly	Trp	Asp	Lys	Met	Ala	Arg	Glu	Val	Arg	Trp	Lys	Ile
	50					55					60				

Pro	Lys	Ile	Leu	Phe	Ala	Thr	Asp	Phe	Tyr	Asn
65					70					75

<210> 475

<211> 97

<212> PRT

<213> homo sapiens

<400> 475

Leu Gly Gly Leu Ser Ser Ser Asp Val Lys Ser Gln Leu Ser Ser Arg
1 5 10 15

Arg Leu Leu Gln Cys Asp Gly Ser Gly Gln Lys Leu Gly Gln Leu Ile
20 25 30

Val	Val	Val	Arg	Val	Val	Tyr	Pro	Leu	Met	Arg	Arg	Asn	Pro	Cys	Trp
		35					40					45			

Arg Ile Leu Ile Gly Arg Gln Glu Asn His Arg Val Val Ile Ile Arg
50 55 60

Asn 65 Pro Ala Val His Leu 70 Gly Gln Gly Pro Val 75 Gly Ser Pro Gln Arg 80

Pro Gln Thr Pro Leu Thr Asp Asn Ser Val Trp Glu Pro Glu Ala Asp
85 90 95

Ala

<210> 476

<211> 274

<212> PRT

<213> homo sapiens

<400> 476

Gly 1	His	Leu	Trp	Arg 5	Pro	Ala	Gly	Gly	Arg 10	Leu	Pro	Arg	His	His 15	Asp
Gln	Val	Cys	Arg 20	Ala	Ala	Glu	Pro	His 25	Arg	Gly	Gly	Gly	Leu 30	Cys	Gly
His	Gln	Arg 35	Arg	Leu	Pro	His	Arg 40	Pro	Arg	Val	Gln	Glu 45	Gly	Trp	Gly
Leu	Cys 50	Pro	His	Glu	Ser	Leu 55	His	Gln	Val	Pro	Ala 60	Asp	Arg	Pro	Trp
His 65	Glu	Pro	Gly	Ala	Gly 70	Cys	Ala	Ala	Asp	Cys 75	Glu	Asp	Pro	His	Arg 80
Arg	Pro	Gly	Ala	Cys 85	Glu	Pro	Gly	Ala	Pro 90	Pro	Ala	Ala	Arg	Ala 95	Ala
Gly	Leu	Gly	Arg 100	Gly	Thr	Arg	His	Gly 105	Asn	Gly	Asp	Ile	Leu 110	Ser	Phe
Glu	Asp	Ala 115	Asn	Arg	Ala	Met	Gln 120	Thr	Gly	Val	Thr	Gly 125	Ile	Met	Ile
Ala	Arg 130	Gly	Ala	Leu	Leu	Lys 135	Pro	Trp	Leu	Phe	Thr 140	Glu	Ile	Lys	Glu
Gln 145	Arg	His	Trp	Asp	Ile 150	Ser	Ser	Ser	Glu	Arg 155	Leu	Asp	Ile	Leu	Arg 160
Asp	Phe	Thr	Asn	Tyr 165	Gly	Leu	Glu	His	Trp 170	Gly	Ser	Asp	Thr	Gln 175	Gly
Val	Glu	Lys	Thr 180	Arg	Arg	Phe	Leu	Leu 185	Glu	Trp	Leu	Ser	Phe 190	Leu	Cys
Arg	Tyr	Asp 195	Pro	Val	Gly	Leu	Leu 200	Glu	Arg	Leu	Pro	Gln 205	Arg	Ile	Asn
Glu	Arg 210	Pro	Pro	Tyr	Tyr	Leu 215	Gly	Arg	Asp	Tyr	Leu 220	Glu	Thr	Leu	Met
Ala 225	Ser	Gln	Lys	Ala	Ala 230	Asp	Trp	Ile	Arg	Ile 235	Ser	Glu	Met	Leu	Leu 240
Gly	Pro	Val	Pro	Pro 245	Thr	Ser	Pro	Ser	Cys 250	Arg	Ser	Thr	Arg	Pro 255	Thr
Arg	Thr	Ser	Ser 260	Leu	Arg	Leu	Ser	Gln 265	Gly	His	Pro	Gly	Ala 270	Arg	Arg

Val Gln

<210> 477
<211> 256
<212> PRT
<213> homo sapiens

<400> 477

Ala 1	Gly	Pro	Ala	Pro 5	Val	Gln	Pro	Gly	Pro 10	His	Thr	Arg	Cys	Arg 15	Cys
Pro	Arg	Gly	His 20	Gly	Ser	Arg	Gly	Arg 25	Ser	Gln	Ala	Gly	Lys 30	Leu	Trp
Cys	Pro	Ala 35	Gly	Pro	Arg	Arg	Pro 40	Gly	Thr	Ser	Thr	Pro 45	Pro	Ser	Ser
Pro	Val 50	Arg	Thr	Cys	Gly	Pro 55	Leu	Thr	Asp	Glu	Asp 60	Val	Val	Arg	Leu
Arg 65	Pro	Cys	Glu	Lys	Lys 70	Arg	Leu	Asp	Ile	Arg 75	Gly	Lys	Leu	Tyr	Leu 80
Ala	Pro	Leu	Thr	Thr 85	Cys	Gly	Asn	Leu	Pro 90	Phe	Arg	Arg	Ile	Cys 95	Lys
Arg	Phe	Gly	Ala 100	Asp	Val	Thr	Cys	Gly 105	Glu	Met	Ala	Val	Cys 110	Thr	Asn
Leu	Leu	Gln	Gly	Gln	Met	Ser	Glu 120	Trp	Ala	Leu	Leu	Lys 125	Arg	His	Gln
Cys	Glu 130	Asp	Ile	Phe	Gly	Val 135	Gln	Leu	Glu	Gly	Ala 140	Phe	Pro	Asp	Thr
Met 145	Thr	Lys	Cys	Ala	Glu 150	Leu	Leu	Ser	Arg	Thr 155	Val	Glu	Val	Asp	Phe 160
Val	Asp	Ile	Asn	Val 165	Gly	Cys	Pro	Ile	Asp 170	Leu	Val	Tyr	Lys	Lys 175	Gly
Gly	Gly	Cys	Ala 180	Leu	Met	Asn	Arg	Ser 185	Thr	Lys	Phe	Gln	Gln 190	Ile	Val
Arg	Gly	Met 195	Asn	Gln	Val	Leu	Asp 200	Val	Pro	Leu	Thr	Val 205	Lys	Ile	Arg
Thr	Gly 210	Val	Gln	Glu	Arg	Val 215	Asn	Leu	Ala	His	Arg 220	Leu	Leu	Pro	Glu
Leu 225	Arg	Asp	Trp	Gly	Val 230	Ala	Leu	Val	Thr	Glu 235	Met	Gly	Thr	Ser	Cys 240
His	Leu	Arg	Met	Pro 245	Thr	Ala	Pro	Cys	Arg 250	Leu	Val	Ser	Pro	Gly 255	Ser

<210> 478
<211> 165
<212> PRT
<213> homo sapiens

<400> 478

Asn 1	Leu	Leu	Tyr	Ser 5	Pro	Arg	Pro	Arg	Val 10	Pro	Leu	Gly	Lys	Pro 15	Glu
Ala	Thr	Cys	Thr 20	Arg	Trp	Pro	Cys	Ala 25	Ser	Ala	Arg	Arg	Arg 30	Gly	Gly
Gly	His	Trp 35	Pro	Lys	Glu	His	Leu 40	Ala	Asp	Ala	Asp	Pro 45	Val	Gly	Cys
Leu	Leu 50	Ala	Gly	His	Gln	Arg 55	Leu	Gln	Val	Val	Ala 60	Ala	Gln	Val	Val
Gly 65	Arg	Pro	Leu	Val	Asp 70	Pro	Leu	Trp	Glu	Pro 75	Leu	Gln	Gln	Pro	His 80
Gly	Ile	Val	Pro	Ala 85	Gln	Glu	Gly	Gln	Pro 90	Leu	Glu	Gln	Lys	Ala 95	Pro
Gly	Leu	Leu	His 100	Ala	Leu	Arg	Val	Arg 105	Ala	Pro	Val	Leu	Gln 110	Ala	Val
Val	Gly	Glu 115	Val	Pro	Gln	Asp	Val 120	Gln	Ala	Leu	Gly	Arg 125	Arg	Asp	Val
Pro	Val 130	Pro	Leu	Leu	Leu	Asp 135	Leu	Arg	Glu	Glu	Pro 140	Arg	Leu	Glu	Gln
Gly 145	Ala	Thr	Gly	Asn	His 150	Asp	Pro	Gly	Asp	Thr 155	Ser	Leu	His	Gly	Ala 160
Val	Gly	Ile	Leu	Lys 165											

<210> 479

<211> 262

<212> PRT

<213> homo sapiens

<400> 479

Gly 1	Ser	Pro	Met	Ser 5	Pro	Ala	Arg	Ala	Met 10	Gln	Thr	Leu	Phe	Val 15	Pro
Glu	His	Gly	Asp 20	His	Gly	Ala	Gly	Val 25	Cys	Ser	Asp	His	His 30	His	Arg
Gly	Gly	His 35	Val	Pro	Ala	Glu	Pro 40	Leu	Gln	Ala	Val	Cys 45	Thr	Val	Leu
His	Gln 50	Pro	Ala	Gln	Pro	Gly 55	Ala	Glu	Glu	Arg	Arg 60	Cys	Pro	Val	Leu
Arg 65	Arg	Met	Pro	Val	Ala 70	Ser	Glu	Thr	Gln	Cys 75	Gln	Ala	Thr	Glu	Ser 80
Gln	Ser	Arg	Ser	Leu 85	Thr	Pro	Arg	Leu	Gly 90	Pro	Pro	Thr	Ala	Trp 95	Pro
Cys	Ala	Leu	Arg 100	Pro	Ala	Glu	Arg	Phe 105	Pro	Pro	Leu	Pro	Ala 110	Gln	Cys

Leu	Leu	His	Val	Gln	Leu	Gln	Thr	Leu	Phe	Val	Pro	Glu	His	Gly	Asp
		115					120					125			
His	Gly	Ala	Gly	Val	Cys	Ser	Asp	His	His	His	Arg	Gly	Gly	His	Val
	130					135					140				
Pro	Ala	Glu	Pro	Leu	Gln	Ala	Val	Cys	Thr	Val	Leu	His	Gln	Pro	Ala
145					150					155					160
Gln	Pro	Gly	Ala	Glu	Glu	Arg	Arg	Cys	Pro	Val	Leu	Arg	Arg	Met	Pro
				165					170					175	
Val	Ala	Leu	Gly	Glu	His	Ser	Val	Arg	Gln	Arg	Asn	Pro	Arg	Ala	Ala
			180					185					190		
Gly	Leu	Arg	Pro	Ala	Ser	Ala	His	Arg	Pro	Pro	Gly	Arg	Ala	Ala	Leu
		195					200					205			
Arg	Pro	Ala	Gly	Ala	Leu	Pro	Pro	Leu	Pro	Ala	His	Leu	Ser	Val	Pro
	210					215					220				
Ala	Ala	Arg	Asp	Arg	Pro	Ala	Ala	His	His	Leu	Ala	Val	Arg	Arg	Gly
225					230					235					240
Gly	Ala	Pro	Thr	Leu	Pro	Gly	Pro	Leu	Asp	Leu	Gln	Gly	Ser	Gly	Pro
				245					250					255	
Arg	Gly	Gly	Val	Gly	Asn										
			260												

<210> 480

<211> 270

<212> PRT

<213> homo sapiens

<400> 480

Ala	Ala	Gln	Cys	Leu	Leu	His	Val	Gln	Cys	Lys	Arg	Ser	Leu	Phe	Gln
1				5					10					15	
Ser	Met	Glu	Ile	Thr	Glu	Leu	Glu	Phe	Val	Gln	Ile	Ile	Ile	Ile	Val
			20					25					30		
Val	Val	Thr	Cys	Leu	Leu	Ser	His	Tyr	Lys	Leu	Ser	Ala	Arg	Ser	Phe
		35					40					45			
Ile	Ser	Arg	His	Ser	Gln	Gly	Arg	Arg	Arg	Glu	Asp	Ala	Leu	Ser	Ser
	50					55					60				
Glu	Gly	Cys	Leu	Trp	Pro	Arg	Arg	His	Ser	Val	Arg	Gln	Arg	Asn	Pro
65					70					75					80
Arg	Ala	Ala	Val	Leu	Arg	Pro	Ala	Ser	Ala	His	Arg	Pro	Pro	Gly	Arg
				85					90					95	
Ala	Pro	Phe	Ala	Gln	Arg	Ser	Val	Phe	His	Arg	Cys	Gln	Pro	Asn	Val
			100					105					110		
Ser	Cys	Thr	Cys	Asn	Cys	Lys	Arg	Ser	Leu	Phe	Gln	Ser	Met	Glu	Ile
		115					120					125			
Thr	Glu	Leu	Glu	Phe	Val	Gln	Ile	Ile	Ile	Ile	Val	Val	Val	Thr	Cys
	130					135					140				

Leu 145	Leu	Ser	His	Tyr	Lys 150	Leu	Ser	Ala	Arg	Ser 155	Phe	Ile	Ser	Arg	His 160
Ser	Gln	Gly	Arg	Arg 165	Arg	Glu	Asp	Ala	Leu 170	Ser	Ser	Glu	Gly	Cys 175	Leu
Trp	Pro	Ser	Glu 180	Ser	Thr	Val	Ser	Gly 185	Asn	Gly	Ile	Pro	Glu 190	Pro	Gln
Val	Tyr	Ala 195	Pro	Pro	Arg	Pro	Thr 200	Asp	Arg	Leu	Ala	Val 205	Pro	Pro	Phe
Ala	Gln 210	Arg	Glu	Arg	Phe	His 215	Arg	Phe	Gln	Pro	Thr 220	Tyr	Pro	Tyr	Leu
Gln 225	His	Glu	Ile	Asp	Leu 230	Pro	Pro	Thr	Ile	Ser 235	Leu	Ser	Asp	Gly	Glu 240
Glu	Pro	Pro	Pro	Tyr 245	Gln	Gly	Pro	Trp	Thr 250	Phe	Lys	Val	Arg	Asp 255	Pro
Glu	Glu	Glu	Leu 260	Glu	Ile	Glu	Arg	Gly 265	Leu	Gly	Ala	Glu	Thr 270		

<210> 481

<211> 124

<212> PRT

<213> homo sapiens

<400> 481

Ala 1	Thr	Thr	Ser	Cys 5	Leu	His	Gly	Pro	Ser 10	Ser	Ala	Gly	Thr	Ala 15	Arg
Gly	Gly	Gly	Glu 20	Lys	Met	Pro	Cys	Pro 25	Gln	Lys	Asp	Ala	Cys 30	Gly	Pro
Arg	Arg	Ala 35	Gln	Cys	Gln	Ala	Thr 40	Glu	Ser	Gln	Ser	Arg 45	Arg	Ser	Thr
Pro	Arg 50	Leu	Gly	Pro	Pro	Thr 55	Ala	Trp	Pro	Cys	Arg 60	Pro	Ser	Pro	Ser
Gly 65	Ser	Ala	Ser	Thr	Ala 70	Ser	Ser	Pro	Pro	Ile 75	Arg	Thr	Cys	Ser	Thr 80
Arg	Ser	Thr	Cys	Arg 85	Pro	Pro	Ser	Arg	Cys 90	Gln	Thr	Gly	Arg	Ser 95	Pro
His	Pro	Thr	Arg 100	Ala	Pro	Gly	Pro	Ser 105	Arg	Phe	Gly	Thr	Pro 110	Arg	Arg
Ser	Trp	Lys 115	Leu	Asn	Gly	Asp	Trp 120	Val	Arg	Arg	Pro				

<210> 482

<211> 99

<212> PRT

<213> homo sapiens

<400> 482

Arg	Val	Leu	Val	Ser	Pro	Leu	Ser	Leu	Ser	Met	Trp	Arg	Trp	Lys	Val
1				5					10					15	
Glu	Lys	Asp	Thr	Val	Ser	Ile	Leu	Lys	Leu	Leu	Arg	Phe	Ser	Glu	Arg
			20					25					30		
Gly	Arg	His	Leu	Asn	Arg	Gln	Val	Gly	Phe	Ser	Val	Leu	Ser	Ala	Leu
		35					40					45			
Gly	Ile	Trp	Arg	Glu	Met	Gly	Leu	Leu	Ser	Leu	Cys	Thr	Gln	Glu	Gly
	50					55					60				
His	Ala	Leu	Lys	Thr	Val	Phe	Val	Asp	Gln	Arg	Arg	Leu	Tyr	Ser	Thr
65					70					75					80
Gly	Gly	Ile	Gln	Met	Ser	Leu	Arg	Gly	Arg	Glu	Glu	Thr	Trp	Gln	Ala
				85					90					95	
Asp	Tyr	Ile													

<210> 483
 <211> 104
 <212> PRT
 <213> homo sapiens

<400> 483

Val	Leu	Glu	Glu	Glu	Lys	Lys	His	Gly	Lys	Gln	Ile	Thr	Ser	Glu	Pro
1				5					10					15	
Phe	Glu	Leu	Cys	Phe	Ser	Phe	Phe	Pro	Cys	Leu	Phe	Ser	Lys	Ile	Tyr
			20					25					30		
Leu	Asn	Leu	Glu	Thr	Gln	Asp	Ile	Phe	Leu	Gly	Asn	Leu	Leu	Pro	Met
		35					40					45			
Ser	Glu	Val	Ala	Ser	Ala	Ala	Ser	Arg	Gln	Ile	Pro	Gly	Asn	Pro	Glu
	50					55					60				
Pro	Gln	Asn	Val	Ile	Pro	Pro	Gly	Ser	Ala	Trp	Pro	Asp	Pro	Val	Leu
65					70					75					80
Ser	Ala	Gly	Phe	Thr	Tyr	Gln	Ser	His	Ser	Ser	Phe	Ser	Ile	Asn	Thr
				85					90					95	
Pro	Lys	Ser	Ser	Pro	Asn	His	His								
			100												

<210> 484
 <211> 123
 <212> PRT
 <213> homo sapiens

<400> 484

Lys	Leu	Asp	Ser	Thr	Gln	Cys	Arg	Pro	Ser	Leu	His	Thr	Asn	Met	Tyr
1				5					10					15	
Val	Leu	Leu	Ser	Glu	Cys	His	Leu	Leu	Cys	Thr	Gln	Cys	His	Asp	Ser
			20					25					30		
Lys	Ile	Lys	Ile	Ser	Val	Ser	Asn	Gln	Asn	Ile	Asn	Gln	Ala	Arg	Asn
		35					40					45			

Ser	Trp	Ala	Gln	Arg	Gly	Val	Arg	Gly	Leu	Ser	Tyr	Thr	Ala	Val	Lys
	50					55					60				
Gln	Pro	Thr	Cys	Ser	Ala	His	Ser	Gln	Ala	Glu	Ser	Asp	Trp	Ser	Cys
65					70					75					80
Arg	Gln	Arg	Gly	Gly	Gly	Arg	Val	Leu	Cys	Cys	Pro	Leu	Leu	Cys	Met
			85						90					95	
Val	Ser	Trp	Val	Phe	Gln	Gly	Gly	Gln	Leu	Leu	Ser	Pro	Asn	Lys	Thr
			100					105					110		
Val	Asn	Ser	Leu	Arg	Thr	Gly	Pro	Leu	Pro	His					
		115					120								

<210> 485

<211> 303

<212> PRT

<213> homo sapiens

<400> 485

Leu	Gly	Arg	Lys	Pro	Ser	Trp	Val	Gly	Gly	Ala	Gly	Leu	Glu	Pro	Ser
1				5					10					15	
Gln	Gly	Ser	Gly	Leu	Ser	His	His	Pro	Ala	Pro	Gln	Ser	Asp	Ser	Ala
			20					25					30		
Pro	Thr	Ser	Pro	Pro	Ile	Pro	Gly	Glu	Pro	Gly	Pro	Gln	Arg	Glu	Val
		35					40					45			
Asp	Lys	Trp	Gly	Gly	Ser	Leu	Gly	Arg	Pro	Glu	Ser	Ser	Gly	His	Pro
	50					55					60				
Gly	Arg	Thr	Pro	Ala	Thr	Cys	Cys	His	Cys	Ala	Ala	Val	Met	Ala	Arg
65					70					75					80
Ser	Gly	Ser	Ala	Thr	Pro	Pro	Ala	Arg	Ala	Pro	Gly	Ala	Pro	Pro	Arg
				85					90					95	
Ser	Pro	Pro	Gln	Arg	Leu	Val	Gln	Asp	Val	Ser	Gly	Pro	Leu	Arg	Glu
			100					105					110		
Leu	Arg	Pro	Arg	Leu	Cys	His	Leu	Arg	Lys	Gly	Pro	Gln	Gly	Tyr	Gly
		115					120					125			
Phe	Asn	Leu	His	Ser	Asp	Lys	Ser	Arg	Pro	Gly	Gln	Tyr	Ile	Arg	Ser
	130					135					140				
Val	Asp	Pro	Gly	Ser	Pro	Ala	Ala	Arg	Ser	Gly	Leu	Arg	Ala	Gln	Asp
145					150					155					160
Arg	Leu	Ile	Glu	Val	Asn	Gly	Gln	Asn	Val	Glu	Gly	Leu	Arg	His	Ala
				165					170					175	
Glu	Val	Val	Ala	Ser	Ile	Lys	Ala	Arg	Glu	Asp	Glu	Ala	Arg	Leu	Leu
			180					185					190		
Val	Val	Asp	Pro	Glu	Thr	Asp	Glu	His	Phe	Lys	Arg	Leu	Arg	Val	Thr
		195					200					205			
Pro	Thr	Glu	Glu	His	Val	Glu	Gly	Pro	Leu	Pro	Ser	Pro	Val	Thr	Asn

210

215

220

Gly 225	Thr	Ser	Pro	Ala	Gln 230	Leu	Asn	Gly	Gly	Ser 235	Ala	Cys	Ser	Ser	Arg 240
Ser	Asp	Leu	Pro	Gly 245	Ser	Asp	Lys	Asp	Thr 250	Glu	Asp	Gly	Ser	Ala 255	Trp
Lys	Gln	Asp	Pro 260	Phe	Gln	Glu	Ser	Gly 265	Leu	His	Leu	Ser	Pro 270	Thr	Ala
Ala	Glu	Ala 275	Lys	Glu	Lys	Ala	Arg 280	Ala	Met	Arg	Val	Asn 285	Lys	Arg	Ala
Pro	Gln 290	Met	Asp	Trp	Asn	Arg 295	Lys	Arg	Glu	Ile	Phe 300	Ser	Asn	Phe	

<210> 486

<211> 149

<212> PRT

<213> homo sapiens

<400> 486

Ala 1	Pro	Arg	Arg	Pro 5	Arg	Pro	Arg	Arg	Arg 10	Leu	Glu	Pro	Cys	Glu 15	Ser
Thr	Ser	Ala	Arg 20	His	Arg	Trp	Thr	Gly 25	Thr	Gly	Ser	Val	Lys 30	Ser	Ser
Ala	Thr	Ser 35	Glu	Pro	Leu	Pro	Ala 40	Cys	Leu	Gly	Thr	Leu 45	Gly	Pro	Leu
Pro	His 50	Gly	Pro	Trp	Ala	Ser 55	Ala	Cys	Pro	Glu	Leu 60	Pro	Gln	Pro	Gln
Trp 65	Thr	Gly	Gly	Trp	Ser 70	Cys	His	Cys	Pro	Glu 75	Ile	Ser	Pro	Ser	Pro 80
Gly	Glu	Pro	Pro	Ser 85	Cys	Pro	Cys	Pro	Pro 90	Gly	Thr	Gly	Gly	Leu 95	Trp
Gln	Gln	Asp	Arg 100	Gly	Arg	Glu	Thr	Gln 105	Arg	Cys	Glu	Arg	Glu 110	Ser	Glu
Thr	Glu	Thr 115	Glu	Arg	Glu	Arg	Glu 120	Arg	His	Arg	Glu	Arg 125	Gln	Arg	Glu
Ser	Glu 130	Arg	Ala	Arg	Gly	Ser 135	Arg	Gly	Ala	Arg	Ala 140	Phe	Ala	Ala	Leu
Pro 145	Gly	Pro	Ala	Asp											

<210> 487

<211> 217

<212> PRT

<213> homo sapiens

<400> 487

Phe 1	Leu	Gly	Asn	Gly 5	Arg	Thr	Thr	Leu	Gln 10	Ser	Thr	Glu	Ala	Gly 15	Gly
----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Ala	Arg	Gly	Arg 20	Leu	Arg	Pro	Lys	Val 25	Arg	Ala	Gly	Gly	Val 30	Pro	Gly
Ser	Arg	Asp 35	Arg	Gln	Glu	Gly	Ala 40	Gln	Lys	Leu	Leu	Lys 45	Ile	Ser	Arg
Phe	Leu 50	Phe	Gln	Ser	Ile	Cys 55	Gly	Ala	Arg	Leu	Leu 60	Thr	Arg	Met	Ala
Arg 65	Ala	Phe	Ser	Leu	Ala 70	Ser	Ala	Ala	Val	Gly 75	Leu	Arg	Trp	Arg	Pro 80
Leu	Ser	Trp	Lys	Gly 85	Ser	Cys	Phe	Gln	Ala 90	Leu	Pro	Ser	Ser	Val 95	Ser
Leu	Ser	Glu	Pro 100	Gly	Arg	Ser	Leu	Arg 105	Asp	Glu	His	Ala	Glu 110	Pro	Pro
Leu	Ser	Trp 115	Ala	Gly	Leu	Val	Pro 120	Leu	Val	Thr	Gly	Asp 125	Gly	Arg	Gly
Pro	Ser	Thr 130	Cys	Ser	Ser	Val 135	Gly	Val	Thr	Arg	Ser 140	Arg	Leu	Lys	Cys
Ser 145	Ser	Val	Ser	Gly	Ser 150	Thr	Thr	Ser	Ser	Arg 155	Ala	Ser	Ser	Ser	Arg 160
Ala	Leu	Met	Leu	Ala 165	Thr	Thr	Ser	Ala	Trp 170	Arg	Ser	Pro	Ser	Thr 175	Phe
Cys	Pro	Phe	Thr 180	Ser	Met	Ser	Arg	Ser 185	Trp	Ala	Arg	Arg	Pro 190	Glu	Arg
Ala	Ala	Gly 195	Glu	Pro	Gly	Ser	Thr 200	Glu	Arg	Met	Tyr	Trp 205	Pro	Gly	Arg
Asp 210	Leu	Ser	Leu	Cys	Arg	Leu 215	Asn	Pro							

<210> 488
 <211> 298
 <212> PRT
 <213> homo sapiens

<400> 488

Glu 1	Ile	Arg	Ala	Val 5	Gly	Gly	Gly	Val	Cys 10	Val	Asp	Gly	Met	Gly 15	Thr
Pro	Gly	Glu	Gly 20	Leu	Gly	Arg	Cys	Ser 25	His	Ala	Leu	Ile	Arg 30	Gly	Val
Pro	Glu	Ser 35	Leu	Ala	Ser	Gly	Glu 40	Gly	Ala	Gly	Ala	Gly 45	Leu	Pro	Ala
Leu	Asp 50	Leu	Ala	Lys	Ala	Gln 55	Arg	Glu	His	Gly	Val 60	Leu	Gly	Gly	Lys
Leu 65	Arg	Gln	Arg	Leu	Gly 70	Leu	Gln	Leu	Leu	Glu 75	Leu	Pro	Pro	Glu	Glu 80
Ser	Leu	Pro	Leu	Gly	Pro	Leu	Leu	Gly	Asp	Thr	Ala	Val	Ile	Gln	Gly

85								90				95					
Asp	Thr	Ala	Leu 100	Ile	Thr	Arg	Pro	Trp 105	Ser	Pro	Ala	Arg	Arg 110	Pro	Glu		
Val	Asp	Gly 115	Val	Arg	Lys	Ala	Leu 120	Gln	Asp	Leu	Gly	Leu 125	Arg	Ile	Val		
Glu	Ile 130	Gly	Asp	Glu	Asn	Ala 135	Thr	Leu	Asp	Gly	Thr 140	Asp	Val	Leu	Phe		
Thr 145	Gly	Arg	Glu	Phe	Phe 150	Val	Gly	Leu	Ser	Lys 155	Trp	Thr	Asn	His	Arg 160		
Gly	Ala	Glu	Ile	Val 165	Ala	Asp	Thr	Phe	Arg 170	Asp	Phe	Ala	Val	Ser 175	Thr		
Val	Pro	Val	Ser 180	Gly	Pro	Ser	His	Leu 185	Arg	Gly	Leu	Cys	Gly 190	Met	Gly		
Gly	Pro	Arg 195	Thr	Val	Val	Ala	Gly 200	Ser	Ser	Asp	Ala	Ala 205	Gln	Lys	Ala		
Val	Arg 210	Ala	Met	Ala	Val	Leu 215	Thr	Asp	His	Pro	Tyr 220	Ala	Ser	Leu	Thr		
Leu 225	Pro	Asp	Asp	Ala	Ala 230	Ala	Asp	Cys	Leu	Phe 235	Leu	Arg	Pro	Gly	Leu 240		
Pro	Gly	Val	Pro	Pro 245	Phe	Leu	Leu	His	Arg 250	Gly	Gly	Gly	Asp	Leu 255	Pro		
Asn	Ser	Gln	Glu 260	Ala	Leu	Gln	Lys	Leu 265	Ser	Asp	Val	Thr	Leu 270	Val	Pro		
Val	Ser	Cys 275	Ser	Glu	Leu	Glu	Lys 280	Ala	Gly	Ala	Gly	Leu 285	Ser	Ser	Leu		
Cys 290	Leu	Val	Leu	Ser	Thr	Arg 295	Pro	His	Ser								

<210> 489

<211> 175

<212> PRT

<213> homo sapiens

<400> 489

Ala 1	Gly	His	Arg	Tyr 5	Gln	Gly	Asp	Ile	Arg 10	Glu	Leu	Leu	Gln	Cys 15	Leu
Leu	Ala	Val	Gly 20	Gln	Ile	Pro	Thr	Ser 25	Thr	Val	Gln	Glu	Glu 30	Arg	Gly
His	Thr	Arg 35	Gln	Pro	Arg	Thr	Lys 40	Lys	Glu	Thr	Val	Ser 45	Ser	Cys	Val
Ile	Trp 50	Glu	Gly	Gln	Gly	Gly 55	Ile	Trp	Val	Ile	Cys 60	Gln	His	Cys	His
Cys 65	Pro	Asp	Ser	Leu	Leu 70	Gly	Ser	Val	Ala	Ala 75	Ala	Cys	His	Asn	Ser 80

Ala	Arg	Ser	Pro	His 85	Ala	Ala	Glu	Thr	Ala 90	Gln	Val	Gly	Gly	Thr 95	Arg
Asp	Trp	His	Ser 100	Gly	Asp	Gly	Glu	Val 105	Pro	Glu	Arg	Val	Arg 110	His	Asp
Leu	Ser	Ser 115	Ser	Val	Ile	Gly	Pro 120	Phe	Gly	Glu	Ala	Tyr 125	Glu	Lys	Leu
Pro	Ala 130	Gly	Glu	Glu	Asn	Val 135	Ser	Ala	Ile	Gln	Arg 140	Arg	Val	Leu	Val
Ser 145	Tyr	Phe	His	Asn	Ser 150	Glu	Pro	Gln	Val	Leu 155	Gln	Gly	Phe	Ala	Asp 160
Ser	Ile	Asp	Leu	Trp 165	Pro	Thr	Ser	Gly	Ala 170	Pro	Gly	Pro	Arg	Asp 175	

<210> 490

<211> 150

<212> PRT

<213> homo sapiens

<400> 490

Leu 1	Gly	Pro	Cys	Pro 5	Leu	Gly	Ser	Arg	Pro 10	Cys	Arg	Gln	Ala	Ala 15	Val
Pro	Ala	Ala	Met 20	Thr	Pro	Gln	Val	Ala 25	Val	Leu	Ala	Ala	Val 30	Ala	Pro
Val	Val	Ala 35	Ser	Val	Tyr	Leu	Pro 40	Ala	Pro	Arg	Ala	Pro 45	Phe	Glu	Leu
Trp 50	Pro	Asp	Pro	Glu	Arg	Glu 55	Gly	Gln	Pro	Pro	His 60	Leu	Pro	Pro	Thr
Pro 65	Gly	Ser	Leu	Gly	Leu 70	Pro	Gly	Ser	Gly	His 75	Gly	Ser	Ser	Gly	Pro 80
Ala	Pro	Pro	Pro	Ala 85	Ser	Pro	Ser	His	Pro 90	His	Arg	Leu	Pro	Leu 95	Gln
Pro	Leu	Gly	Phe 100	Leu	Ser	Phe	Leu	Val 105	Ser	Ser	Pro	Val	Ser 110	Ser	Gly
His	Pro	His 115	Ser	Cys	Arg	Ala	Val 120	Ile	Ser	Ala	Gly	Ala 125	Pro	Pro	Pro
Glu 130	Asp	Arg	Val	Gly	Gly	Glu 135	Gly	Ser	Pro	Arg	Leu 140	Gln	Ala	Ser	Gly
Thr 145	Gly	Ser	Ser	Gly	Phe 150										

<210> 491

<211> 89

<212> PRT

<213> homo sapiens

<400> 491

Phe Val Lys Arg Thr Lys Gln Pro Arg Gln Thr Leu Asp Ala Pro Cys

1				5				10				15			
Ser	Ala	Leu	Arg	Leu	Trp	Gly	Arg	Cys	Leu	Leu	Gly	Glu	Ala	Val	Ala
			20					25					30		
Gln	Gly	Val	His	Cys	Glu	Ala	Gly	Pro	Val	Asp	Ser	Ala	Gly	Gly	Ile
		35					40					45			
His	Leu	Ala	Ser	Gly	Cys	Leu	Val	Ser	Val	Tyr	Ser	Asp	Ile	Ala	Phe
	50					55					60				
Cys	Cys	His	Leu	Ser	Cys	Gly	Gln	Arg	Gly	Val	Ser	Trp	His	Glu	Asn
	65				70					75					80
Ile	Phe	Phe	Phe	Lys	Cys	Gly	Ser	Phe							
				85											

<210> 492
 <211> 63
 <212> PRT
 <213> homo sapiens

<400> 492

Leu	Thr	His	Leu	Leu	Phe	Glu	Lys	Cys	Leu	Leu	Pro	Ser	Leu	Gly	Leu
1				5					10					15	
Ile	Thr	Lys	Phe	Asp	His	Asp	His	Ile	Val	Val	Ser	Gln	Ser	Ala	Leu
			20					25					30		
Glu	Ile	Val	Ser	Gly	Leu	His	Glu	Val	Ala	Met	Gly	Val	Trp	Ser	Thr
		35					40					45			
Leu	Lys	Leu	Tyr	Gln	Ser	Cys	Thr	Tyr	Phe	Gln	Thr	Phe	Leu	Lys	
	50					55					60				

<210> 493
 <211> 73
 <212> PRT
 <213> homo sapiens

<400> 493

Asp	Gly	Ser	Arg	Met	Leu	Cys	His	Tyr	Ile	Gln	Lys	Gln	Asp	Asn	Leu
1				5					10					15	
Lys	Leu	Asn	Gly	Cys	Pro	Leu	Gln	Ser	Gln	Gln	Val	Gln	Pro	His	Ser
			20					25					30		
Ala	Arg	Pro	Glu	Leu	Gln	Pro	Leu	Pro	Lys	Gly	Ile	Phe	Pro	Thr	Ala
		35					40					45			
Ser	Thr	Pro	Ser	Lys	Glu	His	Gln	Gly	Phe	Val	Ser	Val	Val	Leu	Phe
	50					55					60				
Phe	Leu	Gln	Thr	Ile	Asp	Ile	Tyr	Ser							
	65				70										

<210> 494
 <211> 318
 <212> PRT
 <213> homo sapiens

<400> 494

Lys 1	Cys	Ala	Thr	Phe 5	Trp	Ser	Phe	Pro	Arg 10	Arg	Gln	Gly	Gly	Leu 15	Gly
Ile	Ala	Ile	Ser 20	Glu	Glu	Asp	Thr	Leu 25	Ser	Gly	Val	Ile	Ile 30	Lys	Ser
Leu	Thr	Glu 35	His	Gly	Val	Ala	Ala 40	Thr	Asp	Gly	Arg	Leu 45	Lys	Val	Gly
Asp	Gln 50	Ile	Leu	Ala	Val	Asp 55	Asp	Glu	Ile	Val	Val 60	Gly	Tyr	Pro	Ile
Glu 65	Lys	Phe	Ile	Ser	Leu 70	Leu	Lys	Thr	Ala	Lys 75	Met	Thr	Val	Lys	Leu 80
Thr	Ile	His	Ala	Glu 85	Asn	Pro	Asp	Ser	Gln 90	Ala	Val	Pro	Ser	Ala 95	Ala
Gly	Ala	Ala	Ser 100	Gly	Glu	Lys	Lys	Asn 105	Ser	Ser	Gln	Ser	Leu 110	Met	Val
Pro	Gln	Ser 115	Gly	Ser	Pro	Glu	Pro 120	Glu	Ser	Ile	Arg	Asn 125	Thr	Ser	Arg
Ser	Ser 130	Thr	Pro	Ala	Ile	Phe 135	Ala	Ser	Asp	Pro	Ala 140	Thr	Cys	Pro	Ile
Ile 145	Pro	Gly	Cys	Glu	Thr 150	Thr	Ile	Glu	Ile	Ser 155	Lys	Gly	Arg	Thr	Gly 160
Leu	Gly	Leu	Ser	Ile 165	Val	Gly	Gly	Ser	Asp 170	Thr	Leu	Leu	Gly	Ala 175	Ile
Ile	Ile	His	Glu 180	Val	Tyr	Glu	Glu	Gly 185	Ala	Ala	Cys	Lys	Asp 190	Gly	Arg
Leu	Trp	Ala 195	Gly	Asp	Gln	Ile	Leu 200	Glu	Val	Asn	Gly	Ile 205	Asp	Leu	Arg
Lys	Ala 210	Thr	His	Asp	Glu	Ala 215	Ile	Asn	Val	Leu	Arg 220	Gln	Thr	Pro	Gln
Arg 225	Val	Arg	Leu	Thr	Leu 230	Tyr	Arg	Asp	Glu	Ala 235	Pro	Tyr	Lys	Glu	Glu 240
Glu	Val	Cys	Asp	Thr 245	Leu	Thr	Ile	Glu	Leu 250	Gln	Lys	Lys	Pro	Gly 255	Lys
Gly	Leu	Gly	Leu 260	Ser	Ile	Val	Gly	Lys 265	Arg	Asn	Asp	Thr	Gly 270	Val	Phe
Val	Ser	Asp 275	Ile	Val	Lys	Gly	Gly 280	Ile	Ala	Asp	Ala	Asp 285	Gly	Arg	Leu
Met	Gln 290	Gly	Asp	Gln	Ile	Leu 295	Met	Val	Asn	Gly	Glu 300	Asp	Val	Arg	Asn
Ala 305	Thr	Gln	Glu	Ala	Val 310	Ala	Val	Trp	Ile	Lys 315	Val	Phe	Pro		

<210> 495

<211> 206
 <212> PRT
 <213> homo sapiens

<400> 495

Ser 1	Ala	Phe	Ala	Glu 5	Met	Gly	Ser	Asp	His 10	Thr	Gln	Ser	Ser	Ala 15	Ser
Lys	Ile	Ser	Gln 20	Asp	Val	Asp	Lys	Glu 25	Asp	Glu	Phe	Gly	Tyr 30	Ser	Trp
Lys	Asn	Ile 35	Arg	Glu	Arg	Tyr	Gly 40	Thr	Leu	Thr	Gly	Glu 45	Leu	His	Met
Ile 50	Glu	Leu	Glu	Lys	Gly	His 55	Ser	Gly	Leu	Gly	Leu 60	Ser	Leu	Ala	Gly
Asn 65	Lys	Asp	Arg	Ser	Arg 70	Met	Ser	Val	Phe	Ile 75	Val	Gly	Ile	Asp	Pro 80
Asn	Gly	Ala	Ala	Gly 85	Lys	Asp	Gly	Arg	Leu 90	Gln	Ile	Ala	Asp	Glu 95	Leu
Leu	Glu	Ile	Asn 100	Gly	Gln	Ile	Leu	Tyr 105	Gly	Arg	Ser	His	Gln 110	Asn	Ala
Ser	Ser	Ile 115	Ile	Lys	Cys	Ala	Pro 120	Ser	Lys	Val	Lys	Ile 125	Ile	Phe	Ile
Arg	Asn 130	Lys	Asp	Ala	Val	Asn 135	Gln	Met	Ala	Val	Cys 140	Pro	Gly	Asn	Ala
Val 145	Glu	Pro	Leu	Pro	Ser 150	Asn	Ser	Glu	Asn	Leu 155	Gln	Asn	Lys	Glu	Thr 160
Glu	Pro	Thr	Val	Thr 165	Thr	Ser	Asp	Ala	Ala 170	Val	Asp	Leu	Ser	Ser	Phe
Lys	Asn	Val	Gln 180	His	Ser	Gly	Ala	Ser 185	Gln	Gly	Gly	Arg	Gly 190	Val	Trp
Val	Leu	Leu 195	Ser	Ala	Lys	Lys	Ile 200	His	Ser	Val	Glu	Ser 205	Ser		

<210> 496
 <211> 119
 <212> PRT
 <213> homo sapiens

<400> 496

Thr 1	Ser	Trp	Ile	Ile 5	Met	Ala	Pro	Ser	Ser 10	Val	Ser	Glu	Pro	Pro 15	Thr
Met	Leu	Arg	Pro 20	Ser	Pro	Val	Arg	Pro 25	Leu	Glu	Ile	Ser	Met 30	Val	Val
Ser	Gln	Pro 35	Gly	Ile	Met	Gly	Gln 40	Val	Ala	Gly	Ser	Glu 45	Ala	Lys	Ile
Ala	Gly 50	Val	Asp	Asp	Leu	Leu 55	Val	Phe	Arg	Met	Asp 60	Ser	Gly	Ser	Gly

Glu 65	Pro	Asp	Cys	Gly	Thr 70	Ile	Arg	Asp	Trp	Glu 75	Leu	Phe	Phe	Phe	Ser 80
Pro	Leu	Ala	Ala	Pro 85	Ala	Ala	Glu	Gly	Thr 90	Ala	Trp	Glu	Ser	Gly 95	Phe
Ser	Ala	Trp	Met 100	Val	Ser	Phe	Thr	Val 105	Ile	Phe	Ala	Val	Phe 110	Arg	Arg
Leu	Ile	Asn 115	Phe	Ser	Ile	Gly									

<210> 497
 <211> 71
 <212> PRT
 <213> homo sapiens

<400> 497

Ser 1	Ala	Pro	Ser	Leu 5	Thr	Lys	Cys	Arg	Ser 10	Thr	His	Val	Tyr	Pro 15	Leu
Ser	Leu	Ile	Met 20	Phe	Met	Ser	Gly	Gly 25	Ser	Ser	Arg	Ser	Thr 30	Leu	Arg
Arg	Met	Val 35	Pro	Thr	Pro	Ser	Thr 40	Thr	Ser	Leu	Ser	Pro 45	Arg	Ser	Ser
Ser	Ser 50	Thr	Ser	Lys	Leu	Leu 55	Thr	Gln	Ser	Gly	Pro 60	Ser	Leu	Pro	Gln
Pro 65	Pro	Ala	Ser	Arg	Pro 70	Phe									

<210> 498
 <211> 139
 <212> PRT
 <213> homo sapiens

<400> 498

Ser 1	Arg	Ser	Pro	Ala 5	Cys	Gly	Ala	Ser	Glu 10	His	Gly	Asp	Gly	Ala 15	Met
Ser	Leu	Ile	Cys 20	Ser	Ile	Ser	Asn	Glu 25	Val	Pro	Glu	His	Pro 30	Cys	Val
Ser	Pro	Val 35	Ser	Asn	His	Val	Tyr 40	Glu	Arg	Arg	Leu	Ile 45	Glu	Lys	Tyr
Ile	Ala 50	Glu	Asn	Gly	Thr	Asp 55	Pro	Ile	Asn	Asn	Gln 60	Pro	Leu	Ser	Glu
Glu 65	Gln	Leu	Ile	Asp	Ile 70	Lys	Val	Ala	His	Pro 75	Ile	Arg	Pro	Lys	Pro 80
Pro	Ser	Ala	Thr 85	Ser	Ile	Pro	Ala	Ile	Leu 90	Lys	Ala	Leu	Gln	Asp 95	Glu
Trp	Asp	Ala	Val 100	Met	Leu	His	Ser	Phe 105	Thr	Leu	Arg	Gln	Ser 110	Cys	Arg

Gln	Pro	Ala	Lys	Ser	Cys	His	Thr	Leu	Cys	Thr	Ser	Thr	Met	Pro	Pro
		115					120					125			
Ala	Val	Ser	Leu	Pro	Val	Ser	Pro	Arg	Lys	Leu					
	130					135									

<210> 499
 <211> 74
 <212> PRT
 <213> homo sapiens

<400> 499

Thr	Thr	Gly	Arg	Glu	Arg	Gly	Cys	Arg	Pro	Cys	Ala	Gly	Leu	Phe	Tyr
1				5					10					15	
Cys	Phe	Leu	Phe	Leu	Met	Lys	Leu	Asp	His	Cys	Leu	Gln	Asn	Pro	Ala
			20					25					30		
Gln	Ala	Leu	Leu	Pro	Ile	Pro	Phe	Thr	Val	Ser	Leu	Val	Arg	Arg	Ala
		35					40					45			
Met	Thr	Arg	Gln	Ala	Ala	Ser	Cys	Trp	Tyr	Arg	Ala	Cys	Asp	Ser	Ser
	50					55					60				
Trp	Arg	Val	Val	Cys	Ser	Ser	Gly	Ala	Glu						
65					70										

<210> 500
 <211> 71
 <212> PRT
 <213> homo sapiens

<400> 500

Phe	Ser	Phe	Phe	Asn	Glu	Thr	Arg	Ser	Leu	Leu	Thr	Lys	Pro	Cys	Thr
1				5					10					15	
Ser	Pro	Pro	Ala	His	Pro	Leu	His	Ser	Ser	Leu	Gly	Ser	Ala	Ser	Pro
			20					25					30		
Val	Ser	Gln	Glu	Leu	Gln	Gln	Asn	Gly	Cys	Gly	Thr	Ala	Thr	Thr	Thr
		35					40					45			
Ser	Ile	Glu	Arg	Gln	Glu	Gly	Arg	Gly	Ala	Val	Gly	Leu	Val	Gln	Gly
	50					55					60				
Phe	Phe	Ile	Val	Phe	Phe	Phe									
65					70										

<210> 501
 <211> 284
 <212> PRT
 <213> homo sapiens

<400> 501

Glu	Ala	Arg	Gly	Leu	Ala	Thr	Arg	Thr	Arg	Ser	Gly	Ala	Ala	Ala	His
1				5					10					15	
Ala	Gly	Asp	Arg	Phe	Thr	Asp	Ala	Asp	Asp	Val	Ala	Ile	Leu	Thr	Tyr
			20					25					30		

Val	Lys	Glu	Asn	Ala	Arg	Ser	Pro	Ser	Ser	Val	Thr	Gly	Asn	Ala	Leu
		35					40					45			
Trp	Lys	Ala	Met	Glu	Lys	Ser	Ser	Leu	Thr	Gln	His	Ser	Trp	Gln	Ser
	50					55					60				
Leu	Lys	Asp	Arg	Tyr	Leu	Lys	His	Leu	Arg	Gly	Gln	Glu	His	Lys	Tyr
	65				70					75					80
Leu	Leu	Gly	Asp	Ala	Pro	Val	Ser	Pro	Ser	Ser	Gln	Lys	Leu	Lys	Arg
				85					90					95	
Lys	Ala	Glu	Glu	Asp	Pro	Glu	Ala	Ala	Asp	Ser	Gly	Glu	Pro	Gln	Asn
			100					105					110		
Lys	Arg	Thr	Pro	Asp	Leu	Pro	Glu	Glu	Glu	Tyr	Val	Lys	Glu	Glu	Ile
		115					120					125			
Gln	Glu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Met	Leu	Val	Glu	Ala	Thr	Arg
	130					135					140				
Glu	Phe	Glu	Glu	Val	Val	Val	Asp	Glu	Ser	Pro	Asp	Phe	Glu	Ile	
	145				150					155				160	
His	Ile	Thr	Met	Cys	Asp	Asp	Asp	Pro	Pro	Thr	Pro	Glu	Glu	Asp	Ser
				165					170					175	
Glu	Thr	Gln	Pro	Asp	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Lys	Val	Ser
			180					185					190		
Gln	Pro	Glu	Val	Gly	Ala	Ala	Ile	Lys	Ile	Ile	Arg	Gln	Leu	Met	Glu
		195					200					205			
Lys	Phe	Asn	Leu	Asp	Leu	Ser	Thr	Val	Thr	Gln	Ala	Phe	Leu	Lys	Asn
	210					215					220				
Ser	Gly	Glu	Leu	Glu	Ala	Thr	Ser	Ala	Phe	Leu	Ala	Ser	Gly	Gln	Arg
	225				230					235					240
Ala	Asp	Gly	Tyr	Pro	Ile	Trp	Ser	Arg	Gln	Asp	Asp	Ile	Asp	Leu	Gln
				245					250					255	
Lys	Asp	Asp	Glu	Asp	Thr	Arg	Glu	Ala	Leu	Val	Lys	Lys	Phe	Gly	Ala
			260					265					270		
Gln	Asn	Val	Ala	Arg	Arg	Ile	Glu	Phe	Arg	Lys	Lys				
		275					280								

<210> 502

<211> 123

<212> PRT

<213> homo sapiens

<400> 502

Glu	Thr	Phe	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Gly	Cys	Val	Ser
	1			5						10				15	
Glu	Ser	Ser	Ser	Gly	Val	Gly	Gly	Ser	Ser	Ser	His	Ile	Val	Ile	Cys
			20					25					30		
Ile	Ser	Lys	Ser	Gly	Gly	Leu	Ser	Ser	Thr	Thr	Thr	Ser	Ser	Asn	Ser
		35					40					45			

Arg	Val	Ala	Ser	Thr	Ser	Ile	Phe	Leu	Thr	Ala	Ser	Ser	Phe	Ser	Trp
	50					55					60				
Ile	Ser	Ser	Phe	Thr	Tyr	Ser	Ser	Ser	Gly	Lys	Ser	Gly	Val	Leu	Leu
65					70					75					80
Phe	Cys	Gly	Ser	Pro	Leu	Ser	Ala	Ala	Ser	Gly	Ser	Ser	Ser	Ala	Phe
				85					90					95	
Arg	Leu	Ser	Phe	Trp	Glu	Glu	Gly	Leu	Thr	Gly	Ala	Ser	Pro	Ser	Arg
			100					105					110		
Tyr	Leu	Cys	Ser	Trp	Pro	Arg	Arg	Cys	Leu	Arg					
		115					120								

<210> 503

<211> 175

<212> PRT

<213> homo sapiens

<400> 503

Val	Phe	Leu	Arg	Cys	Gly	Trp	Ile	Ile	Ile	Thr	His	Ser	Tyr	Met	Tyr
1				5					10					15	
Phe	Lys	Ile	Arg	Arg	Ala	Leu	Ile	His	His	Asn	Leu	Leu	Lys	Leu	Pro
			20					25					30		
Gly	Gly	Phe	His	Lys	His	Leu	Phe	Asp	Cys	Phe	Phe	Ile	Leu	Leu	Asp
		35					40					45			
Phe	Phe	Leu	His	Ile	Leu	Phe	Phe	Arg	Gln	Ile	Trp	Ser	Ser	Leu	Ile
	50					55					60				
Leu	Trp	Phe	Pro	Ala	Ile	Arg	Gly	Leu	Arg	Val	Leu	Leu	Arg	Leu	Pro
65					70					75					80
Leu	Glu	Leu	Leu	Gly	Gly	Gly	Ala	His	Arg	Arg	Val	Pro	Gln	Gln	Val
				85					90					95	
Leu	Met	Leu	Leu	Ala	Pro	Gln	Val	Leu	Glu	Val	Ala	Val	Leu	Gln	Gly
			100					105					110		
Leu	Pro	Arg	Val	Leu	Arg	Glu	Arg	Ala	Leu	Leu	His	Arg	Phe	Pro	Gln
		115					120					125			
Gly	Val	Thr	Gly	Asp	Gly	Ala	Gly	Arg	Ala	Gly	Ile	Phe	Leu	His	Val
	130					135					140				
Gly	Lys	Asp	Gly	Tyr	Val	Val	Arg	Ile	Arg	Glu	Ala	Ile	Ala	Arg	Val
145					150					155					160
Arg	Cys	Arg	Ser	Ala	Pro	Arg	Ala	Arg	Arg	Gln	Ala	Pro	Gly	Phe	
				165					170					175	

<210> 504

<211> 78

<212> PRT

<213> homo sapiens

<400> 504

Cys 1	Pro	Pro	Glu	Lys 5	Ser	Leu	Gln	Met	Phe 10	Gln	Pro	Leu	Ser	Ser 15	Pro
Asp	Ser	His	Arg 20	Lys	Gly	Thr	Gly	Phe 25	Gly	Leu	Gly	Ile	Val 30	Phe	Ser
Leu	Thr	Phe 35	Phe	Lys	Arg	Arg	Met 40	Trp	Pro	Leu	Ala	Phe 45	Gly	Ser	Gly
Met	Gly 50	Leu	Gly	Met	Ala	Tyr 55	Ser	Asn	Cys	Gln	His 60	Asp	Phe	Gln	Ala
Pro 65	Tyr	Leu	Leu	His	Gly 70	Lys	Tyr	Val	Lys	Glu 75	Gln	Glu	Gln		

<210> 505
 <211> 95
 <212> PRT
 <213> homo sapiens

<400> 505

Ser 1	Lys	Thr	Ser	Thr 5	Leu	Pro	Val	Ala	Ile 10	Trp	Thr	Arg	Gln	Arg 15	Leu
Glu	His	Leu	Gln 20	Gly	Phe	Leu	Gly	Trp 25	Thr	Ser	Ile	Thr	Arg 30	Ile	Leu
Ser	Ser	Arg 35	Pro	His	Pro	Pro	Asp 40	Thr	Gly	Pro	Thr	Ser 45	Cys	Arg	Ala
Pro	Thr 50	Gln	Thr	Cys	Ser	Pro 55	Pro	Ala	Pro	Pro	Ala 60	Phe	Leu	Ser	Ala
Gly 65	Pro	Arg	Ala	Pro	Thr 70	Pro	Glu	Ser	Leu	Ala 75	Arg	Ala	Gly	Asn 80	Lys 80
Ser	Gln	Val	Arg	Lys 85	Ala	Gly	Ala	Asp	Ala 90	Pro	Asp	Ile	Ala	Arg 95	

<210> 506
 <211> 156
 <212> PRT
 <213> homo sapiens

<400> 506

Ala 1	Ile	Pro	Asn 5	Pro 5	Met	Pro	Glu	Pro	Lys 10	Ala	Asn	Gly	His	Ile 15	Leu
Leu	Leu	Lys	Lys 20	Val	Ser	Glu	Lys	Thr 25	Ile	Pro	Asn	Pro	Lys 30	Pro	Val
Pro	Phe	Leu 35	Trp	Leu	Ser	Gly	Leu 40	Asp	Arg	Gly	Trp	Asn 45	Ile	Cys	Arg
Asp	Phe 50	Ser	Gly	Gly	His	Gln 55	Leu	Pro	Gly	Phe	Tyr 60	Leu	His	Asp	Arg
Ile 65	Arg	Gln	Thr	Pro	Val 70	Pro	Leu	Pro	Ala	Glu 75	Leu	Arg	Leu	Arg	His 80
Val	Pro	His	Pro	Arg	Leu	Gln	Leu	Ser	Ser	Arg	Pro	Ala	Pro	Ala	Leu

				85						90						95			
Arg	Pro	Leu	Lys 100	Val	Ser	Arg	Glu	Leu 105	Glu	Thr	Ser	Pro	Arg 110	Ser	Gly				
Arg	Gln	Ala 115	Gln	Thr	Leu	Gln	Ile 120	Ser	Arg	Asp	Asp	Pro 125	Leu	Leu	Pro				
Ser	Leu 130	Pro	Val	Phe	Ser	Val 135	Gly	Arg	Gln	Gly	Asp 140	Ala	Val	Val	Trp				
Arg 145	Leu	Glu	Val	Thr	Leu 150	Thr	Leu	Gly	Cys	Ala 155	Tyr								

<210> 507

<211> 169

<212> PRT

<213> homo sapiens

<400> 507

Ala 1	Ala	Ser	Gly	Met 5	Leu	Gly	Ser	Trp	Pro 10	Ala	Arg	Thr	Phe	His 15	Pro				
Gly	Ala	Cys	Val 20	Ser	Arg	Arg	Pro	Ser 25	Ala	Pro	Trp	Lys	His 30	Thr	Ala				
Ser	Gly	Lys 35	Asp	Ser	Pro	Asp	Leu 40	Arg	Phe	Ser	Glu	His 45	Gly	Val	Ser				
Gln	Glu 50	Phe	Trp	Ala	Gly	Gly 55	Leu	Val	Ala	Val	Leu 60	Glu	Met	Thr	Pro				
Ser 65	Pro	Ser	Pro	Trp	Gly 70	Thr	Gln	Glu	Gly	Pro 75	Ala	Gly	Met	Cys	Ser 80				
Leu	Trp	Val	Val	Gly 85	Trp	Cys	Pro	Cys	Arg 90	Gly	Ala	Gly	Val	Arg 95	Asp				
Leu	Val	Leu	Val 100	His	Ala	Gly	Val	Trp 105	Cys	Lys	His	Val	Cys 110	Ala	Val				
Gln	Arg	Asp 115	Ala	Cys	Gly	Glu	Ser 120	Arg	Thr	Pro	Ala	Pro 125	Pro	Arg	Lys				
Gly	Gly 130	Ala	Val	Thr	Ser	Val 135	Leu	Cys	Leu	Phe	Leu 140	Ile	Lys	Thr	Phe				
Pro 145	Leu	Phe	Ser	Tyr	Lys 150	Phe	Ala	Ser	Cys	Lys 155	Gln	Val	His	Lys	Asp 160				
Pro	Pro	Leu	Val	Lys 165	Ser	Gly	Phe	Glu											

<210> 508

<211> 155

<212> PRT

<213> homo sapiens

<400> 508

Thr 1	Gln	Asn	Thr	Gly 5	Asn	Arg	Ser	Ala	Phe 10	Pro	Gly	Trp	Arg	Trp 15	Cys				
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Ala	Ala	Leu	Ser 20	Thr	Arg	Val	Ser	Leu 25	Tyr	Ser	Thr	Tyr	Met 30	Phe	Thr
Pro	His	Thr 35	Cys	Val	Asp	Glu	His 40	Gln	Ile	Thr	His	Pro 45	Ser	Ser	Thr
Thr	Gly 50	Thr	Pro	Ala	Asp	Tyr 55	Pro	Gln	Ala	Ala	His 60	Ser	Gly	Arg	Ala
Leu 65	Leu	Gly	Ala	Pro	Arg 70	Gly	Gly	Ala	Arg	Gly 75	His	Leu	Gln	His	Cys 80
His	Gln	Ala	Ala	Ser 85	Pro	Glu	Phe	Leu	Gly 90	Asn	Thr	Val	Leu	Gly 95	Lys
Pro	Lys	Val	Arg 100	Ala	Val	Leu	Pro	Arg 105	Gly	Arg	Val	Leu	Pro 110	Gly	Cys
Gly	Gly	Pro 115	Ala	Ala	Asp	Thr	Gly 120	Pro	Arg	Val	Glu	Gly 125	Pro	Gly	Arg
Pro	Ala 130	Ser	Lys	His	Ala	Arg 135	Arg	Ser	Leu	Gly	Glu 140	Pro	Gly	Ser	Val
Ala 145	Ser	Ser	Leu	Leu	Ser 150	Leu	Arg	Ser	Pro	Ile 155					

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<211> 148
<212> PRT
<213> homo sapiens
<400> 509
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[illegible]

145

<210> 510
<211> 75
<212> PRT
<213> homo sapiens

<400> 510

Asn	Ala	Tyr	Ile	Ser	Gly	Tyr	Glu	Arg	Asp	Phe	Met	Thr	Ile	Gln	Ser
1				5					10					15	
Asn	Ile	Thr	Leu	Ala	Asp	Arg	Glu	Thr	Glu	Val	Phe	His	Asp	Leu	Pro
			20					25					30		
Ser	Leu	Pro	Ala	Ser	Leu	Arg	Gln	Asn	Trp	Ile	Pro	Thr	Leu	Val	Phe
		35					40					45			
Phe	Leu	Pro	Phe	Thr	Ser	Phe	Ser	Leu	Leu	Tyr	Asn	Val	Leu	Arg	Asp
	50					55					60				
Gln	Asn	Ser	His	Gln	Asn	Arg	Leu	Phe	Leu	Arg					
65					70					75					

<210> 511
<211> 67
<212> PRT
<213> homo sapiens

<400> 511

Phe	Arg	Asp	Thr	Glu	Gly	Leu	Leu	Ala	Leu	Met	Thr	Phe	Trp	Met	Gly
1				5					10					15	
Leu	Gln	Leu	Met	Thr	Ile	Leu	Ile	Leu	Glu	Glu	Arg	Thr	Leu	Leu	Ile
			20					25					30		
Phe	Ser	Pro	Ile	Ala	Leu	Leu	Arg	Arg	Ser	Thr	Ser	Tyr	Ser	Glu	Ser
		35					40					45			
Leu	His	Ile	Pro	Leu	Val	Phe	Leu	Gln	Ala	Pro	Glu	Pro	Leu	Val	Gln
	50					55					60				
Met	Leu	Tyr													
65															

<210> 512
<211> 101
<212> PRT
<213> homo sapiens

<400> 512

Ile	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Pro	Leu	Arg	His	Leu	Phe
1				5					10					15	
Asn	Asn	Cys	Arg	Asn	Pro	Lys	Glu	Leu	Ala	Ser	Asn	Leu	Glu	Val	Val
			20					25					30		
Ser	Glu	Ala	Ala	Gly	Trp	Leu	Asp	Trp	Ala	Gln	Pro	Leu	Ser	Cys	Leu
		35					40					45			
Asn	Arg	Pro	Arg	Asn	Gly	Ile	Met	Met	Thr	Met	Arg	Thr	Ser	Ile	Leu

50					55					60					
Ser 65	Ser	Ser	His	Cys	Val 70	Tyr	Tyr	Val	Phe	Ser 75	Phe	Asn	Lys	Ala	Phe 80
Val	Pro	Met	Ala	Leu 85	Glu	Leu	Gly	Gly	Arg 90	Leu	Lys	Glu	Cys	Val 95	Val
Ile	Leu	Ser	Lys 100	Met											

<210> 513
 <211> 179
 <212> PRT
 <213> homo sapiens

<400> 513

Phe 1	Gly	Thr	Met	Gly 5	Gly	Ile	Ser	Asp	Pro 10	Asp	Thr	Leu	His	Ile 15	Trp
Lys	Thr	Asn	Ser 20	Leu	Pro	Leu	Arg	Phe 25	Trp	Val	Asn	Ile	Leu 30	Lys	Asn
Pro	Gln	Phe 35	Val	Phe	Asp	Ile	Asp 40	Lys	Thr	Asp	His	Ile 45	Asp	Ala	Cys
Leu	Ser 50	Val	Ile	Ala	Gln	Ala 55	Phe	Ile	Asp	Ala	Cys 60	Ser	Ile	Ser	Asp
Leu 65	Gln	Leu	Gly	Lys	Asp 70	Ser	Pro	Thr	Asn	Lys 75	Leu	Leu	Tyr	Ala	Lys 80
Glu	Ile	Pro	Glu	Tyr 85	Arg	Lys	Ile	Val	Gln 90	Arg	Tyr	Tyr	Lys	Gln 95	Ile
Gln	Asp	Met	Thr 100	Pro	Leu	Ser	Glu	Gln 105	Glu	Met	Asn	Ala	His 110	Leu	Ala
Glu	Glu	Ser 115	Arg	Lys	Tyr	Gln	Asn 120	Glu	Phe	Asn	Thr	Asn 125	Val	Ala	Met
Ala	Glu 130	Ile	Tyr	Lys	Tyr	Ala 135	Lys	Arg	Tyr	Arg	Pro 140	Gln	Ile	Met	Ala
Ala 145	Leu	Glu	Ala	Asn	Pro 150	Thr	Ala	Arg	Arg	Thr 155	Gln	Leu	Gln	His	Lys 160
Phe	Glu	Gln	Val	Val 165	Ala	Leu	Met	Glu	Asp 170	Asn	Ile	Tyr	Glu	Cys 175	Tyr
Ser	Glu	Ala													

<210> 514
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 <212> PRT
 <213> homo sapiens

<400> 514

Asp 1	Arg	Gly	Ala	Pro 5	Ala	Leu	Thr	Pro	Gly 10	His	Leu	His	Pro	Leu 15	Pro
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Pro	Val	Pro	Arg 20	Ser	Val	Ser	Gly	Met 25	Glu	Ala	Arg	Glu	Leu 30	Val	Arg
Leu	Pro	His 35	Leu	Pro	Ser	Thr	Ala 40	Cys	Thr	Val	Pro	Thr 45	His	Leu	Leu
His	Asn 50	Val	Gln	Leu	Val	Leu 55	Leu	Pro	Arg	Ala	Pro 60	Cys	Ile	Gln	Ala
Ala 65	Lys	His	Lys	Leu	Gly 70	Glu	Arg	Arg	Pro	Pro 75	Ala	Arg	Arg	Leu	Gln 80
Pro	Arg	Asn	Ser	Thr 85	Ser	Ser	Thr	Leu	Val 90	Gln	Gly	Ala	Leu	Leu 95	Glu
Leu	Thr	Phe	Asp 100	Trp	Phe	Leu	Leu	Gln 105	Leu	Pro	Lys	Cys	Tyr 110	Leu	His
Phe	Pro	Leu 115	Thr	Arg	Arg	Gly	Ser 120	Trp	Pro	Gln	Thr	Val 125	Ser	Ser	Ser
Val	Arg 130	Phe	Leu	Leu	Leu	Gly 135	Arg	Leu	Leu	Val	Glu 140	Trp	Ala	Val	Pro
Ala 145	Pro	Trp	Gly	Ala	Leu 150	Trp	Ala	Ser	Pro	Gly 155	Ala	Gly	Arg	Val	Glu 160
Gly	Arg	Asp	Gly	Gly 165	His	Arg	Ser	Trp	Glu 170	Pro	Arg	Leu	Gln	Glu 175	Lys
Glu	Arg	Gly													

<210> 515

<211> 200

<212> PRT

<213> homo sapiens

<400> 515

Ser 1	Gly	Asp	Arg	Trp 5	Glu	Gly	Met	Glu	Val 10	Pro	Arg	Gly	Gln	Gly 15	Gly
Gly	Ala	Pro	Val 20	Ser	Glu	Ser	Ser	Pro 25	Ser	Ser	Cys	Pro	Arg 30	Pro	Ser
Arg	Leu	Cys 35	Ser	Val	Phe	Pro	Ser 40	Leu	Ser	His	Arg	His 45	Gly	Val	Glu
Asp	Gln 50	Val	Glu	Ala	Gln	Trp 55	Ala	Ser	Ile	Ser	Pro 60	Ser	Ser	Ser	Leu
Thr 65	Asn	Ser	Pro	Cys	Val 70	Ser	Gly	Leu	Thr	Val 75	Ala	Leu	Val	Asp	Val 80
Val	Leu	His	Gln	Ser 85	His	His	Leu	Leu	Lys 90	Leu	Val	Leu	Gln	Leu 95	Cys
Pro	Pro	Gly	Arg 100	Gly	Val	Gly	Leu	Gln 105	Arg	Gly	His	Asp	Leu 110	Arg	Pro
Ile	Pro	Leu 115	Gly	Val	Leu	Ile	Asn 120	Leu	Cys	His	Gly	His 125	Ile	Gly	Val

Glu	Leu	Ile	Leu	Val	Phe	Pro	Arg	Leu	Leu	Gly	Gln	Met	Gly	Ile	His
	130					135					140				
Leu	Leu	Leu	Ala	Glu	Arg	Arg	His	Val	Leu	Asp	Leu	Leu	Val	Val	Ala
145					150					155					160
Leu	His	Asp	Leu	Pro	Val	Leu	Arg	Asn	Leu	Leu	Gly	Val	Glu	Glu	Leu
				165					170					175	
Val	Gly	Trp	Arg	Ile	Leu	Ala	Gln	Leu	Gln	Val	Arg	Asp	Gly	Ala	Gly
			180					185					190		
Val	Asp	Glu	Gly	Leu	Arg	Asp	Asp								
		195					200								

<210> 516
 <211> 157
 <212> PRT
 <213> homo sapiens

<400> 516

Thr	Ser	Met	Glu	Ala	Leu	Leu	Phe	Arg	Leu	Phe	Lys	Leu	Pro	Ala	Thr
1				5					10					15	
Thr	Leu	Arg	Cys	Ile	Gly	Leu	Arg	Arg	Pro	Leu	Val	Thr	His	Thr	Leu
			20					25					30		
Arg	Arg	Lys	Cys	Glu	His	Lys	Ala	Ser	Arg	Leu	Cys	His	Gly	Gly	Cys
		35					40					45			
Cys	Cys	Thr	Leu	Glu	Pro	Cys	Val	Gly	Arg	His	Arg	Asp	Trp	Asp	Leu
	50					55					60				
Glu	Arg	Gly	Lys	Ser	Ser	Ala	Lys	Thr	Gly	Gly	Glu	Leu	His	Gly	Arg
65					70					75					80
Arg	Thr	Ala	Ala	Ala	Arg	Gly	Gly	Ser	Glu	Arg	Pro	Val	Leu	Gly	His
				85					90					95	
Arg	Arg	Arg	Asp	Pro	Asp	Ala	Gly	Gly	Leu	Arg	Gly	Gln	Asp	Gly	Glu
			100					105					110		
Ala	Leu	Gln	His	Arg	Gly	Trp	His	Ile	Pro	Gly	Ser	Glu	Thr	Leu	Pro
		115					120					125			
Gly	Arg	Gly	Gly	His	Val	Pro	Trp	Pro	Arg	Pro	Gly	Arg	Arg	His	Pro
	130					135					140				
His	His	Met	Cys	Gly	Phe	Trp	Asp	Ser	Gln	Ser	Leu	Ala			
145					150					155					

<210> 517
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 <212> PRT
 <213> homo sapiens

<400> 517

Arg	Thr	Arg	Cys	Ala	Gly	Ser	Val	Asn	Thr	Lys	Pro	Pro	Gly	Phe	Val
1				5					10					15	
Met	Ala	Ala	Ala	Ala	Ala	Arg	Trp	Asn	His	Val	Trp	Val	Gly	Thr	Glu

20										25					30				
Thr	Gly	Ile 35	Leu	Lys	Gly	Val	Asn 40	Leu	Gln	Arg	Lys	Gln 45	Ala	Ala	Asn				
Phe	Thr 50	Ala	Gly	Gly	Gln	Pro 55	Arg	Arg	Glu	Glu	Ala 60	Val	Ser	Ala	Leu				
Cys 65	Trp	Gly	Thr	Gly	Gly 70	Glu	Thr	Gln	Met	Leu 75	Val	Gly	Cys	Ala	Asp 80				
Arg	Thr	Val	Lys	His 85	Phe	Ser	Thr	Glu	Asp 90	Gly	Ile	Phe	Gln	Gly 95	Gln				
Arg	His	Cys	Pro 100	Gly	Gly	Glu	Gly	Met 105	Phe	Arg	Gly	Leu	Ala 110	Gln	Ala				
Asp	Gly	Thr 115	Leu	Ile	Thr	Cys	Val 120	Asp	Ser	Gly	Ile	Leu 125	Arg	Val	Trp				
His	Asp 130	Lys	Asp	Lys	Asp	Thr 135	Ser	Ser	Asp	Pro	Leu 140	Leu	Glu	Leu	Arg				
Val 145	Gly	Pro	Gly	Val	Cys 150	Arg	Met	Arg	Gln	Asp 155	Pro	Ala	His	Pro	His 160				
Val	Val	Ala	Thr	Gly 165	Gly	Lys	Glu	Asn	Ala 170	Leu	Lys	Ile	Trp	Asp 175	Leu				
Gln	Gly	Ser	Glu 180	Glu	Pro	Val	Phe	Arg 185	Ala	Lys	Asn	Val	Arg 190	Asn	Asp				
Trp	Leu	Asp 195	Leu	Arg	Val	Pro	Ile 200	Trp	Asp	Gln	Asp	Ile 205	Gln	Phe	Leu				
Pro	Gly 210	Ser	Gln	Lys	Leu	Val 215	Thr	Cys	Thr	Gly	Tyr 220	His	Gln	Val	Arg				
Val 225	Tyr	Asp	Pro	Ala	Ser 230	Pro	Gln	Arg	Arg	Pro 235	Val	Leu	Glu	Thr	Thr 240				
Tyr	Gly	Glu	Tyr	Pro 245	Leu	Thr	Ala	Met	Thr 250	Leu	Thr	Pro	Gly	Gly 255	Asn				
Ser	Val	Ile	Val 260	Gly	Asn	Thr	His	Gly 265	Gln	Leu	Ala	Glu	Ile 270	Asp	Leu				
Arg	Gln	Gly 275	Arg	Leu	Leu	Gly	Cys 280	Leu	Lys	Gly	Leu	Ala 285	Gly	Ser	Val				
Arg	Gly 290	Leu	Gln	Cys	His	Pro 295	Ser	Lys	Pro	Leu	Leu 300	Ala	Ser	Cys	Gly				
Leu 305	Asp	Arg	Val	Leu	Arg 310	Ile	His	Arg	Ile	Gln 315	Asn	Pro	Arg	Gly	Leu 320				
Glu	His	Lys	Val	Tyr 325	Leu	Lys	Ser	Gln	Leu 330	Asn	Cys	Leu	Leu	Leu 335	Ser				
Gly	Arg	Asp	Asn 340	Trp	Glu	Asp	Glu	Pro 345	Gln	Glu	Pro	Gln	Glu 350	Pro	Asn				
Lys	Val	Pro	Leu	Glu	Asp	Thr	Glu	Thr	Asp	Glu	Leu	Trp	Ala	Ser	Leu				

		355						360					365				
Glu	Ala	Ala	Ala	Lys	Arg	Lys	Leu	Ser	Gly	Leu	Glu	Gln	Pro	Gln	Gly		
	370					375					380						
Ala	Leu	Gln	Thr	Arg	Arg	Arg	Lys	Lys	Lys	Arg	Pro	Gly	Ser	Thr	Ser		
385					390					395					400		
Pro																	

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 <213> homo sapiens

<400> 518

Ser	Trp	Glu	Lys	Leu	Tyr	Val	Leu	Val	Pro	Asp	Gly	Asn	Pro	Gln	Val		
1				5					10					15			
Gln	Pro	Val	Ile	Pro	His	Val	Leu	Gly	Pro	Glu	His	Arg	Phe	Leu	Arg		
			20					25					30				
Ala	Leu	Gln	Val	Pro	Tyr	Leu	Gln	Ser	Ile	Leu	Phe	Pro	Thr	Cys	Gly		
		35					40					45					
Asn	His	Met	Gly	Val	Cys	Trp	Val	Leu	Ala	His	Pro	Thr	His	Pro	Arg		
	50					55					60						
Ala	His	Ser	Gln	Phe	Gln	Glu	Trp	Val	Arg	Gly	Cys	Val	Leu	Val	Leu		
65					70					75					80		
Val	Met	Pro	Asp	Ser	Glu	Asn	Pro	Arg	Ile	His	Thr	Cys	Asp	Glu	Gly		
				85					90					95			
Ala	Val	Gly	Leu	Gly	Glu	Ala	Thr	Glu	His	Ala	Leu	Pro	Ala	Arg	Ala		
			100					105					110				
Val	Ser	Leu	Thr	Leu	Glu	Tyr	Ala	Ile	Leu	Gly	Ala	Glu	Val	Leu	His		
	115						120					125					
Arg	Pro	Val	Arg	Ala	Ala	His	Gln	His	Leu	Gly	Leu	Ala	Ala	Gly	Ala		
	130					135					140						
Pro	Thr	Gln	Gly	Ala	His	Cys	Leu	Leu	Ala	Pro	Arg	Leu	Ser	Ser	Gly		
145					150					155					160		
Arg	Glu	Val	Arg	Arg	Leu	Phe	Ser	Leu	Lys	Ile	Tyr	Pro	Phe	Gln	Asp		
				165					170					175			
Pro	Ser	Leu	Gly	Ala	Asp	Pro	His	Met	Val	Pro	Ala	Cys	Ser	Ser	Ser		
			180					185					190				
Arg	His	Asp	Lys	Ala	Trp	Arg	Leu	Cys	Val	His	Thr	Ser	Gly	Ala	Ala		
	195						200					205					
Cys	Ala	Ser	Pro	Ala	Gly	Val	Glu	Val	Arg	Cys	Thr	Ala	Val				
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Leu	Thr	Tyr	Leu	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Phe	Leu	Gly	Arg	Ser
1				5					10					15	
Leu	Gly	Phe	Ile	Arg	Ser	Val	Gly	Thr	Leu	Phe	Arg	Ser	Glu	Ala	Pro
			20					25					30		
Pro	Ser	His	Gly	Val	Gly	Asp	Ser	Gly	Gly	Arg	Gly	Asn	Pro	Ser	Glu
		35					40					45			
His	Pro	Gly	Gly	Cys	Val	Val	Ser	Met	Tyr	Phe	Ala	Leu	Pro	His	Leu
		50				55					60				
Phe	His	Gly	Val	Pro	Cys	Gln	Gly	Gln	Ala	Leu	Ile	Cys	Gly	Glu	Gly
65					70					75				80	
Ser	Lys	Gln	Arg	Arg	Arg	Pro	Phe	Arg	Gly	Gly	Glu	Arg	Ala	Val	Ala
				85					90					95	
Pro	Arg	Thr	Pro	Ser	Pro	Ala	His	Asp	Ile	Pro	Glu	Lys	Glu	Thr	Lys
			100					105					110		
Ile	Lys	Pro	Arg	Gly	Leu	Ser	Thr								
		115					120								

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Pro 1	Leu	Leu	Lys	Gly 5	Lys	Lys	Leu	Ser	Ala 10	Ala	Leu	Thr	Asn	Leu 15	Ser
Phe	Phe	Phe	Phe 20	Phe	Phe	Phe	Phe	Phe 25	Gly	Lys	Lys	Pro	Trp 30	Leu	Tyr
Ser	Leu	Cys 35	Gly	Asp	Thr	Val	Pro 40	Phe	Arg	Gly	Pro	Ser 45	Gln	Pro	Trp
Gly	Gly 50	Gly	Gln	Trp	Trp	Ala 55	Trp	Glu	Ser	Gln	Arg 60	Ala	Ser	Trp	Arg
Val 65	Arg	Arg	Leu	His	Val 70	Phe	Cys	Ser	Ser	Pro 75	Ser	Phe	Pro	Trp	Gly 80
Pro	Leu	Pro	Gly	Ser 85	Ser	Thr	Asn	Met	Trp 90						

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Asn 1	Lys	Ala	Pro	Gly 5	Pro	Phe	Tyr	Val	Gly 10	Ala	Pro	Leu	Lys	Tyr 15	Gly
Met	Val	Val	Gly 20	Arg	Glu	Ala	Val	Ala 25	Gln	Gln	Ser	Leu	Ser 30	Pro	Asp
Tyr	Gln	Leu 35	Trp	Gly	Gly	Phe	Gln 40	Gly	Ala	Arg	Ser	Arg 45	Leu	Gly	Ser
Ser	Ser 50	His	Arg	His	Val	Gly 55	Gly	Gly	Arg	Lys	Tyr 60	Leu	Gln	Gly	Gly
Thr 65	Val	Ser	Glu	Glu	Gln 70	Asp	Gly	Arg	Gly	Phe 75	Ser	Ala	Cys	Tyr	Gly 80
Ile	Leu	Phe	Lys	Glu 85	Met	Gly	Val	Lys	Pro 90	Gly	Thr	Val	Ala	His 95	Ala

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Thr 1	Pro	Ala	Leu	Val 5	Gln	Arg	Phe	Arg	Glu 10	Gly	Gly	Ser	Gly	Ala 15	Pro
Glu	Gln	Ala	Glu 20	Cys	Val	Glu	Leu	Leu 25	Leu	Ala	Leu	Gly	Glu 30	Pro	Ala
Glu	Glu	Leu 35	Cys	Glu	Glu	Phe	Leu 40	Ala	His	Ala	Arg	Gly 45	Arg	Leu	Glu
Lys	Glu 50	Leu	Arg	Asn	Leu	Glu 55	Ala	Glu	Leu	Gly	Pro 60	Ser	Pro	Pro	Ala

Pro 65	Asp	Val	Leu	Glu	Phe 70	Thr	Asp	His	Gly	Gly 75	Ser	Gly	Phe	Val	Gly 80
Gly	Leu	Cys	Gln	Val 85	Ala	Ala	Ala	Tyr	Gln 90	Glu	Leu	Phe	Ala	Ala 95	Gln
Gly	Pro	Ala	Gly 100	Ala	Glu	Lys	Leu	Ala 105	Ala	Phe	Ala	Arg	Gln 110	Leu	Gly
Ser	Arg	Tyr 115	Phe	Ala	Leu	Val	Glu 120	Arg	Arg	Leu	Ala	Gln 125	Glu	Gln	Gly
Gly	Gly 130	Asp	Asn	Ser	Leu	Leu 135	Val	Arg	Ala	Leu	Asp 140	Arg	Phe	His	Arg
Arg 145	Leu	Arg	Ala	Pro	Gly 150	Ala	Leu	Leu	Ala	Ala 155	Ala	Gly	Leu	Ala	Asp 160
Ala	Ala	Thr	Glu	Ile 165	Val	Glu	Arg	Val	Ala 170	Arg	Glu	Arg	Leu	Gly 175	His
His	Leu	Gln	Gly 180	Leu	Arg	Ala	Ala	Phe 185	Leu	Gly	Cys	Leu	Thr 190	Asp	Val
Arg	Gln	Ala 195	Leu	Ala	Ala	Pro	Arg 200	Val	Ala	Gly	Lys	Glu 205	Gly	Pro	Gly
Leu	Ala 210	Glu	Leu	Leu	Ala	Asn 215	Val	Ala	Ser	Ser	Ile 220	Leu	Ser	His	Ile
Lys 225	Ala	Ser	Leu	Ala	Ala 230	Val	His	Leu	Phe	Thr 235	Ala	Lys	Glu	Val	Ser 240
Phe	Ser	Asn	Lys	Pro 245	Tyr	Phe	Arg	Gly	Glu 250	Phe	Cys	Ser	Gln	Gly 255	Val
Arg	Glu	Gly	Leu 260	Ile	Val	Gly	Phe	Val 265	His	Ser	Met	Cys	Gln 270	Thr	Ala
Gln	Ser	Phe 275	Cys	Asp	Ser	Pro	Gly 280	Glu	Lys	Gly	Gly	Ala 285	Thr	Pro	Pro
Ala	Leu 290	Leu	Leu	Leu	Leu	Ser 295	Arg	Leu	Cys	Leu	Asp 300	Tyr	Glu	Thr	Ala
Thr 305	Ile	Ser	Tyr	Ile	Leu 310	Thr	Leu	Thr	Asp	Glu 315	Gln	Phe	Leu	Val	Gln 320
Asp	Gln	Phe	Pro	Val 325	Thr	Pro	Val	Ser	Thr 330	Leu	Cys	Ala	Glu	Ala 335	Arg
Glu	Thr	Ala	Arg 340	Arg	Leu	Leu	Thr	His 345	Tyr	Val	Lys	Val	Gln 350	Gly	Leu
Val	Ile	Ser 355	Gln	Met	Leu	Arg	Lys 360	Ser	Val	Glu	Thr	Arg 365	Asp	Trp	Leu
Ser	Thr 370	Leu	Glu	Pro	Arg	Asn 375	Val	Arg	Ala	Val	Met 380	Lys	Arg	Val	Val
Glu 385	Asp	Thr	Thr	Ala	Ile 390	Asp	Val	Gln	Val	Gly 395	Leu	Leu	Tyr	Glu	Glu 400

Gly	Val	Arg	Lys	Ala 405	Gln	Ser	Ser	Asp	Ser 410	Ser	Lys	Arg	Thr	Phe 415	Ser
Val	Tyr	Ser	Ser 420	Ser	Arg	Gln	Gln	Gly 425	Arg	Tyr	Ala	Pro	Ser 430	Tyr	Thr
Pro	Ser	Ala 435	Pro	Met	Asp	Thr	Asn 440	Leu	Leu	Ser	Asn	Ile 445	Gln	Lys	Leu
Phe	Ser 450	Glu	Arg	Ile	Asp	Val 455	Phe	Ser	Pro	Val	Glu 460	Phe	Asn	Lys	Val
Ser 465	Val	Leu	Thr	Gly	Ile 470	Ile	Lys	Ile	Ser	Leu 475	Lys	Thr	Leu	Ala	Gly 480
Ser	Val	Cys	Gly	Leu 485	Arg	Thr	Phe	Leu	Ala 490	Leu	Cys	Gly	Leu	Gln 495	Gln

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Cys 1	Gly	Ser	Gly	Trp 5	Ser	Trp	Pro	His	Trp 10	Pro	Ala	Thr	Arg	Pro 15	Gly
Gln	Gly	Pro	Pro 20	Ser	Gln	Pro	Arg	Glu 25	Val	Leu	Pro	Ala	Pro 30	Gly	Gly
Arg	Leu	Ser 35	Gly	Ser	Pro	Gly	Arg 40	Pro	Pro	Gly	Asp	Pro 45	Ala	Gly	Gly
Gly	Pro 50	Gly	Ala	Arg	Gly	Pro 55	Leu	Val	Pro	Arg	Ser 60	Pro	Trp	Gln	Arg
Leu 65	Arg	Ala	Arg	Gln	Arg 70	Pro	Ala	Gly	Pro	Arg 75	Glu	Pro	Ala	Ser	Ala 80
Gly	Gly	Ser	Gly	Pro 85	Ala	Pro	Ala	Pro	Ala 90	Val	Ser	Cys	His	His 95	His
Pro	Ala	Pro	Ala 100	Pro	Ala	Ala	Ala	Pro 105	Pro	Ala	Gln	Asn	Ser 110	Gly	Cys
Pro	Ala	Ala 115	Gly	Arg	Arg	Pro	Pro 120	Ala	Ser	Arg	His	Leu 125	Leu	Gly	Pro
Gly	Pro 130	Gln	Thr	Ala	Pro	Gly 135	Arg	Pro	Pro	Pro	Pro 140	Gly	Arg	Gly	Arg
Pro 145	Arg	Ser	His	Cys	Leu 150	His	Gly	Arg							

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Tyr 1	Asp	Gln	Ala	Leu 5	His	Leu	His	Val	Val 10	Gly	Gln	Gln	Pro	Pro 15	Arg
Arg	Phe	Pro	Gly 20	Leu	Cys	Thr	Gln	Arg 25	Ala	His	Gly	Arg	His 30	Trp	Glu
Leu	Ile	Leu 35	His	Gln	Lys	Leu	Phe 40	Ile	Ser	Glu	Ser	Glu 45	Asp	Val	Gly
Asp	Gly 50	Gly	Arg	Leu	Val	Val 55	Gln	Ala	Glu	Ala	Gly 60	Glu	Gln	Gln	Glu
Gln 65	Gly	Arg	Trp	Cys	Gly 70	Thr	Pro	Leu	Leu	Pro 75	Arg	Ala	Val	Ala	Glu 80
Ala	Leu	Ser	Arg	Leu 85	Ala	His	Arg	Val	Asp 90	Glu	Ala	His	Asp	Glu 95	Ala
Leu	Thr	Asp	Thr 100	Leu	Thr	Ala	Glu	Leu 105	Thr	Pro	Glu	Val	Gly 110	Leu	Val
Gly	Glu	Gly 115	His	Leu	Phe	Gly	Gly 120	Glu	Lys	Val	His	Cys 125	Cys	Gln	Arg
Gly	Leu 130	Asn	Val	Ala	Gln	Asp 135	Gly	Ala	Gly	His	Ile 140	Gly	Gln	Gln	Leu
Gly 145	Gln	Ala	Arg	Ala	Leu 150	Leu	Pro	Ser	His	Ala 155	Arg	Cys	Cys	Gln	Arg 160
Leu	Ala	Asp	Val	Cys 165	Gln	Ala	Ala	Gln	Glu 170	Gly	Arg	Pro	Glu	Thr 175	Leu
Gln	Val	Val	Ala 180	Gln	Ala	Leu	Ala	Gly 185	His	Ser	Phe	His	Asp 190	Leu	Arg
Gly	Ser	Val 195	Cys	Glu	Pro	Gly	Ser 200	Gly	Gln	Gln	Gly	Pro 205	Gly	Ser	Pro
Gln 210	Ala	Pro	Val	Glu	Ala	Val 215	Gln	Arg	Pro	His	Gln 220	Gln			

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Pro 1	Ser	Ile	Leu	Ile 5	Pro	Met	Thr	Pro	Gly 10	Gly	Phe	Phe	Ser	Val 15	Met
Val	Arg	Ala	Lys 20	Thr	Gly	Ser	Thr	His 25	Arg	Cys	Ser	Pro	Ala 30	Val	Tyr
Pro	Leu	Met 35	Arg	Arg	Ile	Pro	Cys 40	Trp	Arg	Ile	Leu	Ile 45	Gly	Arg	Gln
Glu 50	Thr	Thr	Gly												

<210> 535

Study	Year	Country	Sample Size	Study Design	Intervention	Control	Outcome Measure	Effect Size	Quality of Evidence
1	2010	USA	100	Randomized Controlled Trial	Hand hygiene	Standard care	Reduction in infection rates	0.15	High
2	2012	UK	200	Randomized Controlled Trial	Antibiotic stewardship	Standard care	Reduction in antibiotic resistance	0.20	High
3	2015	Canada	150	Randomized Controlled Trial	Vaccination	Standard care	Reduction in disease incidence	0.10	High
4	2018	Australia	300	Randomized Controlled Trial	Screening	Standard care	Reduction in mortality	0.05	High
5	2020	France	400	Randomized Controlled Trial	Telemedicine	Standard care	Reduction in hospital admissions	0.08	High

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[illegible]

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Ser 1	Gly	Cys	Val	Pro 5	Ser	His	Glu	Glu	Asp 10	Ser	Met	Leu	Glu	Asp 15	Ser
His	Arg	Gln	Ala 20	Arg	Asn	His	Arg	Leu 25	Val	Ile	Ile	Arg	Asn 30	Pro	Val
Val	His	Leu 35	Gly	Gln	Ala	Pro	Leu 40	Ala	Thr	Pro	His	Arg 45	Pro	Gln	Ile
Arg	Ser 50	Leu	Thr	Ile	Gln	Ser 55									

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[illegible]

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Glu 1	Pro	Ala	Asp	Ser 5	Gln	Ala	Arg	Gly	Arg 10	Gln	Cys	Leu	Leu	Leu 15	Leu
His	Gln	Val	Gln 20	Gly	Ile	Trp	Leu	Lys 25	Ala	Cys	Ile	Phe	Pro 30	Gly	His
Lys	Leu	Pro 35	Glu	Pro	Leu	Lys	Trp 40	Glu	Ala	Arg	Gln	Phe 45	Gln	Thr	Asn
Leu	Phe 50	Ser	Thr	His	His	Ser 55	Thr	Phe	Lys	Val	Cys 60	Leu	Leu	Leu	Leu
Pro 65	Val	His	Pro	Pro	Ser 70	Leu	Gln	Phe	Phe	His 75	Ser	Leu	Thr	Ser	Glu 80
Arg	Val	Pro	Gly	Gly 85	Ser	Met	Val	Asn	Lys 90	Leu	Thr	Cys	Met	Leu 95	Gln
Lys	Lys	Lys	Lys 100	Lys											

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Tyr 1	Ser	Leu	Cys	Ser 5	Gln	Cys	Val	Ser	Ala 10	Pro	Leu	Thr	Leu	Asn 15	Arg
His	Arg	Ser	Arg 20	Arg	Lys	Arg	Lys	Trp 25	Trp	Ile	Ala	Gln	Leu 30	Glu	Pro
Gly	Asp	Cys 35	Tyr	Asp	Cys	Leu	Asp 40	Leu	Cys	Gly	His	Arg 45	Ala	Ser	Gln
Pro	Pro 50	Gln	Thr	Leu	Ser	Leu 55	Glu	Cys	Gly	Gly	Thr 60	Gln	Cys	Arg	Phe
Pro 65	Gly	Gly	Leu	Ser	Pro 70	Arg	Pro	Ser	Pro	Cys 75	Pro	Pro	Ser	Ser	Ser 80
Gly	Leu	Leu	Phe	Tyr 85	Arg	Phe	Phe	Leu	Val 90	Ser	Phe	Leu	Gly	Leu 95	Leu
Phe	Thr	Glu	Gly 100	Thr	Ala	Ala	Leu	Gly 105	Phe	Leu	Val	Thr	Ser 110	Ala	Leu
Leu	Gly	Ser 115	Asp	Gly	Ser	Ala	Ser 120	Ala	Ser	Trp	Asp	Leu 125	Gly	Met	Gly
Thr 130	Met	Met	Ala	Ser	Thr	Gln 135	Met	Ser	Trp	Lys	Met 140	Ala	Pro	Arg	Lys

Ser 145	Pro	Tyr	Arg	Ser	Arg 150	Phe	Ser	Arg	Lys	Val 155	Gly	Ser	Gly	Thr	Ser 160
Gly	Gly	Glu	Lys	Ser 165	Arg	Ser	Glu	Ala	Met 170	Ala	Gln	Val	Ala	Cys 175	Cys
Leu	Thr	Ser	Leu 180	Leu	Thr	His	His	Ser 185	Leu	Glu	Pro	Thr	Pro 190	Ala	Pro
Pro	Arg	Arg 195	Ser	Pro	Arg										

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Lys 1	Lys	Asn	Ser	Ser 5	Ala	Leu	Ile	Phe	Leu 10	Glu	Glu	Ala	Ala	Asp 15	Phe
Gly	Cys	Gln	Ile	Ser 20	Leu	Arg	Asn	Gly 25	His	Phe	Leu	Arg	Cys 30	Phe	Phe
Leu	Thr	Glu 35	Ser	Val	Asp	Lys	Leu 40	Ile	Lys	Arg	Leu	Ser 45	His	Phe	Lys
Ile	Thr 50	Pro	Lys	Ser	Ser 55	Thr	Val	Phe	Phe	Phe 60	Phe	Ser	Phe	Cys	
Phe 65	Lys	Ile	Thr	Asn	Gln 70	Val	Arg	Ser	Pro	Thr 75	Ser	Ser	Ser	Met	Asn 80
Ser	Phe	Val	Thr	Glu 85	Leu	Leu	Ser	Val	Cys 90	Ser	Pro	His	Cys	Ala 95	Leu
Asn	Thr	Val	Ser 100	Ala	Ala	Pro	Val	Cys 105	Pro	Leu	Phe	Arg	Lys 110	Glu	Ser
Ile	Phe	Asn 115	Thr	Phe	Thr	Ile	Cys 120	Thr	Pro	Trp	Asn	Leu 125	His	Met	Leu
Thr	Ser 130	Tyr	Tyr	Lys	Pro	Thr 135	His	Pro	Gln	Leu	Ser 140	Ser	Gly	Thr	Gly
His 145	Pro	Leu													

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Lys 1	Asn	Asp	Arg	Phe 5	Pro	Trp	Thr	Ser	Leu 10	Pro	Gly	Leu	Lys	Gly 15	Ala
Leu	Ile	Lys	Leu 20	Phe	Thr	Glu	His	Val 25	Ala	Glu	Lys	His	Ile 30	Tyr	Gly
Leu	Met	Pro	Leu	Leu	Leu	Glu	Ala	Gln	Ser	Thr	Pro	Phe	Gln	Val	Thr

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      35                                40                                45
Pro  Ser  Thr  Met  Ala  Asn  Ile  Val  Lys  Gly  Leu  Tyr  Thr  Leu  Arg  Pro
    50
Glu  Trp  Val  Gln  Met  Ala  Pro  Thr  Leu  Phe  Ser  Lys  Phe  Ile  Pro  Asn
  65    70    80
Ile  Leu  Pro  Pro  Ala  Val  Glu  Ser  Glu  Leu  Ser  Glu  Tyr  Ala  Ala  Gln
    85    95
Asp  Gln  Lys  Phe  Gln  Arg  Glu  Leu  Ile  Gln  Asn  Gly  Phe  Thr  Arg  Gly
    100    105    110
Asp  Gln  Ser  Arg  Lys  Arg  Ala  Gly  Asp  Glu  Leu  Ala  Tyr  Asn  Ser  Ser
    115    120    125
Ser  Ala  Cys  Ala  Ser  Ser  Arg  Gly  Tyr  Arg
    130    135

<210> 542
<211> 179
<212> PRT
<213> homo sapiens

<400> 542
Lys  Ala  Cys  Ile  Pro  Ser  Asp  Gln  Ser  Gly  Phe  Arg  Trp  Leu  Gln  Leu
  1      5
Tyr  Phe  Leu  Asn  Leu  Phe  Gln  Thr  Phe  Ser  Leu  Arg  Arg  Trp  Asn  Leu
    20    25
Asn  Phe  Leu  Asn  Met  Leu  Leu  Lys  Ile  Arg  Asn  Phe  Lys  Glu  Asn  Leu
    35    40
Tyr  Arg  Met  Val  Leu  Gln  Gly  Val  Thr  Ser  Pro  Gly  Arg  Glu  Leu  Gly
    50    55
Met  Ser  Trp  Leu  Ile  Ile  Ala  Arg  Gln  His  Val  Gln  Val  Pro  Gly  Gly
  65    70    80
Thr  Asp  Ser  Glu  Cys  Ile  Glu  Tyr  Ala  Phe  Leu  Pro  Glu  Lys  Arg  Thr
    85    90    95
His  Trp  Ser  Cys  Arg  Asp  Cys  Ile  Gln  Ser  Thr  Val  Gly  Ala  Ala  His
    100    105    110
Thr  Gln  Glu  Leu  Cys  His  Lys  Ala  Val  His  Gly  Arg  Gly  Cys  Trp  Thr
    115    120
Ser  Tyr  Leu  Val  Cys  Asn  Phe  Lys  Thr  Lys  Thr  Lys  Lys  Lys  Lys  Asn
    130    135    140
Ser  Ala  Ala  Arg  Leu  Gly  Gly  Asp  Phe  Glu  Met  Gly  Gln  Ser  Phe  Asn
  145    150    155
Glu  Phe  Ile  Tyr  Arg  Phe  Cys  Glu  Glu  Lys  Ala  Ser  Gln  Lys  Val  Thr
    165    170    175

Ile  Ser  Lys

<210> 543

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<211> 92
 <212> PRT
 <213> homo sapiens

<400> 543

Ile	Gln	Phe	Leu	Glu	Ala	Ala	Phe	Ala	Val	Phe	Leu	His	Cys	Met	Arg
1				5					10					15	
Phe	Gly	Asn	Glu	Cys	Arg	Asn	Leu	Leu	Trp	Ala	Phe	Thr	Phe	Leu	Cys
			20					25					30		
Gln	Phe	Gly	Phe	Tyr	Cys	Leu	Asn	Leu	Met	Leu	Thr	Trp	Arg	Gly	Asp
		35					40					45			
Gly	Gly	Gln	Cys	Cys	Cys	Gly	Ala	Ser	Ser	Glu	Ser	Val	Cys	Gly	Glu
	50					55					60				
Leu	Cys	Cys	Ala	Asp	Val	Ala	Val	Gly	Gly	Gln	Val	Arg	Gly	Ser	Ala
65					70					75					80
Pro	Ser	Trp	Lys	Lys	Ser	Cys	Leu	Arg	Val	Tyr	Val				
				85					90						

<210> 544
 <211> 99
 <212> PRT
 <213> homo sapiens

<400> 544

Lys	Pro	Asn	Trp	His	Arg	Lys	Val	Asn	Ala	His	Ser	Lys	Phe	Leu	His
1				5					10					15	
Ser	Phe	Pro	Asn	Arg	Ile	Gln	Cys	Lys	Lys	Thr	Ala	Lys	Ala	Ala	Ser
			20					25					30		
Arg	Asn	Cys	Ile	Tyr	Trp	Pro	Leu	Pro	Glu	Gln	Gln	Ala	Ala	Met	Pro
		35					40					45			
Ala	Pro	Trp	Pro	Pro	Glu	Leu	Asp	Ala	Cys	Cys	Ala	Asp	Val	Leu	Thr
	50					55					60				
Leu	Met	Arg	Met	Leu	Gly	Tyr	Gly	Ser	Asp	Ser	Glu	Glu	Ile	His	Leu
65					70					75					80
Ser	Tyr	Ser	Ser	Leu	Glu	Arg	Ser	Ser	Cys	Val	Phe	Asn	Met	Lys	His
				85					90					95	

Phe Ile Trp

<210> 545
 <211> 96
 <212> PRT
 <213> homo sapiens

<400> 545

Gln	Ser	Gln	Asn	Thr	Lys	Val	Phe	Val	Pro	Ile	Arg	Ile	Tyr	Thr	Asp
1				5					10					15	
Pro	Leu	Thr	Lys	Val	Leu	Leu	Ile	Met	Gln	Phe	Ala	Ser	Ser	Pro	Ser
			20					25					30		

Ser	Trp	Leu	Gly	Ser	Ser	Pro	Ile	Trp	His	Asp	His	Ile	Lys	Arg	Thr
		35					40					45			
Pro	Ser	Asp	Met	Ile	Ser	Ser	Lys	Lys	Val	Pro	Ser	Leu	Leu	Pro	Asp
	50					55					60				
His	Gln	Arg	Pro	His	Gln	His	Asn	Thr	Thr	Leu	Arg	Ile	Gln	Ile	His
65					70					75					80
Cys	Trp	Pro	His	Asn	Ser	Thr	Val	Pro	His	Leu	Leu	Ser	Arg	Ser	Ala
				85					90					95	

<210> 546
 <211> 108
 <212> PRT
 <213> homo sapiens

<400> 546

Gly	Arg	Asp	Ala	Gly	Gln	Ser	Glu	Pro	Trp	Leu	Ser	Thr	Ser	Gly	Cys
1				5					10					15	
Cys	Ala	Trp	Gly	Gly	Cys	Ala	Pro	Gly	Ala	Arg	Gly	Cys	Trp	Gly	Pro
			20					25					30		
Gly	Pro	Pro	Ser	Leu	Gly	Val	Gly	Arg	Lys	Pro	Gly	Cys	Arg	Val	Ser
		35					40					45			
Ala	Ser	Ser	Val	Pro	Glu	Arg	Trp	Ile	Ala	Trp	Ser	Pro	Arg	Pro	Ser
	50					55					60				
Glu	Ala	Ser	Ala	Thr	Phe	Arg	Gly	Ala	Pro	Lys	Ser	Ile	Leu	Thr	Ala
65					70					75					80
Arg	Leu	Trp	Ala	Ser	Ala	Trp	Arg	Pro	Gln	His	Arg	Gly	Ser	Gln	Asn
				85					90					95	
Glu	Arg	Pro	Trp	Ser	Ser	Ser	Met	Lys	Thr	Ser	Gly				
			100					105							

<210> 547
 <211> 117
 <212> PRT
 <213> homo sapiens

<400> 547

Pro	Gly	Arg	Arg	Ala	Lys	Arg	Ala	Met	Ala	Val	Tyr	Val	Gly	Met	Leu
1				5					10					15	
Arg	Leu	Gly	Arg	Leu	Cys	Ala	Gly	Ser	Ser	Gly	Val	Leu	Gly	Ala	Arg
			20					25					30		
Ala	Ala	Leu	Ser	Arg	Ser	Trp	Gln	Glu	Ala	Arg	Leu	Gln	Gly	Val	Arg
		35					40					45			
Phe	Leu	Ser	Ser	Arg	Glu	Val	Asp	Arg	Met	Val	Ser	Thr	Pro	Ile	Gly
50						55					60				
Gly	Leu	Ser	Tyr	Val	Gln	Gly	Cys	Thr	Lys	Lys	His	Leu	Asn	Ser	Lys
65					70					75					80

Thr	Val	Gly	Gln	Cys 85	Leu	Glu	Thr	Thr	Ala 90	Gln	Arg	Val	Pro	Glu 95	Arg
Glu	Ala	Leu	Val 100	Val	Leu	His	Glu	Asp 105	Val	Arg	Leu	Thr	Phe 110	Ala	Gln
Leu	Lys	Glu 115	Glu	Trp											

<210> 548
 <211> 117
 <212> PRT
 <213> homo sapiens

<400> 548

Pro 1	Leu	Leu	Leu	Glu 5	Leu	Gly	Lys	Gly	Gln 10	Pro	Asp	Val	Phe	Met 15	Glu
Asp	Asp	Gln	Gly 20	Leu	Ser	Phe	Trp	Asp 25	Pro	Leu	Cys	Cys	Gly 30	Leu	Gln
Ala	Leu	Ala 35	His	Ser	Leu	Ala	Val 40	Lys	Met	Leu	Phe	Gly 45	Ala	Pro	Leu
Asn 50	Val	Ala	Glu	Ala	Ser	Asp 55	Gly	Arg	Gly	Asp	His 60	Ala	Ile	His	Leu
Ser 65	Gly	Thr	Glu	Glu	Ala 70	Asp	Thr	Leu	Gln	Pro 75	Gly	Phe	Leu	Pro	Thr 80
Pro	Arg	Glu	Gly	Gly 85	Pro	Gly	Pro	Gln	His 90	Pro	Arg	Ala	Pro	Gly 95	Ala
Gln	Pro	Pro	Gln 100	Ala	Gln	His	Pro	Asp 105	Val	Asp	Ser	His	Gly 110	Ser	Leu
Cys	Pro	Ala 115	Ser	Arg											

<210> 549
 <211> 68
 <212> PRT
 <213> homo sapiens

<400> 549

Arg 1	Leu	Ser	Gly	Pro 5	Ala	Ala	Asn	Pro	Arg 10	Gly	Ala	Ala	Gly	Trp 15	Arg
Ala	Ala	Gly	Ala 20	Gln	Glu	Leu	Gly	Met 25	Ser	Tyr	Lys	Pro	Met 30	Arg	Pro
Trp	Leu	Pro 35	Ser	Ser	Thr	Pro	Trp 40	Ser	Ala	Arg	His	Pro 45	Leu	Gly	Pro
Gly	Ala 50	Pro	Arg	Phe	Pro	Asp 55	Arg	Glu	Ala	Cys	Ala 60	Cys	Ala	Val	Arg
Gly 65	Cys	Ser	Val												

<210> 550

<211> 68
 <212> PRT
 <213> homo sapiens

<400> 550

Gly 1	His	Cys	Ser	Pro 5	Ala	Arg	Arg	Thr	Arg 10	Thr	Pro	Pro	Cys	Gln 15	Gly
Thr	Gly	Val	Pro 20	Arg	Ala	Pro	Gly	Gly 25	Ala	Trp	Gln	Thr	Arg 30	Gly	Cys
Cys	Trp	Ala 35	Ala	Arg	Gly	Ala	Trp 40	Val	Cys	Arg	Thr	Ser 45	Pro	Thr	Pro
Gly	Arg 50	Gln	Arg	His	Ala	Ser 55	Arg	Pro	Leu	Leu	Gly 60	Gly	Trp	Leu	Arg
Gly 65	Arg	Ser	Ala												

<210> 551
 <211> 68
 <212> PRT
 <213> homo sapiens

<400> 551

Asp 1	Thr	Ala	Ala	Pro 5	His	Gly	Ala	Arg	Ala 10	Arg	Leu	Pro	Val	Arg 15	Glu
Pro	Gly	Cys	Pro 20	Gly	Pro	Gln	Gly	Val 25	Pro	Gly	Arg	Pro	Gly 30	Gly	Ala
Ala	Gly	Gln 35	Pro	Gly	Ala	His	Gly 40	Phe	Val	Gly	His	Pro 45	Gln	Leu	Leu
Gly	Ala 50	Ser	Gly	Thr	Pro	Ala 55	Gly	Arg	Ser	Ser	Gly 60	Val	Gly	Cys	Gly
Ala 65	Ala	Gln	Pro												

<210> 552
 <211> 32
 <212> PRT
 <213> homo sapiens

<400> 552

Ser 1	Pro	Ile	Ser	Ile 5	Thr	Glu	Thr	Gln	Gln 10	Phe	Ser	Asn	Asn	Leu 15	Ile
His	Thr	Ile	Thr 20	Cys	Leu	Leu	Arg	Met 25	Ala	Leu	Tyr	Leu	Phe 30	Ser	Leu

<210> 553
 <211> 33
 <212> PRT
 <213> homo sapiens

<400> 553

Ile	Thr	Leu	Gln	Pro	Ile	Ser	Gln	Asn	Met	Phe	Leu	Leu	Leu	Asn	Asn
1				5					10					15	
Thr	Gln	Leu	Phe	Tyr	Leu	Cys	Val	Leu	Phe	Met	Pro	Asp	His	Gln	Tyr
			20					25					30		

Gln

<210> 554
 <211> 43
 <212> PRT
 <213> homo sapiens

<400> 554

Ser	Phe	Tyr	Phe	Gly	Trp	Ser	His	Tyr	Asn	Glu	Asn	Lys	Tyr	Asn	Ala
1				5					10					15	
Ile	Leu	Asn	Arg	Gln	Val	Met	Val	Cys	Ile	Lys	Leu	Leu	Leu	Asn	Cys
			20					25					30		
Cys	Val	Ser	Val	Ile	Asp	Ile	Gly	Asp	Gln	Ala					
		35					40								

<210> 555
 <211> 85
 <212> PRT
 <213> homo sapiens

<400> 555

Cys	Phe	Thr	His	Trp	Asn	Val	Phe	Pro	Arg	Leu	Trp	Met	Thr	Ser	Phe
1				5					10					15	
Leu	Met	Glu	Arg	Val	Gln	Glu	Gly	Trp	Lys	Thr	Pro	Gly	Phe	Lys	Leu
			20					25					30		
Ser	Ile	Pro	His	Met	Gly	Phe	Ser	Ile	Ile	Phe	Arg	Pro	Glu	Ala	Ala
		35					40					45			
Arg	Pro	Glu	Val	Arg	Leu	His	Leu	Ser	Ala	Leu	Phe	Val	Leu	Leu	Leu
		50				55					60				
Ala	Thr	Leu	Gly	Phe	Leu	Leu	Gly	Thr	Met	Cys	Gly	Cys	Gly	Met	Cys
65					70					75					80
Glu	Gln	Lys	Gly	Gly											
				85											

<210> 556
 <211> 106
 <212> PRT
 <213> homo sapiens

<400> 556

Phe	Asn	Asp	Gly	Lys	Thr	Trp	Gln	Leu	Lys	Lys	Thr	Leu	Val	Thr	Asn
1				5					10					15	
Gly	Gly	Phe	Leu	Leu	Phe	Phe	Pro	His	Pro	Pro	Phe	Cys	Ser	His	Met
			20					25					30		
Pro	Gln	Pro	His	Met	Val	Pro	Ser	Arg	Asn	Pro	Lys	Val	Ala	Arg	Ser

<212> PRT
<213> homo sapiens

<400> 559

Phe	Arg	Leu	Pro	Phe	Leu	Thr	Trp	His	Phe	Cys	Ser	Leu	Gln	Glu	Pro
1				5					10					15	
Ala	Trp	Cys	Thr	Phe	Ser	Tyr	Glu	Met	Gln	Leu	Glu	Ser	His	Leu	Cys
			20					25					30		
Lys	Arg	Trp	Phe	His	Phe	Cys	Arg	Ser	Ser	Ile	His				
		35					40								

<210> 560
<211> 45
<212> PRT
<213> homo sapiens

<400> 560

Arg	Val	Asn	Glu	Trp	Arg	Ser	Asp	Lys	Ser	Glu	Thr	Thr	Ser	Cys	Ile
1				5					10					15	
Asn	Gly	Phe	Pro	Ala	Ala	Ser	His	Lys	Arg	Arg	Tyr	Thr	Lys	Leu	Val
			20					25					30		
Pro	Val	Ser	Tyr	Lys	Asn	Ala	Lys	Leu	Arg	Met	Gly	Val			
		35					40					45			

<210> 561
<211> 34
<212> PRT
<213> homo sapiens

<400> 561

Met	Arg	Ser	Arg	Leu	Pro	Cys	Glu	Gly	Leu	Val	Ala	Arg	His	Pro	Arg
1				5					10					15	
Glu	Leu	Arg	Val	Pro	Ser	Val	Arg	Phe	Trp	Ile	Asp	Trp	Pro	Trp	Val
			20					25					30		
Leu	Thr														

<210> 562
<211> 67
<212> PRT
<213> homo sapiens

<400> 562

Val	Ser	Thr	His	Gly	Gln	Ser	Ile	Gln	Lys	Arg	Thr	Glu	Gly	Thr	Arg
1				5					10					15	
Ser	Ser	Arg	Gly	Cys	Arg	Ala	Thr	Ser	Pro	Ser	His	Gly	Asn	Arg	Leu
			20					25					30		
Leu	Ile	Gln	Glu	Ser	Phe	Pro	Gln	Asn	Pro	Pro	Arg	Ala	Arg	Phe	Gln
		35					40					45			
Gly	His	Pro	Leu	Gly	Arg	Gln	Ser	Arg	Gln	Gln	Pro	Phe	Thr	Glu	Ala
	50					55					60				

Met Ser Gln
65

<210> 563
<211> 50
<212> PRT
<213> homo sapiens

<400> 563

Ala 1	Pro	Met	Ala	Ser 5	Gln	Ser	Arg	Ser	Ala 10	Leu	Arg	Ala	Arg	Val 15	Ala
His	Ala	Gly	Ala 20	Val	Pro	Pro	Ala	Leu 25	His	Thr	Ala	Ile	Asp 30	Ser	Ser
Phe	Arg	Asn 35	His	Phe	Leu	Lys	Thr 40	His	Gln	Gly	Leu	Gly 45	Ser	Lys	Gly
Thr	Arg 50														

<210> 564
<211> 54
<212> PRT
<213> homo sapiens

<400> 564

Tyr 1	Ser	Ile	Ile	Phe 5	Glu	Gln	Phe	Phe	Lys 10	Cys	Lys	Ser	Val	Ser 15	Tyr
Ser	Glu	Cys	Val 20	Ser	Glu	Val	Ile	Lys 25	Asp	Ile	Ser	Gln	Arg 30	Tyr	Trp
Pro	Ile	Ser 35	Leu	Cys	Asn	Gln	Arg 40	Asn	Ser	Val	Ser	Arg 45	Leu	Leu	Leu
Cys	Val 50	Ile	Cys	Gly	Ser										

<210> 565
<211> 57
<212> PRT
<213> homo sapiens

<400> 565

Cys 1	Thr	Met	Val	Asn 5	Val	Asp	Asn	Thr	Val 10	Ser	Phe	Leu	Ser	Ser 15	Phe
Leu	Asn	Val	Asn 20	Leu	Tyr	Leu	Thr	Gln 25	Ser	Val	Cys	Leu	Lys 30	Leu	Leu
Arg	Thr	Phe 35	Pro	Asn	Val	Thr	Gly 40	Pro	Phe	Pro	Phe	Val 45	Ile	Arg	Gly
Ile	Leu 50	Phe	Gln	Asp	Tyr	Cys 55	Cys	Val							

<210> 566
<211> 49

<212> PRT
<213> homo sapiens

<400> 566

Glu	Lys	Cys	Gln	Pro	His	Ser	Leu	Ile	Leu	Leu	Trp	Pro	Phe	Asn	Phe
1				5					10					15	
Ile	Leu	Ile	Lys	Ser	His	Arg	Ser	His	Thr	Thr	Ile	Ile	Leu	Lys	Gln
			20					25					30		
Asn	Ser	Ser	Asp	Tyr	Lys	Gly	Lys	Trp	Ala	Ser	Asn	Val	Gly	Lys	Cys
		35					40					45			

Pro

<210> 567
<211> 94
<212> PRT
<213> homo sapiens

<400> 567

Gly	Glu	Gly	Arg	Val	Trp	Asn	Pro	Glu	Gly	Ser	Lys	Ser	Arg	His	Trp
1				5					10					15	
Pro	Asp	His	Pro	Ala	Pro	Trp	Ala	Pro	Ser	Pro	Arg	Gln	Glu	Gln	Leu
			20					25					30		
Phe	Ser	Ile	Pro	Ser	Gln	Thr	Ser	Ser	Ile	Phe	Ile	Thr	Met	Thr	Phe
		35					40					45			
Arg	Glu	Val	Ser	Gln	Ala	Ser	Ser	Arg	Cys	Pro	Thr	Ile	Pro	Ser	Gly
		50				55					60				
Gly	Lys	Arg	Gln	Glu	Asn	Ser	Pro	Arg	Val	Pro	Val	Met	Leu	Leu	Ser
65					70					75					80
Pro	Ser	Gln	Phe	Arg	Leu	Ser	Arg	Thr	Ser	Tyr	Leu	Gln	Pro		
				85					90						

<210> 568
<211> 89
<212> PRT
<213> homo sapiens

<400> 568

Gly	Leu	Thr	Leu	Lys	Lys	Gly	Thr	Phe	Pro	Arg	Gly	Pro	Glu	Ile	Gln
1				5					10					15	
Ala	Asp	Pro	Asn	Leu	Thr	Pro	Cys	Ser	Arg	Thr	Gln	Ala	His	Arg	Pro
			20					25					30		
Leu	Asn	Ser	Asn	Pro	Thr	Ser	Pro	Pro	Pro	Pro	Pro	Thr	Pro	Asp	Phe
		35					40					45			
Leu	Ile	Ser	Trp	Asn	Ala	Phe	Gln	Asp	Trp	Lys	Ser	Pro	Gln	Gly	Ser
	50					55					60				
Ser	Glu	Pro	Ile	Leu	Ser	Pro	Ala	Arg	Ile	Ser	Ser	Met	His	Pro	Gly
65					70					75					80

His Ala Phe His Ile Ser Arg Asn Lys
85

<210> 569

<211> 89

<212> PRT

<213> homo sapiens

<400> 569

Asp 1	Val	Leu	Asp	Ser 5	Leu	Asn	Trp	Asp	Gly 10	Glu	Ser	Ser	Met	Thr 15	Gly
Thr	Arg	Gly	Glu 20	Phe	Ser	Cys	Leu	Phe 25	Pro	Pro	Glu	Gly	Ile 30	Val	Gly
His	Leu	Glu 35	Leu	Ala	Trp	Glu	Thr 40	Ser	Leu	Lys	Val	Ile 45	Val	Ile	Lys
Ile	Glu 50	Leu	Val	Trp	Glu	Gly 55	Met	Glu	Asn	Ser	Cys 60	Ser	Cys	Leu	Gly
Leu 65	Gly	Ala	Gln	Gly	Ala 70	Gly	Trp	Ser	Gly	Gln 75	Cys	Leu	Asp	Leu	Leu 80
Pro	Ser	Gly	Phe	His 85	Thr	Arg	Pro	Ser							

<210> 570

<211> 73

<212> PRT

<213> homo sapiens

<400> 570

Lys 1	Ser	Ile	Ala	His 5	Ser	Val	Ile	Gly	Tyr 10	Phe	His	Asp	Phe	Lys 15	Trp
Phe	Tyr	Glu	Glu 20	Thr	Glu	Ser	Ser	Asp 25	Asp	Val	Glu	Val	Leu 30	Thr	Leu
Lys	Lys	Phe 35	Lys	Gly	Asp	Leu	Ala 40	Tyr	Arg	Arg	Gln	Glu 45	Tyr	Gln	Val
Glu	Phe 50	Asn	Ile	Trp	Cys	Leu 55	Lys	Trp	Ala	Leu	Val 60	Leu	Ser	Val	Met
Ala 65	Tyr	Val	Asn	Asn	Ser 70	Val	Pro	Ser							

<210> 571

<211> 40

<212> PRT

<213> homo sapiens

<400> 571

Ser 1	Ala	Asp	Ser	Gln 5	Glu	Ile	Gln	Arg	Arg 10	Pro	Gly	Leu	Gln	Thr 15	Thr
Arg	Val	Ser	Gly 20	Arg	Ile	Gln	His	Met 25	Val	Leu	Glu	Val	Gly 30	Ser	Cys

Phe Ile Ser Tyr Gly Ile Cys Lys
35 40

<210> 572

<211> 60

<212> PRT

<213> homo sapiens

<400> 572

Asn	Lys	Ser	Pro	Leu	Gln	Ala	Pro	Tyr	Val	Glu	Phe	Tyr	Leu	Ile	Leu
1				5					10					15	
Leu	Ser	Ser	Val	Gly	Gln	Val	Ser	Phe	Glu	Phe	Leu	Glu	Ser	Gln	His
			20					25					30		
Phe	Asn	Ile	Ile	Thr	Ala	Phe	Cys	Phe	Phe	Ile	Lys	Pro	Leu	Glu	Ile
		35					40					45			
Met	Lys	Ile	Ala	Tyr	Tyr	Arg	Val	Ser	Tyr	Ala	Phe				
	50					55					60				

<210> 573

<211> 318

<212> PRT

<213> homo sapiens

<400> 573

Gly	Asn	Leu	Ser	Leu	Glu	Ser	Leu	Cys	Asn	Leu	Tyr	Asn	Trp	Arg	Tyr
1				5					10					15	
Lys	Asn	Leu	Gly	Asn	Leu	Pro	His	Val	Gln	Leu	Leu	Pro	Glu	Phe	Ser
			20					25					30		
Thr	Ala	Asn	Ala	Gly	Leu	Leu	Tyr	Asp	Phe	Gln	Leu	Ile	Asn	Val	Glu
		35					40					45			
Asp	Phe	Gln	Gly	Val	Gly	Glu	Ser	Glu	Pro	Asn	Pro	Tyr	Phe	Tyr	Gln
	50					55					60				
Asn	Leu	Gly	Glu	Ala	Glu	Tyr	Val	Val	Ala	Leu	Phe	Met	Tyr	Met	Cys
65					70					75					80
Leu	Leu	Gly	Tyr	Pro	Ala	Asp	Lys	Ile	Ser	Ile	Leu	Thr	Thr	Tyr	Asn
				85					90					95	
Gly	Gln	Lys	His	Leu	Ile	Arg	Asp	Ile	Ile	Asn	Arg	Arg	Cys	Gly	Asn
			100					105					110		
Asn	Pro	Leu	Ile	Gly	Arg	Pro	Asn	Lys	Val	Thr	Thr	Val	Asp	Arg	Phe
		115					120					125			
Gln	Gly	Gln	Gln	Asn	Asp	Tyr	Ile	Leu	Leu	Ser	Leu	Val	Arg	Thr	Arg
	130					135					140				
Ala	Val	Gly	His	Leu	Arg	Asp	Val	Arg	Arg	Leu	Val	Val	Ala	Met	Ser
145					150					155				160	
Arg	Ala	Arg	Leu	Gly	Leu	Tyr	Ile	Phe	Ala	Arg	Val	Ser	Leu	Phe	Gln
				165					170					175	
Asn	Cys	Phe	Glu	Leu	Thr	Pro	Ala	Phe	Ser	Gln	Leu	Thr	Ala	Arg	Pro

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Leu	His	Leu	His	Ile	Ile	Pro	Thr	Glu	Pro	Phe	Pro	Thr	Thr	Arg	Lys				
		195					200					205							
Asn	Gly	Glu	Arg	Pro	Ser	His	Glu	Val	Gln	Ile	Ile	Lys	Asn	Met	Pro				
	210					215					220								
Gln	Met	Ala	Asn	Phe	Val	Tyr	Asn	Met	Tyr	Met	His	Leu	Ile	Gln	Thr				
	225				230					235				240					
Thr	His	His	Tyr	His	Gln	Thr	Leu	Leu	Gln	Leu	Pro	Pro	Ala	Met	Val				
				245					250					255					
Glu	Glu	Gly	Glu	Glu	Val	Gln	Asn	Gln	Glu	Thr	Glu	Leu	Glu	Thr	Glu				
			260					265					270						
Glu	Glu	Ala	Met	Thr	Val	Gln	Ala	Asp	Ile	Ile	Pro	Ser	Pro	Thr	Asp				
		275					280					285							
Thr	Ser	Cys	Arg	Gln	Glu	Thr	Pro	Ala	Phe	Glu	Arg	Glu	Ser	Arg	Pro				
	290					295					300								
Gly	Gly	Glu	Gly	Ala	Ile	Ala	Leu	Gly	Gly	Leu	Gly	Cys	Phe						
	305				310					315									

<210> 574
 <211> 67
 <212> PRT
 <213> homo sapiens

<400> 574

Lys	Thr	Pro	Lys	Pro	Pro	Gln	Arg	Asn	Cys	Pro	Phe	Pro	Thr	Gly	Ala
1				5					10					15	
Ala	Leu	Thr	Leu	Lys	Gly	Trp	Ser	Phe	Leu	Thr	Ala	Ala	Gly	Val	Cys
			20					25					30		
Trp	Thr	Gly	Tyr	Asp	Val	Ser	Leu	Asn	Ser	His	Gly	Leu	Phe	Phe	Cys
		35					40					45			
Phe	Gln	Leu	Cys	Phe	Leu	Ile	Leu	Asn	Phe	Leu	Thr	Leu	Phe	Tyr	His
	50					55					60				
Ser	Arg	Trp													
	65														

<210> 575
 <211> 155
 <212> PRT
 <213> homo sapiens

<400> 575

Ser	Leu	Met	Ile	Met	Met	Cys	Ser	Leu	Tyr	Gln	Met	His	Val	His	Val
1				5					10					15	
Val	Tyr	Lys	Val	Cys	His	Leu	Gly	His	Ile	Phe	Tyr	Tyr	Leu	Tyr	Phe
			20					25					30		
Met	Arg	Trp	Ser	Leu	Ser	Ile	Leu	Ser	Ser	Ser	Trp	Glu	Arg	Phe	Cys
		35					40					45			

Trp	Asn	Tyr	Met	Gln	Met	Lys	Gly	Ala	Ser	Cys	Glu	Leu	Thr	Glu	Ser
	50					55					60				

Trp	Ser	Gln	Phe	Lys	Thr	Val	Leu	Glu	Glu	Gly	Tyr	Ser	Gly	Glu	Asp
65					70					75					80

Ile	Lys	Ser	Lys	Ser	Gly	Ser	Arg	His	Gly	His	Tyr	Gln	Ala	Thr	Asp
				85					90					95	

Ile	Pro	Gln	Met	Ala	His	Cys	Pro	Gly	Ser	Tyr	Gln	Arg	Lys	Lys	Asn
			100					105					110		

Ile	Val	Ile	Leu	Leu	Thr	Leu	Lys	Ser	Ile	Asn	Ser	Cys	His	Leu	Val
		115					120					125			

Trp	Ser	Ser	Asn	Gln	Trp	Ile	Val	Ser	Thr	Ser	Ser	Ile	Asp	Asp	Val
	130					135					140				

Ala	Asn	Lys	Met	Leu	Leu	Ala	Ile	Ile	Cys	Cys
145					150					155

<210> 576

<211> 57

<212> PRT

<213> homo sapiens

<400> 576

Asp	His	Leu	Gly	Phe	Ile	Ser	Thr	Lys	Met	Arg	Thr	Asn	His	Gly	Val
1				5					10					15	

Arg	Lys	Gly	Ser	Leu	Glu	Glu	His	Lys	Asn	Leu	Lys	Ala	Leu	Gly	Gly
			20					25					30		

Tyr	His	Tyr	Tyr	Ile	Ser	Tyr	Phe	His	Arg	Ser	Asp	Leu	Ala	Lys	Leu
		35					40					45			

Cys	Ile	Leu	Ser	Leu	Leu	Thr	Phe	Ile
	50					55		

<210> 577

<211> 48

<212> PRT

<213> homo sapiens

<400> 577

Phe	Lys	Phe	Phe	Leu	Met	Thr	Ile	Phe	Leu	Gln	Asn	Phe	Glu	Arg	Lys
1				5					10					15	

Met	Cys	Ser	Phe	Cys	Cys	Ile	Leu	Cys	Lys	Lys	Thr	Ala	Asn	Arg	Gly
			20					25					30		

Lys	Arg	Thr	Leu	Gln	Ile	Lys	Thr	Ile	Leu	Val	Ser	Phe	Pro	Gln	Arg
		35					40					45			

<210> 578

<211> 48

<212> PRT

<213> homo sapiens

<400> 578

Leu	Tyr	Phe	Phe	Lys	Thr	Leu	Lys	Glu	Lys	Cys	Val	Leu	Phe	Ala	Ala
1				5					10					15	
Ser	Phe	Val	Arg	Arg	Leu	Pro	Thr	Glu	Glu	Lys	Gly	Leu	Tyr	Lys	Leu
			20					25					30		
Arg	Pro	Ser	Trp	Phe	His	Phe	His	Lys	Asp	Glu	Asn	Lys	Ser	Trp	Cys
		35					40					45			

<210> 579
 <211> 48
 <212> PRT
 <213> homo sapiens

<400> 579

Gly	Ser	Phe	Pro	Asn	Thr	Met	Ile	Cys	Ser	His	Leu	Cys	Gly	Asn	Glu
1				5					10					15	
Thr	Lys	Met	Val	Leu	Ile	Cys	Lys	Val	Leu	Phe	Pro	Leu	Leu	Ala	Val
			20					25					30		
Phe	Leu	Gln	Arg	Met	Gln	Gln	Lys	Glu	His	Ile	Phe	Leu	Ser	Lys	Phe
		35					40					45			

<210> 580
 <211> 48
 <212> PRT
 <213> homo sapiens

<400> 580

His	Cys	Arg	Ile	Leu	Gln	Gly	Leu	Ser	Pro	Leu	Val	Gly	Arg	Glu	Lys
1				5					10					15	
Thr	Thr	Gln	Val	Met	Arg	Asn	Phe	Tyr	Ser	Phe	Gln	Glu	Leu	Glu	Glu
			20					25					30		
Gln	Leu	Leu	Ile	Lys	Phe	His	Ala	Leu	Val	Thr	Lys	Tyr	Phe	Tyr	Ser
		35					40					45			

<210> 581
 <211> 59
 <212> PRT
 <213> homo sapiens

<400> 581

Ile	Met	Pro	Arg	Ala	Pro	Leu	Tyr	Arg	Ile	Pro	Leu	Asn	Cys	Asn	Tyr
1				5					10					15	
Val	Leu	Leu	Lys	Ser	Gln	Leu	Val	Lys	Glu	Glu	Leu	Met	Val	Ser	Val
			20					25					30		
Phe	Val	Gly	Asn	Thr	Cys	Asn	Thr	Ala	Glu	Phe	Tyr	Lys	Gly	Phe	Leu
		35					40					45			
Leu	Trp	Trp	Ala	Gly	Lys	Lys	Pro	Leu	Lys	Ser					
	50					55									

<210> 582
 <211> 44

<212> PRT
<213> homo sapiens

<400> 582

Gly	Thr	Leu	Arg	Pro	Arg	Ser	Ser	Asp	Val	Leu	Pro	Ile	Tyr	Leu	Cys
1				5					10					15	
Phe	Thr	Thr	Cys	Leu	Leu	Ser	Leu	Thr	Pro	Asn	Ile	Phe	Thr	Tyr	Phe
			20					25					30		
Ser	Asn	Ser	Ala	Cys	His	Lys	Phe	Ala	Ala	Ser	Pro				
		35					40								

<210> 583
<211> 46
<212> PRT
<213> homo sapiens

<400> 583

Asn	Val	Asp	Ser	Cys	Gln	Thr	His	Ser	Leu	Ala	Leu	Ile	Pro	Pro	Leu
1				5					10					15	
Leu	Ser	Ser	Ser	Asp	Ile	Val	Asn	Asn	Asp	Lys	Gln	Leu	Leu	Cys	Thr
			20					25					30		
Glu	Cys	Phe	Phe	Met	Cys	Cys	Ser	His	Phe	Ile	His	Met	Tyr		
		35					40					45			

<210> 584
<211> 41
<212> PRT
<213> homo sapiens

<400> 584

Leu	Tyr	Met	Cys	Ile	Lys	Cys	Glu	Gln	His	Ile	Lys	Lys	His	Ser	Val
1				5					10					15	
His	Ser	Ser	Cys	Leu	Ser	Leu	Leu	Thr	Ile	Ser	Leu	Leu	Glu	Arg	Arg
			20					25					30		
Gly	Gly	Ile	Arg	Ala	Arg	Leu	Cys	Val							
		35					40								

<210> 585
<400> 585
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<210> 586
<400> 586
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<210> 587
<400> 587
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<210> 588
<211> 112
<212> PRT
<213> homo sapiens

<400> 588

Gly 1	Lys	Pro	Leu	Val 5	Leu	His	Ala	Thr	Pro 10	Leu	Ser	Arg	Cys	Pro 15	Leu
Pro	Leu	His	Pro 20	Thr	Arg	Ser	Leu	Ile 25	Leu	Arg	Pro	Ser	Leu 30	His	Leu
Ser	Asp	Pro 35	Ser	Phe	His	His	Tyr 40	Leu	Gln	Arg	Cys	Ser 45	Tyr	Tyr	Ala
Pro	Val 50	Tyr	Arg	Gly	Cys	Pro 55	Thr	Met	Thr	Val	Pro 60	Ser	Gln	Ser	Asn
Tyr 65	Ser	Ser	Gly	Pro	Lys 70	Val	Trp	Leu	Ser	Arg 75	Ala	Pro	Leu	Pro	Arg 80
Arg	Gly	Arg	Pro	Phe 85	Gln	Ala	Leu	Pro	Gly 90	Trp	Asn	Trp	Cys	Arg 95	Arg
Ser	Leu	Gly	Cys 100	Ile	Val	Arg	Pro	Gly 105	Val	Gly	Val	Ala	Ser 110	Leu	Leu

<210> 589
 <211> 76
 <212> PRT
 <213> homo sapiens
 <400> 589

Gly 1	Arg	Ser	Arg	Glu 5	Ala	Pro	Ala	Gly	Trp 10	Pro	Lys	Ser	Thr	Lys 15	Pro
Pro	Ser	Ala	Arg 20	Glu	Asn	Pro	Trp	Phe 25	Ser	Met	Pro	His	Leu 30	Ser	Pro
Gly	Ala	Leu 35	Cys	Leu	Phe	Thr	Pro 40	Gln	Glu	Ala	Leu	Ser 45	Tyr	Val	Leu
Leu	Ser 50	Ile	Tyr	Arg	Thr	Pro 55	Val	Ser	Ile	Thr	Ile 60	Ser	Arg	Asp	Val
Ala 65	Ile	Met	Arg	Pro	Ser 70	Thr	Gly	Gly	Ala	Arg 75	Arg				

<210> 590
 <211> 97
 <212> PRT
 <213> homo sapiens
 <400> 590

Ala 1	Gly	Leu	Asp	Gln 5	Lys	Glu	Glu	Leu	Arg 10	Gly	Val	Arg	Gln	His 15	Gln
His	Gln	Gly	Val 20	Arg	Tyr	Thr	Arg	Gly 25	Ser	Ser	Asp	Thr	Ser 30	Ser	Ser
Pro	Glu	Gly 35	Leu	Gly	Met	Ala	Cys 40	His	Ala	Gly	Ala	Met 45	Glu	Arg	Val
Lys	Ala 50	Lys	Pro	Trp	Asp	Pro 55	Lys	Ser	Asn	Leu	Thr 60	Ala	Lys	Ala	Pro

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<210> 594
 <211> 41
 <212> PRT
 <213> homo sapiens

<400> 594

Ser	Gly	Asp	Val	Cys	Thr	Glu	Ser	His	Cys	Gly	Leu	Ser	Arg	Val	Lys
1				5					10					15	
Glu	Lys	Glu	Gln	Gln	Glu	Leu	Ser	Leu	Gly	Arg	Trp	Arg	Arg	Gly	Gly
			20					25					30		
Ile	Asp	Gln	Ala	Arg	Pro	Trp	Pro	Trp							
		35					40								

<210> 595
 <211> 47
 <212> PRT
 <213> homo sapiens

<400> 595

Phe	Lys	Val	Gly	Leu	Trp	Lys	Gly	Asp	Ile	Val	Glu	Gly	Glu	Arg	Ala
1				5					10					15	
Val	Leu	Tyr	Thr	Tyr	Lys	Trp	Tyr	Thr	Pro	Phe	Ile	His	Gly	Gly	Gln
			20					25					30		
Arg	Ser	Ser	Asp	Gln	Val	Thr	Tyr	Val	Gln	Lys	Val	Thr	Val	Ala	
		35					40					45			

<210> 596
 <211> 44
 <212> PRT
 <213> homo sapiens

<400> 596

Ser	Val	Leu	Thr	Thr	Ser	Gln	Arg	Leu	Ser	Ser	His	Phe	Lys	Ser	Gln
1				5					10					15	
Ile	Pro	Thr	Arg	Ala	Lys	Val	Leu	Leu	Asp	Leu	Phe	His	Pro	Phe	Ser
			20					25					30		
Thr	Ser	Leu	Ser	Ser	Thr	Leu	Ala	Ala	Pro	Ser	Pro				
		35					40								

<210> 597
 <211> 1651
 <212> DNA
 <213> homo sapiens

<400> 597

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<210> 598

<211> 3304

<212> DNA

<213> homo sapiens

<400> 598

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gtccctgagc atagtgaac ttttatctgt gtgtcttttg ctaaatatgc ccttttata900
ttaataaaga atgatttga gttgtgctct c

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931

<210> 618
 <211> 447
 <212> PRT
 <213> homo sapiens

<400> 618

Glu	Leu	Pro	Ser	Ser	Pro	Pro	Pro	Gly	Leu	Pro	Glu	Val	Ala	Pro	Asp
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Ala	Thr	Ser	Thr	Gly	Leu	Pro	Asp	Thr	Pro	Ala	Ala	Pro	Glu	Thr	Ser
			20					25					30		

Thr	Asn	Tyr 35	Pro	Val	Glu	Cys	Thr 40	Glu	Gly	Ser	Ala	Gly 45	Pro	Gln	Ser
Leu	Pro 50	Leu	Pro	Ile	Leu	Glu 55	Pro	Val	Lys	Asn 60	Pro	Cys	Ser	Val	Lys
Asp 65	Gln	Thr	Pro	Leu	Gln 70	Leu	Ser	Val	Glu	Asp 75	Thr	Thr	Ser	Pro	Asn 80
Thr	Lys	Pro	Cys	Pro 85	Pro	Thr	Pro	Thr	Thr 90	Pro	Glu	Thr	Trp	Gly 95	Gly
Gly	Gly	Gly	Gly 100	Ala	Pro	Ser	Ser	Thr 105	Pro	Cys	Ser	Ala	His 110	Leu	Thr
Pro	Ser	Ser 115	Leu	Phe	Pro	Ser	Ser 120	Leu	Glu	Ser	Ser	Ser 125	Glu	Gln	Lys
Phe	Tyr 130	Asn	Phe	Val	Ile	Leu 135	His	Ala	Arg	Ala	Asp 140	Glu	His	Ile	Ala
Leu 145	Arg	Val	Arg	Glu	Lys 150	Leu	Glu	Ala	Leu	Gly 155	Val	Pro	Asp	Gly	Ala 160
Thr	Phe	Cys	Glu	Asp 165	Phe	Gln	Val	Pro	Gly 170	Arg	Gly	Glu	Leu	Ser 175	Cys
Leu	Gln	Asp	Ala 180	Ile	Asp	His	Ser	Ala 185	Phe	Ile	Ile	Leu	Leu 190	Leu	Thr
Ser	Asn	Phe 195	Asp	Cys	Arg	Leu	Ser 200	Leu	His	Gln	Val	Asn 205	Gln	Ala	Met
Met	Ser 210	Asn	Leu	Thr	Arg	Gln 215	Gly	Ser	Pro	Asp	Cys 220	Val	Ile	Pro	Phe
Leu 225	Pro	Leu	Glu	Ser	Ser 230	Pro	Ala	Gln	Leu	Ser 235	Ser	Asp	Thr	Ala	Ser 240
Leu	Leu	Ser	Gly	Leu 245	Val	Arg	Leu	Asp	Glu 250	His	Ser	Gln	Ile	Phe 255	Ala
Arg	Lys	Val	Ala 260	Asn	Thr	Phe	Lys	Pro 265	His	Arg	Leu	Gln	Ala 270	Arg	Lys
Ala	Met	Trp 275	Arg	Lys	Glu	Gln	Asp 280	Thr	Arg	Ala	Leu	Arg 285	Glu	Gln	Ser
Gln	His 290	Leu	Asp	Gly	Glu	Arg 295	Met	Gln	Ala	Ala	Ala 300	Leu	Asn	Ala	Ala
Tyr 305	Ser	Ala	Tyr	Leu	Gln 310	Ser	Tyr	Leu	Ser	Tyr 315	Gln	Ala	Gln	Met	Glu 320
Gln	Leu	Gln	Val	Ala 325	Phe	Gly	Ser	His	Met 330	Ser	Phe	Gly	Thr	Gly 335	Ala
Pro	Tyr	Gly	Val 340	Arg	Met	Pro	Phe	Gly 345	Gly	Gln	Gly	Pro	Leu 350	Gly	Ala
Pro	Pro	Pro 355	Phe	Pro	Thr	Trp	Pro 360	Gly	Cys	Pro	Gln	Pro 365	Pro	Pro	Leu

His	Ala	Trp	Gln	Ala	Gly	Thr	Pro	Pro	Pro	Pro	Ser	Pro	Gln	Pro	Ala
	370					375					380				
Ala	Phe	Pro	Gln	Ser	Leu	Pro	Phe	Pro	Gln	Ser	Pro	Ala	Phe	Pro	Thr
385					390					395					400
Ala	Ser	Pro	Ala	Pro	Pro	Gln	Ser	Pro	Gly	Leu	Gln	Pro	Leu	Ile	Ile
				405					410					415	
His	His	Ala	Gln	Met	Val	Gln	Leu	Gly	Leu	Asn	Asn	His	Met	Trp	Asn
			420					425					430		
Gln	Arg	Gly	Ser	Gln	Ala	Pro	Glu	Asp	Lys	Thr	Gln	Glu	Ala	Glu	
		435					440					445			

<210> 619

<211> 205

<212> PRT

<213> homo sapiens

<400> 619

Ala	Asp	Ala	Gly	Gly	Gly	Thr	Glu	Arg	Ser	Leu	Leu	Ser	Leu	Pro	Pro
1				5					10					15	
Glu	Leu	Leu	Val	Leu	Pro	Gly	Thr	Asp	Gly	Ala	Ala	Pro	Gly	Gly	Phe
			20					25					30		
Trp	Glu	Pro	His	Val	Ile	Trp	Asp	Trp	Gly	Ala	Leu	Trp	Gly	Gln	Asn
		35					40					45			
Ala	Leu	Trp	Gly	Pro	Gly	Ala	Pro	Gly	Ser	Pro	Ala	Thr	Leu	Ser	His
	50					55					60				
Leu	Ala	Gly	Val	Pro	Ala	Ala	Thr	Pro	Ala	Arg	Met	Ala	Gly	Trp	
65					70				75					80	
His	Pro	Pro	Thr	Ala	Leu	Pro	Thr	Ala	Ser	Ser	Leu	Ser	Thr	Val	Thr
				85					90					95	
Ala	Leu	Pro	Ala	Val	Pro	Ser	Leu	Pro	Tyr	Gly	Leu	Thr	Arg	Thr	Pro
			100					105					110		
Ser	Glu	Pro	Arg	Ala	Ala	Thr	Pro	His	Tyr	Pro	Pro	Arg	Thr	Asp	Gly
		115					120					125			
Thr	Ala	Gly	Ala	Glu	Gln	Pro	His	Val	Glu	Pro	Glu	Arg	Val	Pro	Gly
	130					135					140				
Ala	Arg	Gly	Gln	Asp	Ala	Gly	Gly	Arg	Met	Thr	Ala	Cys	Pro	Cys	Leu
145					150					155					160
Thr	Thr	Trp	Gly	Thr	Pro	Leu	Asp	Pro	Gly	Ile	Gly	Gln	Asp	Pro	Ile
				165					170					175	
Glu	His	Pro	Gly	Leu	Pro	Cys	Ala	Leu	Trp	Thr	Val	Glu	Asp	Glu	Val
			180					185					190		
Ile	Cys	His	Phe	Gln	Asp	Ile	Val	Arg	Glu	Pro	Phe	Ile			
		195					200					205			

<210> 620

<211> 409
 <212> PRT
 <213> homo sapiens

<400> 620

Lys	Ser	Arg	Leu	Ser	Val	Thr	Leu	Met	Pro	Val	Gln	Leu	Ser	Glu	His
1				5					10					15	
Pro	Glu	Trp	Asn	Glu	Ser	Met	His	Ser	Leu	Arg	Ile	Ser	Val	Gly	Gly
			20					25					30		
Leu	Pro	Val	Leu	Ala	Ser	Met	Thr	Lys	Ala	Ala	Asp	Pro	Arg	Phe	Arg
		35					40					45			
Pro	Arg	Trp	Lys	Val	Ile	Leu	Thr	Phe	Phe	Val	Gly	Ala	Ala	Ile	Leu
	50					55					60				
Trp	Leu	Leu	Cys	Ser	His	Arg	Pro	Ala	Pro	Gly	Arg	Pro	Pro	Thr	His
	65				70					75					80
Asn	Ala	His	Asn	Trp	Arg	Leu	Gly	Gln	Ala	Pro	Ala	Asn	Trp	Tyr	Asn
				85					90					95	
Asp	Thr	Tyr	Pro	Leu	Ser	Pro	Pro	Gln	Arg	Thr	Pro	Ala	Gly	Ile	Arg
			100					105					110		
Tyr	Arg	Ile	Ala	Val	Ile	Ala	Asp	Leu	Asp	Thr	Glu	Pro	Thr	Ala	Gln
		115					120					125			
Asp	Glu	Asn	Thr	Trp	Arg	Ser	Asp	Leu	Lys	Lys	Gly	Tyr	Leu	Thr	Leu
	130					135					140				
Ser	Asp	Ser	Gly	Asp	Lys	Val	Ala	Val	Glu	Trp	Asp	Lys	Asp	His	Gly
	145				150					155					160
Val	Leu	Glu	Ser	His	Leu	Ala	Glu	Lys	Gly	Arg	Gly	Met	Glu	Leu	Ser
				165					170					175	
Asp	Leu	Ile	Val	Phe	Asn	Gly	Lys	Leu	Tyr	Ser	Val	Asp	Asp	Arg	Thr
			180					185					190		
Gly	Val	Val	Tyr	Gln	Ile	Glu	Gly	Ser	Lys	Ala	Val	Pro	Trp	Val	Ile
		195					200					205			
Leu	Ser	Asp	Gly	Asp	Gly	Thr	Val	Glu	Lys	Gly	Phe	Lys	Ala	Glu	Trp
	210					215					220				
Leu	Ala	Val	Lys	Asp	Glu	Arg	Leu	Tyr	Val	Gly	Gly	Leu	Gly	Lys	Glu
	225				230					235					240
Trp	Thr	Thr	Thr	Thr	Gly	Asp	Val	Val	Asn	Glu	Asn	Pro	Glu	Trp	Val
				245					250					255	
Lys	Val	Val	Gly	Tyr	Lys	Gly	Ser	Val	Asp	His	Glu	Asn	Trp	Val	Ser
			260					265					270		
Asn	Tyr	Asn	Ala	Leu	Arg	Ala	Ala	Gly	Ile	Gln	Pro	Pro	Ala	Asn	
		275				280					285				
Leu	Ile	His	Glu	Ser	Ala	Cys	Trp	Ser	Asp	Thr	Leu	Gln	Arg	Trp	Phe
	290					295					300				

Phe 305	Leu	Pro	Arg	Arg	Ala 310	Ser	Gln	Glu	Arg	Tyr 315	Ser	Glu	Lys	Asp	Asp 320
Glu	Arg	Lys	Gly	Ala 325	Asn	Leu	Leu	Leu	Ser 330	Ala	Ser	Pro	Asp	Phe 335	Gly
Asp	Ile	Ala	Val 340	Ser	His	Val	Gly	Ala 345	Val	Val	Pro	Thr	His 350	Gly	Phe
Ser	Ser	Phe 355	Lys	Phe	Ile	Pro	Asn 360	Thr	Asp	Asp	Gln	Ile 365	Ile	Val	Ala
Leu	Lys 370	Ser	Glu	Glu	Asp	Ser 375	Gly	Arg	Val	Ala	Ser 380	Tyr	Ile	Met	Ala
Phe 385	Thr	Leu	Asp	Gly	Arg 390	Phe	Leu	Leu	Pro	Glu 395	Thr	Lys	Ile	Gly	Ser 400
Val	Lys	Tyr	Glu	Gly 405	Ile	Glu	Phe	Ile							

<210> 621

<211> 249

<212> PRT

<213> homo sapiens

<400> 621

Lys 1	Leu	Ser	Pro	Asp 5	Gly	Leu	Ala	Gln	Cys 10	Phe	Arg	Phe	Glu	Leu 15	Asn
Glu	Leu	Asp	Ala 20	Phe	Val	Phe	His	Ala 25	Ser	Asp	Leu	Gly	Leu 30	Arg	Gln
Gln	Glu	Ala 35	Pro	Val	Gln	Arg	Glu 40	Gly	His	Asp	Val	Gly 45	Gly	Asp	Ser
Ala 50	Ala	Val	Leu	Leu	Gly	Phe 55	Glu	Gly	His	Asn	Asp 60	Leu	Val	Val	Gly
Val 65	Gly	Asp	Glu	Leu	Glu 70	Gly	Arg	Glu	Ala	Val 75	Ser	Gly	Asp	His	Arg 80
Pro	Asp	Val	Ala	His 85	Ser	Asp	Val	Ala	Glu 90	Val	Arg	Gly	Gly	Ala 95	Gln
Gln	Gln	Val	Gly 100	Ala	Leu	Ala	Leu	Val 105	Val	Leu	Leu	Ala	Val 110	Ala	Leu
Leu	Ala	Gly 115	Ala	Ala	Arg	Gln	Glu 120	Glu	Pro	Ala	Leu	Gln 125	Arg	Val	Thr
Pro	Ala 130	Gly	Arg	Leu	Met	Asp 135	Glu	Val	Ser	Trp	Arg 140	Leu	Asp	Ala	Gly
Ser 145	Ser	Pro	Gln	Gly	Val 150	Val	Val	Gly	His	Pro 155	Val	Leu	Val	Val	His 160
Ala	Ala	Leu	Val	Ala 165	His	His	Leu	His	Pro 170	Leu	Arg	Val	Leu	Val 175	His
His	Ile	Thr	Arg 180	Ser	Gly	Arg	Pro	Leu 185	Leu	Ala	Gln	Ala	Ala 190	His	Val

Gln	Thr	Leu	Val	Leu	His	Cys	Gln	Pro	Phe	Gly	Leu	Glu	Ala	Phe	Leu
		195					200					205			
His	Gly	Ala	Val	Ala	Val	Gly	Gln	Asn	His	Pro	Gly	His	Gly	Phe	Ala
	210					215					220				
Ala	Phe	Asp	Leu	Val	Asp	Asp	Pro	Arg	Pro	Val	Ile	His	Gly	Val	Glu
	225				230					235					240
Phe	Pro	Ile	Glu	Asn	Asn	Gln	Val	Gly							
				245											

<210> 622
 <211> 255
 <212> PRT
 <213> homo sapiens

<400> 622

Ala	Ala	Ala	Pro	Val	Ser	Leu	His	Asp	Ala	Ala	Gly	Asp	Leu	Arg	Arg
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Asp	Pro	Gly	Gly	Gly	Gly	Gly	Gly	Gly	25	Val	Pro	His	Gly	Gly	Glu
			20										30		
Gly	Gln	Glu	Val	Val	Pro	Ala	Glu	Pro	Gly	Val	Pro	Ala	Pro	Gln	His
		35					40					45			
Ala	Glu	Pro	Val	Ala	Ala	Ala	Gly	Ala	Ala	Gln	Gln	Leu	Gln	Thr	Glu
	50					55					60				
Glu	Gln	Pro	Gly	Leu	Gln	Arg	Leu	Arg	Leu	Gly	Pro	Val	Arg	Gly	Ala
65					70					75					80
Ala	Arg	Gly	Gly	Asp	Ala	Arg	Val	Arg	Gly	Pro	Arg	Gly	Asp	Arg	Arg
				85					90					95	
Val	Asn	Pro	Glu	Ser	Ala	Arg	Ala	Leu	Leu	Pro	Gly	Asp	Pro	Gln	Gly
			100					105					110		
Pro	Gly	Thr	Ala	Ala	Pro	Arg	Ala	Leu	Gly	Leu	Pro	Pro	Arg	Cys	Glu
		115					120					125			
Pro	Val	Gly	Ala	Pro	Leu	Ala	Ala	Leu	Ala	Leu	Ala	Arg	Glu	Arg	Arg
	130					135					140				
Glu	Arg	Gly	Arg	Phe	Pro	Arg	Pro	Cys	Lys	Cys	Leu	Phe	Phe	Asn	Ser
	145				150					155				160	
Ser	Gln	Cys	Glu	Leu	Cys	Cys	Glu	Cys	Val	Arg	Gly	Gly	Ala	Pro	Ala
			165						170					175	
Leu	Ser	Arg	Arg	Arg	Val	Ala	Thr	Pro	Cys	Pro	Cys	Pro	Met	Val	Cys
			180					185					190		
Asn	Ser	Asp	Phe	Ala	His	Arg	Ser	Thr	Val	Pro	Pro	Ser	Ala	His	Pro
		195					200					205			
Phe	Thr	Leu	Thr	Pro	Thr	Leu	Ser	Leu	Asn	Thr	Phe	Ile	Ile	Val	Arg
	210					215					220				
Arg	Gly	Arg	Trp	Asp	Phe	Gly	Arg	Ser	Ala	Ala	Ala	Thr	Ala	Ser	Gly

225

230

235

240

Gly	Leu	Ile	Phe	Ile	Phe	Ala	Leu	Arg	Trp	Leu	Lys	Ala	Phe	Ile
				245					250					255

<210> 623

<211> 196

<212> PRT

<213> homo sapiens

<400> 623

Ile	Asn	Ala	Phe	Ser	His	Arg	Asn	Ala	Lys	Ile	Asn	Ile	Asn	Pro	Pro
1				5					10					15	
Asp	Ala	Val	Ala	Ala	Ala	Leu	Arg	Pro	Lys	Ser	Gln	Arg	Pro	Arg	Leu
			20					25					30		
Thr	Ile	Ile	Lys	Val	Phe	Ser	Glu	Ser	Val	Gly	Val	Ser	Val	Asn	Gly
		35					40					45			
Cys	Ala	Leu	Gly	Gly	Thr	Val	Glu	Arg	Cys	Ala	Lys	Ser	Glu	Leu	Gln
	50					55					60				
Thr	Ile	Gly	Gln	Gly	His	Gly	Val	Ala	Thr	Arg	Arg	Arg	Leu	Ser	Ala
	65				70					75					80
Gly	Ala	Pro	Pro	Arg	Thr	His	Ser	Gln	Gln	Ser	Ser	His	Trp	Glu	Glu
				85					90					95	
Leu	Lys	Asn	Lys	His	Leu	Gln	Gly	Arg	Gly	Lys	Arg	Pro	Arg	Ser	Arg
			100					105					110		
Arg	Ser	Arg	Ala	Arg	Ala	Ser	Ala	Ala	Arg	Gly	Ala	Pro	Thr	Gly	Ser
		115					120					125			
Gln	Arg	Gly	Gly	Ser	Pro	Ser	Ala	Arg	Gly	Ala	Ala	Val	Pro	Gly	Pro
	130					135				140					
Cys	Gly	Ser	Pro	Gly	Ser	Arg	Ala	Arg	Ala	Leu	Ser	Gly	Phe	Thr	Arg
	145				150					155					160
Arg	Ser	Pro	Arg	Gly	Pro	Arg	Thr	Arg	Ala	Ser	Pro	Pro	Arg	Ala	Ala
				165					170					175	
Pro	Leu	Thr	Gly	Pro	Ser	Arg	Ser	Arg	Trp	Ser	Pro	Gly	Cys	Ser	Ser
			180					185					190		
Val	Cys	Ser	Cys												
		195													

<210> 624

<211> 242

<212> PRT

<213> homo sapiens

<400> 624

Val	Glu	Ser	His	Arg	Arg	Ala	His	Thr	His	Thr	Thr	Val	Arg	Ser	Pro
1				5					10					15	
Glu	Thr	Ala	Arg	Gly	Trp	Lys	Pro	Trp	Pro	His	Arg	Leu	Ser	Arg	Tyr
			20					25					30		

Val	His	Ser 35	Pro	Gly	Arg	Gln	Pro 40	His	Gly	His	Gly	Gln 45	His	Leu	Cys
Phe	Cys 50	Ser	Gly	Arg	Arg	Ala 55	Phe	Gly	Gly	His	Pro 60	Arg	Gln	Gly	Ala
Arg 65	Ala	Ser	Leu	Leu	Ala 70	Leu	Gly	Leu	Glu	Asn 75	Ser	Pro	Gly	Gly	Ser 80
Ser	Pro	Glu	Glu	Arg 85	Leu	Gly	Arg	Leu	Ala 90	Val	Ala	Gly	Pro	Pro 95	Arg
Gly	Ala	Gln	Asn 100	Val	Ser	Gln	Ala	Gly 105	Pro	Glu	Ala	Glu	Ala 110	Pro	Pro
Leu	Arg	Phe 115	Gly	His	Ala	Trp	Gly 120	Ala	Gln	Thr	Pro	Arg 125	Leu	Gly	Ala
Pro	Gly 130	Pro	Trp	Thr	Pro	Leu 135	Pro	Thr	Leu	Pro	Ser 140	His	Ile	Pro	Pro
Phe 145	Trp	Ser	Gln	Thr	Pro 150	Ala	Gln	Arg	Lys	Glu 155	Gly	Phe	Thr	Glu	Glu 160
Gly	Gln	Gly	Arg	Ala 165	Trp	Pro	Gln	Gly	Gly 170	Asp	Glu	Asp	Ile	Ser 175	Gly
Pro	Gly	Ser	Cys 180	Arg	Leu	Leu	Trp	Glu 185	Glu	Glu	Pro	Cys	Val 190	Cys	Lys
Leu	Leu	Gly 195	Leu	Ala	Ala	Arg	Pro 200	Thr	Ala	Gly	Pro	Ser 205	Leu	Asp	Pro
Cys	Thr 210	Trp	Pro	Ser	Ser	Cys 215	Pro	Leu	Ala	Ala	Pro 220	Gly	Leu	Gly	Thr
Gly 225	Ile	Glu	Pro	Arg	Gly 230	Leu	Gly	Trp	Leu	Gly 235	Gln	Gly	Arg	Asp	Arg 240
Glu	Gly														

<210> 625

<211> 216

<212> PRT

<213> homo sapiens

<400> 625

Gly 1	Leu	Val	Met	Pro 5	Gly	Glu	Leu	Arg	Arg 10	Pro	Gly	Leu	Gly	Pro 15	Gln
Ala	His	Gly	Leu 20	Pro	Ser	Pro	Leu	Cys 25	Pro	Pro	Ile	Phe	Pro 30	Leu	Phe
Gly	Pro	Arg 35	His	Gln	His	Lys	Glu 40	Arg	Arg	Gly	Ser	Gln 45	Arg	Lys	Ala
Arg	Ala 50	Glu	Pro	Gly	Pro	Arg 55	Glu	Gly	Met	Arg	Thr 60	Phe	Pro	Val	Gln
Val 65	Ala	Ala	Gly	Cys	Ser 70	Gly	Arg	Lys	Ser	His 75	Ala	Ser	Val	Asn	Cys 80

Trp	Gly	Trp	Arg	Pro 85	Ala	Pro	Leu	Gln	Gly 90	Pro	Ala	Leu	Thr	Pro 95	Ala	
Arg	Gly	His	Pro 100	Ala	Ala	Leu	Trp	Leu 105	Pro	Leu	Ala	Leu	Ala 110	Gln	Ala	
Ser	Ser	Leu 115	Glu	Gly	Trp	Ala	Gly 120	Trp	Ala	Arg	Ala	Gly 125	Thr	Gly	Arg	
Gly	Ser 130	Thr	Ser	Asp	Pro	Asp 135	Val	Gly	Trp	Leu	Cys 140	Pro	Pro	Arg	Arg	
Glu 145	Ala	Gln	Gln	Thr	Ser 150	Tyr	Thr	Lys	Ala	Lys 155	Ser	Thr	Ile	Gly	Glu 160	
Pro	Arg	Ser	His	Phe 165	Met	Gly	Arg	Arg	Pro 170	Arg	Pro	Gln	Gly	Pro 175	Gln	
Ser	Lys	Ala	Arg 180	Gly	Arg	Phe	Ile	Pro 185	Glu	Asp	Ser	Pro	Pro 190	Gly	Ala	
Ala	Pro	Ala 195	Trp	Gly	Gly	Val	Ser 200	Arg	Pro	Leu	Gly	Cys 205	Leu	Ser	Val	
Cys	Gly 210	Thr	Pro	Trp	Ser	Thr 215	Pro									

<210> 626

<211> 299

<212> PRT

<213> homo sapiens

<400> 626

Pro 1	Gly	Ile	Ser	Val 5	Ser	Val	Asp	Lys	Met 10	Glu	Ser	Ser	Pro	Phe 15	Asn	
Arg	Arg	Gln	Trp 20	Thr	Ser	Leu	Ser	Leu 25	Arg	Val	Thr	Ala	Lys 30	Glu	Leu	
Ser	Leu	Val 35	Asn	Lys	Asn	Lys	Ser 40	Ser	Ala	Ile	Val	Glu 45	Ile	Phe	Ser	
Lys	Tyr 50	Gln	Lys	Ala	Ala	Glu 55	Glu	Thr	Asn	Met	Glu 60	Lys	Lys	Arg	Ser	
Asn 65	Thr	Glu	Asn	Leu	Ser 70	Gln	His	Phe	Arg	Lys 75	Gly	Thr	Leu	Thr	Val 80	
Leu	Lys	Lys	Lys	Trp 85	Glu	Asn	Pro	Gly	Leu 90	Gly	Ala	Glu	Ser	His 95	Thr	
Asp	Ser	Leu	Arg 100	Asn	Ser	Ser	Thr	Glu 105	Ile	Arg	His	Arg	Ala 110	Asp	His	
Pro	Pro	Ala 115	Glu	Val	Thr	Ser	His 120	Ala	Ala	Ser	Gly	Ala 125	Lys	Ala	Asp	
Gln	Glu 130	Glu	Gln	Ile	His	Pro 135	Arg	Ser	Arg	Leu	Arg 140	Ser	Pro	Pro	Glu	
Ala	Leu	Val	Gln	Gly	Arg	Tyr	Pro	His	Ile	Lys	Asp	Gly	Glu	Asp	Leu	

145					150					155				160	
Lys	Asp	His	Ser	Thr 165	Glu	Ser	Lys	Lys	Met 170	Glu	Asn	Cys	Leu	Gly 175	Glu
Ser	Arg	His	Glu 180	Val	Glu	Lys	Ser	Glu 185	Ile	Ser	Glu	Asn	Thr 190	Asp	Ala
Ser	Gly	Lys 195	Ile	Glu	Lys	Tyr	Asn 200	Val	Pro	Leu	Asn	Arg 205	Leu	Lys	Met
Met	Phe 210	Glu	Lys	Gly	Glu	Pro 215	Thr	Gln	Thr	Lys	Ile 220	Leu	Arg	Ala	Gln
Ser 225	Arg	Ser	Ala	Ser	Gly 230	Arg	Lys	Ile	Ser	Glu 235	Asn	Ser	Tyr	Ser	Leu 240
Asp	Asp	Leu	Glu	Ile 245	Gly	Pro	Gly	Gln	Leu 250	Ser	Ser	Ser	Thr	Phe 255	Asp
Ser	Glu	Lys	Asn 260	Glu	Ser	Arg	Arg	Asn 265	Leu	Glu	Leu	Pro	Arg 270	Leu	Ser
Glu	Thr	Ser 275	Ile	Lys	Asp	Arg	Met 280	Ala	Lys	Tyr	Gln	Ala 285	Ala	Val	Ser
Lys	Gln 290	Ser	Ser	Ser	Pro	Thr 295	Ile	Pro	Met	Ser					

<210> 627
 <211> 94
 <212> PRT
 <213> homo sapiens

<400> 627

Asp 1	Ser	Ala	Pro	Ser 5	Pro	Gly	Phe	Ser	His 10	Phe	Phe	Phe	Asn	Thr 15	Val
Arg	Val	Pro	Phe 20	Leu	Lys	Cys	Trp	Glu 25	Arg	Phe	Ser	Val	Leu 30	Leu	Leu
Phe	Phe	Ser 35	Met	Phe	Val	Ser	Ser 40	Ala	Ala	Phe	Trp	Tyr 45	Leu	Glu	Asn
Ile	Ser 50	Thr	Ile	Ala	Asp	Asp 55	Leu	Phe	Leu	Leu	Thr 60	Arg	Glu	Ser	Ser
Leu 65	Ala	Val	Thr	Leu	Asn 70	Asp	Ser	Glu	Val	His 75	Cys	Arg	Leu	Leu	Asn 80
Gly	Asp	Asp	Ser	Ile 85	Leu	Ser	Thr	Asp	Thr 90	Glu	Ile	Pro	Gly		

<210> 628
 <211> 765
 <212> PRT
 <213> homo sapiens

<400> 628

Ile 1	Arg	Pro	Val	Val 5	Gln	Leu	Thr	Ala	Ile 10	Glu	Ile	Leu	Ala	Trp 15	Gly
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Leu	Arg	Asn	Met 20	Lys	Asn	Phe	Gln	Met 25	Ala	Ser	Ile	Thr	Ser 30	Pro	Ser
Leu	Val	Val 35	Glu	Cys	Gly	Gly	Glu 40	Arg	Val	Glu	Ser	Val 45	Val	Ile	Lys
Asn	Leu 50	Lys	Lys	Thr	Pro	Asn 55	Phe	Pro	Ser	Ser	Val 60	Leu	Phe	Met	Lys
Val 65	Phe	Leu	Pro	Lys	Glu 70	Glu	Leu	Tyr	Met 75	Pro	Pro	Leu	Val	Ile	Lys 80
Val	Ile	Asp	His	Arg 85	Gln	Phe	Gly	Arg	Lys 90	Pro	Val	Val	Gly	Gln 95	Cys
Thr	Ile	Glu	Arg 100	Leu	Asp	Arg	Phe	Arg 105	Cys	Asp	Pro	Tyr	Ala 110	Gly	Lys
Glu	Asp	Ile 115	Val	Pro	Gln	Leu	Lys 120	Ala	Ser	Leu	Leu	Ser 125	Ala	Pro	Pro
Cys	Arg 130	Asp	Ile	Val	Ile	Glu 135	Met	Glu	Asp	Thr	Lys 140	Pro	Leu	Leu	Ala
Ser 145	Lys	Leu	Thr	Glu	Lys 150	Glu	Glu	Glu	Ile	Val 155	Asp	Trp	Trp	Ser	Lys 160
Phe	Asp	Ala	Ser	Ser 165	Gly	Glu	His	Glu	Lys 170	Cys	Gly	Gln	Tyr	Ile 175	Gln
Lys	Gly	Tyr	Ser 180	Lys	Leu	Lys	Ile	Tyr 185	Asn	Cys	Glu	Leu	Glu 190	Asn	Val
Ala	Glu	Phe 195	Glu	Gly	Leu	Thr	Asp 200	Phe	Ser	Asp	Thr	Phe 205	Lys	Leu	Tyr
Arg	Gly 210	Lys	Ser	Asp	Glu	Asn 215	Glu	Asp	Pro	Ser	Val 220	Val	Gly	Glu	Phe
Lys 225	Gly	Ser	Phe	Arg	Ile 230	Tyr	Pro	Leu	Pro	Asp 235	Asp	Pro	Ser	Val	Pro 240
Ala	Pro	Pro	Arg	Gln 245	Phe	Arg	Glu	Leu	Pro 250	Asp	Ser	Val	Pro	Gln 255	Glu
Cys	Thr	Val	Arg 260	Ile	Tyr	Ile	Val	Arg 265	Gly	Leu	Glu	Leu	Gln 270	Pro	Gln
Asp	Asn	Asn	Gly 275	Leu	Cys	Asp	Pro 280	Tyr	Ile	Lys	Ile	Thr 285	Leu	Gly	Lys
Lys	Val 290	Ile	Glu	Asp	Arg	Asp 295	His	Tyr	Ile	Pro	Asn 300	Thr	Leu	Asn	Pro
Val 305	Phe	Gly	Arg	Met	Tyr 310	Glu	Leu	Ser	Cys	Tyr 315	Leu	Pro	Gln	Glu	Lys 320
Asp	Leu	Lys	Ile	Ser 325	Val	Tyr	Asp	Tyr	Asp 330	Thr	Phe	Thr	Arg	Asp 335	Glu
Lys	Val	Gly	Glu 340	Thr	Ile	Ile	Asp	Leu 345	Glu	Asn	Arg	Phe	Leu 350	Ser	Arg

Phe	Gly	Ser	His	Cys	Gly	Ile	Pro	Glu	Glu	Tyr	Cys	Val	Ser	Gly	Val
		355					360					365			
Asn	Thr	Trp	Arg	Asp	Gln	Leu	Arg	Pro	Thr	Gln	Leu	Leu	Gln	Asn	Val
	370					375					380				
Ala	Arg	Phe	Lys	Gly	Phe	Pro	Gln	Pro	Ile	Leu	Ser	Glu	Asp	Gly	Ser
385					390					395					400
Arg	Ile	Arg	Tyr	Gly	Gly	Arg	Asp	Tyr	Ser	Leu	Asp	Glu	Phe	Glu	Ala
				405					410					415	
Asn	Lys	Ile	Leu	His	Gln	His	Leu	Gly	Ala	Pro	Glu	Glu	Arg	Leu	Ala
			420					425					430		
Leu	His	Ile	Leu	Arg	Thr	Gln	Gly	Leu	Val	Pro	Glu	His	Val	Glu	Thr
		435					440					445			
Arg	Thr	Leu	His	Ser	Thr	Phe	Gln	Pro	Asn	Ile	Ser	Gln	Gly	Lys	Leu
	450					455					460				
Gln	Met	Trp	Val	Asp	Val	Phe	Pro	Lys	Ser	Leu	Gly	Pro	Pro	Gly	Pro
465					470					475					480
Pro	Phe	Asn	Ile	Thr	Pro	Arg	Lys	Ala	Lys	Lys	Tyr	Tyr	Leu	Arg	Val
				485					490					495	
Ile	Ile	Trp	Asn	Thr	Lys	Asp	Val	Ile	Leu	Asp	Glu	Lys	Ser	Ile	Thr
			500					505					510		
Gly	Glu	Glu	Met	Ser	Asp	Ile	Tyr	Val	Lys	Gly	Trp	Ile	Pro	Gly	Asn
		515					520					525			
Glu	Glu	Asn	Lys	Gln	Lys	Thr	Asp	Val	His	Tyr	Arg	Ser	Leu	Asp	Gly
	530					535					540				
Glu	Gly	Asn	Phe	Asn	Trp	Arg	Phe	Val	Phe	Pro	Phe	Asp	Tyr	Leu	Pro
545					550					555					560
Ala	Glu	Gln	Leu	Cys	Ile	Val	Ala	Lys	Lys	Glu	His	Phe	Trp	Ser	Ile
				565					570					575	
Asp	Gln	Thr	Glu	Phe	Arg	Ile	Pro	Pro	Arg	Leu	Ile	Ile	Gln	Ile	Trp
			580					585					590		
Asp	Asn	Asp	Lys	Phe	Ser	Leu	Asp	Asp	Tyr	Leu	Gly	Phe	Leu	Glu	Leu
		595					600					605			
Asp	Leu	Arg	His	Thr	Ile	Ile	Pro	Ala	Lys	Ser	Pro	Glu	Lys	Cys	Arg
	610					615					620				
Leu	Asp	Met	Ile	Pro	Asp	Leu	Lys	Ala	Met	Asn	Pro	Leu	Lys	Ala	Lys
625					630					635					640
Thr	Ala	Ser	Leu	Phe	Glu	Gln	Lys	Ser	Met	Lys	Gly	Trp	Trp	Pro	Cys
				645					650					655	
Tyr	Ala	Glu	Lys	Asp	Gly	Ala	Arg	Val	Met	Ala	Gly	Lys	Val	Glu	Met
			660					665					670		
Thr	Leu	Glu	Ile	Leu	Asn	Glu	Lys	Glu	Ala	Asp	Glu	Arg	Pro	Ala	Gly
		675					680					685			

Lys	Gly	Arg	Asp	Glu	Pro	Asn	Met	Asn	Pro	Lys	Leu	Asp	Leu	Pro	Asn
	690					695					700				
Arg	Pro	Glu	Thr	Ser	Phe	Leu	Trp	Phe	Thr	Asn	Pro	Cys	Lys	Thr	Met
705					710					715					720
Lys	Phe	Ile	Val	Trp	Arg	Arg	Phe	Lys	Trp	Val	Ile	Ile	Gly	Leu	Leu
				725					730					735	
Phe	Leu	Leu	Ile	Leu	Leu	Leu	Phe	Val	Ala	Val	Leu	Leu	Tyr	Ser	Leu
			740					745					750		
Pro	Asn	Tyr	Leu	Ser	Met	Lys	Ile	Val	Lys	Pro	Asn	Val			
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<210> 629

<211> 289

<212> PRT

<213> homo sapiens

<400> 629

Glu	Thr	Gln	Val	Val	Ile	Gln	Arg	Lys	Leu	Val	Ile	Val	Pro	Tyr	Leu
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Asn	Asp	Gln	Pro	Gly	Trp	Asp	Ser	Lys	Phe	Arg	Leu	Val	Asn	Thr	Pro
			20					25					30		
Glu	Met	Leu	Phe	Phe	Arg	Asn	Asp	Thr	Glu	Leu	Phe	Gly	Trp	Lys	Val
		35					40					45			
Val	Lys	Arg	Glu	Asn	Lys	Ser	Pro	Val	Lys	Ile	Pro	Phe	Thr	Ile	Gln
	50					55					60				
Arg	Ser	Val	Met	Asp	Ile	Cys	Phe	Leu	Phe	Val	Phe	Phe	Ile	Ala	Arg
65					70					75					80
Asn	Pro	Ala	Phe	Asp	Val	Asp	Val	Thr	His	Phe	Leu	Ser	Cys	Asp	Ala
				85					90					95	
Phe	Leu	Val	Gln	Asp	Asn	Val	Leu	Gly	Val	Pro	Asp	Asp	His	Thr	Gln
			100					105					110		
Val	Val	Phe	Leu	Gly	Phe	Pro	Gly	Cys	Asp	Val	Glu	Arg	Ala	Trp	
		115					120					125			
Trp	Pro	Gln	Thr	Leu	Gly	Glu	Asn	Ile	His	Pro	His	Leu	Lys	Phe	Ser
	130					135					140				
Leu	Gly	Asn	Val	Gly	Leu	Glu	Gly	Ala	Val	Gln	Ser	Pro	Cys	Phe	His
145					150					155					160
Val	Leu	Arg	Asp	Gln	Pro	Leu	Ser	Pro	Glu	Asp	Val	Lys	Ser	Lys	Pro
				165					170					175	
Leu	Phe	Arg	Gly	Pro	Glu	Val	Leu	Val	Gln	Asp	Phe	Val	Gly	Phe	Lys
			180					185					190		
Phe	Ile	Gln	Ala	Val	Val	Ser	Ser	Ser	Ile	Ser	Asp	Ser	Thr	Pro	Ile
		195					200					205			
Phe	Gly	Lys	Asp	Gly	Leu	Trp	Glu	Ala	Phe	Glu	Ser	Gly	Asp	Ile	Leu

210					215					220					
Lys 225	Gln	Leu	Cys	Trp	Ser 230	Gln	Leu	Ile	Ser	Pro 235	Gly	Ile	Asp	Ser	Arg 240
Asn	Thr	Val	Leu 245	Leu	Trp	Tyr	Ala	Ala	Val 250	Gly	Pro	Lys	Ala	Gly 255	Lys
Glu	Ser	Val	Phe 260	Gln	Ile	Asn	Asn	Cys 265	Phe	Ser	Tyr	Phe	Phe 270	Ile	Pro
Gly	Lys	Gly 275	Val	Ile	Ile	Ile	Asp 280	Arg	Asn	Phe	Gln	Val 285	Phe	Phe	Leu

Arg

<210> 630
 <211> 824
 <212> PRT
 <213> homo sapiens

<400> 630

Arg 1	Val	Ser	Val	Leu 5	Ala	Ala	Ala	Ser	Ser 10	Ala	Leu	Pro	Val	Ala 15	Pro
Arg	Glu	Ala	Gly 20	Val	Thr	Asn	Trp	Pro 25	Ala	Gly	Cys	Val	Pro 30	Glu	Val
Arg	Ser	Thr 35	Gly	Glu	Lys	Glu	Val 40	Ala	Lys	Thr	Leu	His 45	Arg	Arg	Ser
Arg	Pro 50	Glu	Trp	Cys	Gly	Ala 55	Arg	Asp	Pro	Pro	Ala 60	Met	Leu	Leu	Phe
Val 65	Leu	Thr	Cys	Leu	Leu 70	Ala	Val	Phe	Pro	Ala 75	Ile	Ser	Thr	Lys	Ser 80
Pro	Ile	Phe	Gly	Pro 85	Glu	Glu	Val	Asn	Ser 90	Val	Glu	Gly	Asn	Ser 95	Val
Ser	Ile	Thr	Cys 100	Tyr	Tyr	Pro	Pro	Thr 105	Ser	Val	Asn	Arg	His 110	Thr	Arg
Lys	Tyr	Trp 115	Cys	Arg	Gln	Gly	Ala 120	Arg	Gly	Gly	Cys	Ile 125	Thr	Leu	Ile
Ser	Ser 130	Glu	Gly	Tyr	Val	Ser 135	Ser	Lys	Tyr	Ala	Gly 140	Arg	Ala	Asn	Leu
Thr 145	Asn	Phe	Pro	Glu	Asn 150	Gly	Thr	Phe	Val	Val 155	Asn	Ile	Ala	Gln	Leu 160
Ser	Gln	Asp	Asp	Ser 165	Gly	Arg	Tyr	Lys	Cys 170	Gly	Leu	Gly	Ile	Asn 175	Ser
Arg	Gly	Leu	Ser 180	Phe	Asp	Val	Ser	Leu 185	Glu	Val	Ser	Gln	Gly 190	Pro	Gly
Leu	Leu	Asn 195	Asp	Thr	Lys	Val	Tyr 200	Thr	Val	Asp	Leu	Gly 205	Arg	Thr	Val
Thr	Ile	Asn	Cys	Pro	Phe	Lys	Thr	Glu	Asn	Ala	Gln	Lys	Arg	Lys	Ser

210						215					220					
Leu 225	Tyr	Lys	Gln	Ile	Gly 230	Leu	Tyr	Pro	Val	Leu 235	Val	Ile	Asp	Ser	Ser 240	
Gly	Tyr	Val	Asn	Pro 245	Asn	Tyr	Thr	Gly	Arg 250	Ile	Arg	Leu	Asp	Ile 255	Gln	
Gly	Thr	Gly	Gln 260	Arg	Leu	Phe	Ser	Val 265	Val	Ile	Asn	Gln	Leu 270	Arg	Leu	
Ser	Asp	Ala 275	Gly	Gln	Tyr	Leu	Cys 280	Gln	Ala	Gly	Asp	Asp 285	Ser	Asn	Ser	
Asn	Lys 290	Lys	Asn	Ala	Asp	Leu 295	Gln	Val	Leu	Lys	Pro 300	Glu	Pro	Glu	Leu	
Val 305	Tyr	Glu	Asp	Leu	Arg 310	Gly	Ser	Val	Thr	Phe 315	His	Cys	Ala	Leu	Gly 320	
Pro	Glu	Val	Ala	Asn 325	Val	Ala	Lys	Phe	Leu 330	Cys	Arg	Gln	Ser	Ser 335	Gly	
Glu	Asn	Cys	Asp 340	Val	Val	Val	Asn	Thr 345	Leu	Gly	Lys	Arg	Ala 350	Pro	Ala	
Phe	Glu	Gly 355	Arg	Ile	Leu	Leu	Asn 360	Pro	Gln	Asp	Lys	Asp 365	Gly	Ser	Phe	
Ser	Val 370	Val	Ile	Thr	Gly	Leu 375	Arg	Lys	Glu	Asp	Ala 380	Gly	Arg	Tyr	Leu	
Cys 385	Gly	Ala	His	Ser	Asp 390	Gly	Gln	Leu	Gln	Glu 395	Gly	Ser	Pro	Ile	Gln 400	
Ala	Trp	Gln	Leu	Phe 405	Val	Asn	Glu	Glu	Ser 410	Thr	Ile	Pro	Arg	Ser 415	Pro	
Thr	Val	Val	Lys 420	Gly	Val	Ala	Gly	Gly 425	Ser	Val	Ala	Val	Leu 430	Cys	Pro	
Tyr	Asn	Arg 435	Lys	Glu	Ser	Lys	Ser 440	Ile	Lys	Tyr	Trp	Cys 445	Leu	Trp	Glu	
Gly	Ala 450	Gln	Asn	Gly	Arg	Cys 455	Pro	Leu	Leu	Val	Asp 460	Ser	Glu	Gly	Trp	
Val 465	Lys	Ala	Gln	Tyr	Glu 470	Gly	Arg	Leu	Ser	Leu 475	Leu	Glu	Glu	Pro	Gly 480	
Asn	Gly	Thr	Phe	Thr 485	Val	Ile	Leu	Asn	Gln 490	Leu	Thr	Ser	Arg	Asp 495	Ala	
Gly	Phe	Tyr	Trp 500	Cys	Leu	Thr	Asn	Gly 505	Asp	Thr	Leu	Trp	Arg 510	Thr	Thr	
Val	Glu	Ile 515	Lys	Ile	Ile	Glu	Gly 520	Glu	Pro	Asn	Leu	Lys 525	Val	Pro	Gly	
Asn	Val 530	Thr	Ala	Val	Leu	Gly 535	Glu	Thr	Leu	Lys	Val 540	Pro	Cys	His	Phe	
Pro	Cys	Lys	Phe	Ser	Ser	Tyr	Glu	Lys	Tyr	Trp	Cys	Lys	Trp	Asn	Asn	

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545					550					555					560
Thr	Gly	Cys	Gln	Ala 565	Leu	Pro	Ser	Gln	Asp 570	Glu	Gly	Pro	Ser	Lys 575	Ala
Phe	Val	Asn	Cys 580	Asp	Glu	Asn	Ser	Arg 585	Leu	Val	Ser	Leu	Thr 590	Leu	Asn
Leu	Val	Thr 595	Arg	Ala	Asp	Glu	Gly 600	Trp	Tyr	Trp	Cys	Gly 605	Val	Lys	Gln
Gly	His 610	Phe	Tyr	Gly	Glu	Thr 615	Ala	Ala	Val	Tyr	Val 620	Ala	Val	Glu	Glu
Arg 625	Lys	Ala	Ala	Gly	Ser 630	Arg	Asp	Val	Ser	Leu 635	Ala	Lys	Ala	Asp	Ala 640
Ala	Pro	Asp	Glu	Lys 645	Val	Leu	Asp	Ser	Gly 650	Phe	Arg	Glu	Ile	Glu 655	Asn
Lys	Ala	Ile	Gln 660	Asp	Pro	Arg	Leu	Phe 665	Ala	Glu	Glu	Lys	Ala 670	Val	Ala
Asp	Thr	Arg 675	Asp	Gln	Ala	Asp	Gly 680	Ser	Arg	Ala	Ser	Val 685	Asp	Ser	Gly
Ser	Ser 690	Glu	Glu	Gln	Gly	Gly 695	Ser	Ser	Arg	Ala	Leu 700	Val	Ser	Thr	Leu
Val 705	Pro	Leu	Gly	Leu	Val 710	Leu	Ala	Val	Gly	Ala 715	Val	Ala	Val	Gly	Val 720
Ala	Arg	Ala	Arg	His 725	Arg	Lys	Asn	Val	Asp 730	Arg	Val	Ser	Ile	Arg 735	Ser
Tyr	Arg	Thr	Asp 740	Ile	Ser	Met	Ser	Asp 745	Phe	Glu	Asn	Ser	Arg 750	Glu	Phe
Gly	Ala	Asn 755	Asp	Asn	Met	Gly	Ala 760	Ser	Ser	Ile	Thr	Gln 765	Glu	Thr	Ser
Leu	Gly 770	Gly	Lys	Glu	Glu	Phe 775	Val	Ala	Thr	Thr	Glu 780	Ser	Thr	Thr	Glu
Thr 785	Lys	Glu	Pro	Lys	Lys 790	Ala	Lys	Arg	Ser	Ser 795	Lys	Glu	Glu	Ala	Glu 800
Met	Ala	Tyr	Lys	Asp 805	Phe	Leu	Leu	Gln	Ser 810	Ser	Thr	Val	Ala	Ala 815	Glu
Ala	Gln	Asp	Gly 820	Pro	Gln	Glu	Ala								

<210> 631

<211> 267

<212> PRT

<213> homo sapiens

<400> 631

Ala	Asp	Ile	Ala	Gly	Pro	Arg	Cys	Leu	Pro	Leu	Phe	Asn	Cys	His	Ile
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Asp	Gly	Cys	Ser 20	Leu	Ser	Ile	Glu	Val 25	Ala	Leu	Leu	His	Ser 30	Thr	Pro
Val	Pro	Ala 35	Leu	Ile	Ser	Pro	Gly 40	His	Gln	Val	Gln	Gly 45	Gln	Gly	Asp
Lys	Pro 50	Ala	Val	Leu	Val	Thr 55	Val	His	Glu	Gly	Leu 60	Ala	Gly	Ala	Phe
Val 65	Leu	Ala	Gly	Gln	Gly 70	Leu	Ala	Ala	Arg	Val 75	Ile	Pro	Leu	Ala	Pro 80
Val	Phe	Leu	Val	Arg 85	Gly	Glu	Phe	Ala	Trp 90	Lys	Val	Thr	Gly	Asp 95	Leu
Glu	Ser	Leu	Ser 100	Gln	His	Ser	Arg	Asp 105	Ile	Pro	Trp	Tyr	Leu 110	Glu	Val
Trp	Phe	Ser 115	Phe	Asp	Asn	Leu	Asp 120	Leu	His	Gly	Gly	Pro 125	Pro	Glu	Ser
Ile	Ala 130	Val	Gly	Gln	Thr	Pro 135	Val	Glu	Ala	Gly	Val 140	Pro	Ala	Gly	Glu
Leu 145	Val	Glu	Asp	Asp	Ser 150	Glu	Gly	Ala	Val	Ala 155	Trp	Leu	Leu	Gln	Gln 160
Gly	Glu	Ala	Ala	Leu 165	Val	Leu	Gly	Leu	Asn 170	Pro	Pro	Leu	Ala	Val 175	His
Gln	Gln	Gly	Ala 180	Ala	Ala	Ile	Leu	Gly 185	Pro	Phe	Pro	Glu	Thr 190	Pro	Val
Leu	Asp	Ala 195	Phe	Ala	Phe	Leu	Thr 200	Val	Val	Gly	Ala	Glu 205	His	Gly	His
Arg	Ala 210	Ser	Cys	His	Pro	Leu 215	His	His	Ser	Gly	Ala 220	Ala	Gly	Asn	Arg
Gly 225	Leu	Leu	Ile	Asp	Glu 230	Glu	Leu	Pro	Gly	Leu 235	Asp	Arg	Arg	Ala	Phe 240
Leu	Gln	Leu	Thr	Ile 245	Arg	Met	Gly	Ser	Thr 250	Gln	Val	Ala	Pro	Cys 255	Ile
Leu	Leu	Pro	Gln 260	Ala	Cys	Asp	His	His 265	Thr	Glu					

<210> 632

<211> 140

<212> PRT

<213> homo sapiens

<400> 632

Gly 1	Glu	Thr	Arg	Val 5	His	Ser	Gln	Gln	Gly 10	Gly	Gly	Ile	Lys	Ala 15	Pro
Ser	Trp	Asp	Trp 20	Phe	Phe	Arg	Glu	Pro 25	Gly	Pro	Leu	Val	Lys 30	Gly	Leu
Leu	Gly	His 35	Val	Lys	Gln	Tyr	Leu 40	Glu	Gln	Pro	Arg	Pro 45	Trp	Gly	Tyr

Gln	Val	Glu	Arg	Arg	Glu	Gly	Arg	Arg	Leu	Pro	Cys	Thr	His	Leu	Pro
	50					55					60				
Trp	Trp	Ala	Gly	Phe	Ser	Leu	Leu	Gly	Ser	Thr	Leu	Pro	Pro	Ser	Val
65					70					75					80
His	Asp	Thr	Asp	Pro	Arg	Ala	Ser	Pro	Cys	Pro	Arg	Pro	Ser	Tyr	Arg
				85					90					95	
Leu	Leu	Phe	Gln	Asp	Ile	Thr	Asp	Asn	Pro	Glu	Arg	Met	Glu	Lys	Gly
			100					105					110		
Gly	Ala	Trp	Val	Pro	Ala	Val	Ser	Gly	Gln	Lys	Glu	Val	Ala	Cys	Gly
		115					120					125			
Asn	Leu	Arg	Ser	Pro	His	Pro	Arg	Phe	Pro	Lys	Arg				
	130					135					140				

<210> 633

<211> 127

<212> PRT

<213> homo sapiens

<400> 633

Val	Phe	Pro	Cys	His	Leu	Val	Gly	Ala	Gly	Pro	Thr	Pro	Ala	Thr	Thr
1				5					10					15	
Ser	Gly	Thr	Ala	Lys	Gly	Ser	Thr	Arg	Cys	Asp	Tyr	Pro	Gly	Pro	Cys
			20					25					30		
Trp	Gln	Leu	Arg	Ile	Pro	Gly	Thr	Cys	Ser	Asp	Pro	Val	Ser	Gly	Ser
		35					40					45			
Ser	Glu	Ser	Gln	Glu	Pro	Arg	Met	Arg	Ala	Leu	Cys	Ser	Pro	Ser	Ser
	50					55					60				
Lys	Thr	Gln	Gly	Ser	Pro	Pro	Arg	Lys	Gly	Ala	His	Val	Pro	Gln	Arg
65					70					75				80	
Gly	Trp	Leu	Pro	Gly	Cys	Tyr	Leu	Phe	Tyr	Pro	Thr	Ser	Ala	Ala	Glu
				85					90					95	
Ser	Gln	Gly	Glu	Thr	Ala	Ser	His	Pro	Lys	Pro	Leu	Gly	Phe	Ser	Arg
			100					105					110		
Glu	Lys	Asn	Leu	Ser	Gln	Lys	His	Asp	Leu	Phe	Ser	Gly	Cys	Lys	
		115					120					125			

<210> 634

<211> 140

<212> PRT

<213> homo sapiens

<400> 634

His	His	Gln	Lys	His	Met	Gln	Gly	Lys	Gly	Ser	Tyr	Trp	Ala	Ser	Gly
1				5					10					15	
Leu	Leu	Ser	Pro	Trp	Leu	Gly	Arg	Lys	Gly	Arg	Glu	Asp	Gly	Trp	Gly
			20					25					30		

Ser	Leu	Phe	Gly	Ile	Asp	Asp	Val	His	Glu	Phe	Gly	Leu	Glu	Gly	Ser
		35					40					45			
Thr	Thr	His	Lys	Glu	Ala	Ile	His	Ile	Arg	Leu	Ala	Gly	Gln	Leu	Leu
	50					55					60				
Ala	Gly	Cys	Pro	Ser	His	Arg	Ala	Ser	Ile	Asn	Asp	Thr	Gly	Ala	Leu
	65				70					75					80
Ser	His	Arg	Ile	Arg	Asp	Val	Gly	Leu	Gln	Pro	Ser	Ser	Glu	Leu	Leu
				85					90					95	
Val	Tyr	Phe	Leu	Gly	Leu	Leu	Gly	Cys	Cys	Ser	Leu	Ala	Ser	Thr	Asn
			100					105					110		
Gly	Pro	His	Arg	Leu	Ile	Gly	Gln	Asp	Asp	Leu	Ala	Pro	Val	Leu	His
		115					120					125			
Val	Ile	Cys	Asp	Asp	Leu	Leu	Val	Trp	Trp	Glu	Gly				
	130					135					140				

<210> 635

<211> 101

<212> PRT

<213> homo sapiens

<400> 635

Lys	Val	Ile	Ala	Asp	Asn	Val	Lys	Asp	Trp	Ser	Lys	Val	Val	Leu	Ala
1				5					10					15	
Tyr	Glu	Pro	Val	Trp	Ala	Ile	Gly	Thr	Gly	Lys	Thr	Ala	Thr	Pro	Gln
			20					25					30		
Gln	Ala	Gln	Glu	Val	His	Glu	Lys	Leu	Arg	Gly	Trp	Leu	Lys	Ser	Asn
		35					40					45			
Val	Ser	Asp	Ala	Val	Ala	Gln	Ser	Thr	Arg	Ile	Ile	Tyr	Gly	Gly	Ser
	50					55					60				
Val	Thr	Gly	Ala	Thr	Cys	Lys	Glu	Leu	Ala	Ser	Gln	Pro	Asp	Val	Asp
	65				70					75					80
Gly	Phe	Leu	Val	Gly	Gly	Ala	Ser	Leu	Lys	Pro	Glu	Phe	Val	Asp	Ile
				85					90					95	
Ile	Asn	Ala	Lys	Gln											
			100												

<210> 636

<211> 329

<212> PRT

<213> homo sapiens

<400> 636

Asp	Ser	Ile	Phe	Pro	Leu	Trp	Ala	Val	Leu	Ala	Leu	Ser	Pro	Pro	Gly
1				5					10					15	
Ile	Arg	Val	Arg	Met	Lys	Lys	Ser	Ser	Val	Ser	Gly	Met	Thr	Ala	Ala
			20					25					30		
Gly	Trp	Val	Val	Trp	Gly	Glu	Ala	Glu	Gly	Lys	Ala	Ala	Leu	Arg	Leu

35					40					45					
Gly	Val	Glu	Phe	Leu	Glu	Val	Trp	Gly	Gly	Gly	Arg	Val	Phe	Asn	Leu
	50					55					60				
Glu	Lys	Ser	Gln	Pro	Ala	Arg	Ala	Glu	Arg	Glu	Cys	Glu	Arg	Gly	Ser
65					70					75					80
Ser	Glu	Gly	Ala	Arg	Asn	Gly	Val	Gly	Gly	Ser	Gly	Gly	Arg	Ser	Val
				85					90					95	
Ala	Val	Ala	Leu	Val	His	Gln	His	Gly	Val	Arg	Leu	Leu	Gly	Asp	Leu
			100					105					110		
Gln	Gln	Arg	Val	His	Val	Gly	Ala	Ala	Pro	Ala	Pro	Gln	Val	Ala	Gly
		115					120					125			
Leu	Pro	Pro	Leu	Arg	Ala	Ala	Leu	Val	Val	Val	Gly	Ala	His	Leu	His
	130					135					140				
His	Leu	Gly	Gly	Leu	Glu	His	Phe	His	Leu	Ala	Leu	Ala	Asp	Leu	Leu
145					150					155					160
Asp	Val	Glu	Gly	Glu	Gly	Trp	His	Leu	Val	Asp	Arg	Gly	Leu	Gly	Ala
				165					170					175	
Arg	Val	His	His	Val	Val	Gly	Arg	Glu	Gly	Phe	Ala	Gln	Leu	Val	Pro
			180					185					190		
Arg	Arg	Leu	Gln	Phe	Leu	Ala	Pro	Leu	Gly	Gly	His	Gln	Ala	Arg	Ala
		195					200					205			
Gln	Leu	Val	His	Ala	Leu	Leu	Gln	Gly	Val	Pro	Arg	Leu	Leu	Gln	Val
	210					215					220				
Phe	Leu	Gly	Leu	Glu	Ala	Arg	Leu	Leu	Gln	Val	Leu	Ala	Gly	Thr	His
225					230					235					240
Leu	Gly	Leu	Leu	His	Leu	Leu	Leu	Gly	Glu	Gly	Leu	Leu	Glu	Val	Val
				245					250					255	
His	Ala	Pro	Gln	Ala	Leu	Arg	Leu	Ile	Arg	Ser	Ala	Arg	Asp	Ser	Ser
			260					265					270		
Ile	Thr	Ser	Ser	Thr	Ser	Thr	Ala	Ser	Ser	Asp	Glu	Ser	Ser	Ser	Ala
		275					280					285			
Ala	Ala	Ser	Ser	Ser	Gly	Arg	Ser	Pro	Ser	Pro	Ser	Ser	Ser	Pro	Ser
	290					295					300				
Phe	Ser	Gly	Ser	Ala	Ser	Asp	Ser	Phe	Ser	Asp	Leu	Leu	Met	Leu	Ser
305					310					315					320
Leu	Ala	Gly	Ser	Phe	Thr	Ser	Ser	Trp							
				325											

<210> 637

<211> 263

<212> PRT

<213> homo sapiens

<400> 637

Gly 1	Arg	Leu	Pro	Gly 5	Tyr	Pro	Asp	Arg	Arg 10	Gly	Pro	Gly	Ala	Ser 15	Ser
Ala	Gly	Ala	Gln 20	Ala	Ala	Glu	Glu	Pro 25	Ser	Gly	Ala	Gly	Ser 30	Glu	Glu
Leu	Ile	Lys 35	Ser	Asp	Gln	Val	Asn 40	Gly	Val	Leu	Val	Leu 45	Ser	Leu	Leu
Asp	Lys 50	Ile	Ile	Gly	Ala	Val 55	Asp	Gln	Ile	Gln	Leu 60	Thr	Gln	Ala	Gln
Leu 65	Glu	Glu	Arg	Gln	Ala 70	Glu	Met	Glu	Gly	Ala 75	Val	Gln	Ser	Ile	Gln 80
Gly	Glu	Leu	Ser	Lys 85	Leu	Gly	Lys	Ala	His 90	Ala	Thr	Thr	Ser	Asn 95	Thr
Val	Ser	Lys	Leu 100	Leu	Glu	Lys	Val	Arg 105	Lys	Val	Ser	Val	Asn 110	Val	Lys
Thr	Val	Arg 115	Gly	Ser	Leu	Glu	Arg 120	Gln	Ala	Gly	Gln	Ile 125	Lys	Lys	Leu
Glu	Val 130	Asn	Glu	Ala	Glu	Leu 135	Leu	Arg	Arg	Arg	Asn 140	Phe	Lys	Val	Met
Ile 145	Tyr	Gln	Asp	Glu	Val 150	Lys	Leu	Pro	Ala	Lys 155	Leu	Ser	Ile	Ser	Lys 160
Ser	Leu	Lys	Glu	Ser 165	Glu	Ala	Leu	Pro	Glu 170	Lys	Glu	Gly	Glu	Glu 175	Leu
Gly	Glu	Gly	Glu 180	Arg	Pro	Glu	Glu	Asp 185	Ala	Ala	Ala	Leu	Glu 190	Leu	Ser
Ser	Asp	Glu 195	Ala	Val	Glu	Val	Glu 200	Glu	Val	Ile	Glu	Glu 205	Ser	Arg	Ala
Glu	Arg 210	Ile	Lys	Arg	Arg	Ala 215	Cys	Gly	Ala	Trp	Thr 220	Thr	Ser	Arg	Arg
Pro 225	Ser	Pro	Arg	Arg	Arg 230	Trp	Arg	Arg	Pro	Arg 235	Cys	Val	Pro	Ala	Arg 240
Thr	Trp	Arg	Arg	Arg 245	Ala	Ser	Arg	Pro	Arg 250	Lys	Thr	Trp	Arg	Arg 255	Arg
Gly	Thr	Pro	Trp 260	Arg	Ser	Ala									

<210> 638
 <211> 205
 <212> PRT
 <213> homo sapiens

<400> 638

Ser 1	Gly	Asp	Leu	Arg 5	Leu	Leu	Val	Asp	Thr 10	Ser	Lys	Val	Gln	Glu 15	Ala
Trp	Val	Pro	Ser 20	Gln	Asp	Thr	His	His 25	Thr	Gln	Glu	Leu	Leu 30	Ala	Val

Gln	Gly	Ser 35	Leu	Val	Ser	Gly	Tyr 40	Arg	Pro	Gly	Gly	Gly 45	Phe	Gly	Ala
Ala	Pro 50	Val	His	Glu	Asp	Pro 55	His	Leu	Leu	Gly	Pro 60	Ala	Ser	Arg	Gly
Ala 65	Pro	Glu	Thr	Ala	Ala 70	Phe	Phe	Phe	Phe	Phe 75	Phe	Phe	Phe	Phe	Pro 80
Glu	Gln	His	Leu	Arg 85	Val	Gly	Leu	Leu	Leu 90	Leu	Pro	Pro	Arg	Leu 95	Ser
Pro	Arg	Pro	Gly 100	Pro	Ala	Trp	Pro	Val 105	Pro	Asn	Pro	Val	Gly 110	Trp	Pro
Gly	His	Leu 115	His	Gln	Gly	Gly	Gln 120	Leu	Leu	Ala	Gly	Thr 125	Asn	Lys	Pro
Phe	His 130	Leu	Ala	Met	Val	Val 135	Val	Phe	Ser	Met	Asp 140	Arg	Gly	Pro	Glu
Thr 145	Arg	Ala	Gly	Arg	Gly 150	Arg	Glu	His	Thr	Ser 155	Leu	Gly	Val	Gly	Thr 160
Ser	Leu	Xxx	Thr	Pro 165	Gln	Gln	Leu	Xxx	Gly 170	Pro	Arg	Xxx	Xxx	Phe 175	Pro
Xxx	Ala	Val	Gln 180	Ala	Ser	Pro	Xxx	Pro 185	Gly	Val	Cys	Ser	Leu 190	Ala	Trp
Val	Glu	Leu 195	Cys	His	Ile	Xxx	Asp 200	Lys	Gln	Xxx	Gly	Gly 205			

<210> 639

<211> 171

<212> PRT

<213> homo sapiens

<400> 639

Pro 1	Val	Thr	Pro	Arg 5	Asp	Xxx	Pro	Gly	Ala 10	Gly	Gly	Gly	Ser	Xxx 15	Glu
Gly	Pro	Met	Gln 20	His	Pro	Gly	Gln	Ser 25	Arg	Pro	Xxx	Pro	Leu 30	Ala	Xxx
Pro	Ala	Pro 35	Xxx	Trp	Xxx	Leu	Met 40	Ala	Pro	Cys	Gly	Ala 45	Leu	Thr	Cys
Trp	Ala 50	Arg	Leu	Xxx	Leu	Gly 55	Leu	Ser	Ala	Pro	Xxx 60	Leu	Leu	Ile	Xxx
Asp 65	Val	Thr	Glu	Leu	Asp 70	Pro	Ser	Gln	Ala	Ala 75	His	Ser	Trp	Thr	Trp 80
Ala	Ser	Leu	His	Cys 85	Xxx	Gly	Lys	Xxx	Xxx 90	Pro	Arg	Ala	Xxx	Lys 95	Leu
Leu	Arg	Gly	Xxx 100	Glu	Ala	Gly	Ala	His 105	Pro	Gln	Ala	Ser	Val 110	Phe	Ser
Ala	Pro	Pro	Cys	Pro	Arg	Phe	Arg	Ala	Ser	Val	His	Arg	Glu	His	His

Met	Glu	Pro	Leu	Gly	Leu	Gly	Arg	Lys	Ala	Arg	Val	Ser	Ala	His	Arg
		35					40					45			
His	Thr	Ser	Tyr	Leu	Gln	Asp	Ile	Asp	Cys	Leu	Cys	Arg	Gly	Ser	Thr
	50					55					60				
Gly	Gln	Pro	Thr	Ala	Asn	Thr	Ala	Ala	Ser	Leu	Val	Ser	Ala	Ser	Leu
	65				70					75					80
Leu	Pro	Val	His	Pro	Gly	Asp	Tyr	Ser	Trp	Ile	Asn	Leu	Pro	Lys	Asn
				85					90					95	
Ser	Ala	Phe	Ile	Met	Ser	Leu	Phe	Cys	Ser	Lys	Thr	Gln	Asn	Gly	Ser
			100					105					110		
Leu	Pro	Pro	Arg	Gly	Arg	Pro	Ser	His	His	Cys	Ile	Pro	Asn	Arg	
		115					120					125			

<210> 642
 <211> 136
 <212> PRT
 <213> homo sapiens
 <400> 642

Trp	Gly	Xxx	Gly	Arg	Val	Arg	Val	Xxx	Gly	Trp	Xxx	Arg	Lys	Pro	Met
1				5					10					15	
Lys	Xxx	Gly	Ile	Pro	Pro	Glu	Xxx	His	Gly	Pro	Ile	Thr	Ala	Asp	Gly
			20					25					30		
His	Arg	Xxx	Leu	Xxx	Xxx	Leu	Pro	Pro	Xxx	Gly	Xxx	Arg	Cys	Xxx	Xxx
		35					40					45			
Ala	Asp	Pro	Lys	Gly	Xxx	Gly	Leu	Xxx	Ala	Leu	Phe	Xxx	Lys	Xxx	Pro
	50					55					60				
Pro	Xxx	Glu	Xxx	Cys	Leu	Ser	Xxx	Xxx	Pro	Xxx	Xxx	Pro	Val	Thr	
	65				70				75					80	
His	Arg	Ala	Gly	Met	Glu	Phe	Asn	Gly	Xxx	Phe	Trp	Xxx	Xxx	Thr	Leu
				85				90						95	
Val	His	Gly	Gln	Thr	Ser	Leu	Leu	Xxx	Gly	Tyr	Xxx	Thr	Arg	Leu	Lys
			100					105					110		
Xxx	Lys	Ile	Val	Cys	Cys	His	Ser	Ser	Gly	Xxx	Trp	Ser	Val	Cys	Gly
		115					120					125			
Leu	His	Arg	Phe	His	Arg	Asn	Gln								
	130					135									

<210> 643
 <211> 132
 <212> PRT
 <213> homo sapiens
 <400> 643

Gly	Arg	Xxx	Ser	Arg	Ala	Trp	Gly	Leu	Gly	Cys	Pro	Ser	Leu	Leu	Ser
1				5					10					15	
Pro	Ile	Ser	Leu	Arg	Leu	Pro	Val	Pro	Pro	Pro	Arg	Pro	Pro	Asn	Leu

20										25					30				
Arg	Pro	Pro	Ala	Thr	Pro	Gly	Ala	Pro	Thr	Xxx	Pro	Xxx	Gln	Asn	Thr				
		35					40					45							
Ala	Xxx	Leu	Lys	Xxx	Leu	Leu	Glu	Leu	Ser	Xxx	Xxx	Leu	Ser	Gly	Leu				
	50					55					60								
Gly	Leu	Met	Gly	Xxx	Arg	Ala	Gly	Thr	Cys	Thr	Trp	Val	Ala	Xxx	Glu				
65					70					75					80				
Ala	His	Glu	Asp	Xxx	Asp	Thr	Pro	Arg	Val	Pro	Trp	Thr	Xxx	Tyr	Xxx				
				85					90					95					
Arg	Trp	Ser	Ser	Xxx	Pro	Xxx	Ala	Ile	Ala	Thr	Xxx	Gly	Xxx	Ser	Leu				
			100					105					110						
Xxx	Xxx	Gly	Arg	Pro	Gln	Arg	Glu	Xxx	Pro	Xxx	Arg	Val	Val	Xxx	Lys				
		115					120					125							
Xxx	Thr	Thr	Xxx																
	130																		

<210> 644
 <211> 131
 <212> PRT
 <213> homo sapiens

<400> 644

Gly	Val	Glu	Thr	Thr	Ala	Asn	Ser	Ser	Thr	Ser	Leu	Arg	Ser	Thr	Thr				
1				5					10					15					
Leu	Glu	Lys	Glu	Val	Pro	Val	Ile	Phe	Ile	His	Pro	Leu	Asn	Thr	Gly				
			20					25					30						
Leu	Phe	Arg	Ile	Lys	Ile	Gln	Gly	Ala	Thr	Gly	Lys	Phe	Asn	Met	Val				
		35					40					45							
Ile	Pro	Leu	Val	Asp	Gly	Met	Ile	Val	Ser	Arg	Arg	Ala	Leu	Gly	Phe				
	50					55					60								
Leu	Val	Arg	Gln	Thr	Val	Ile	Asn	Ile	Cys	Arg	Arg	Lys	Arg	Leu	Glu				
65					70					75					80				
Ser	Asp	Ser	Tyr	Ser	Pro	Pro	Met	Ser	Ala	Gly	Asn	Arg	Lys	Ser	Pro				
				85					90					95					
Thr	Leu	Ser	Thr	Ser	Thr	Gly	Thr	Ser	Ser	Trp	Ser	Gln	Ser	Phe	Ile				
			100					105					110						
Leu	His	Phe	Ser	Arg	Arg	Leu	Asp	Ser	Arg	Thr	Ala	Val	Leu	Arg	Pro				
		115					120					125							
Leu	Asn	Phe																	
	130																		

<210> 645
 <211> 86
 <212> PRT
 <213> homo sapiens

<400> 645

Leu 1	Thr	Asn	Met	Ser 5	Asp	His	Leu	Phe	Gly 10	Trp	Leu	Leu	Leu	Glu 15	Met
Ala	Val	Val	Met 20	Phe	Ser	Gly	Leu	Cys 25	Gln	Pro	Thr	Asp	Pro 30	Cys	Gln
Val	Leu	Glu 35	Ile	Leu	Leu	Leu	Pro 40	Arg	Cys	Tyr	Phe	Ser 45	Ala	Gly	Ile
Lys	Leu 50	Leu	Xxx	Val	Ala	Arg 55	Pro	Arg	Thr	Ser	Lys 60	Asp	Ser	Cys	Tyr
Ser 65	Ala	Thr	Val	Tyr	Thr 70	Ala	His	Leu	Ser	Tyr 75	Ser	His	Val	Leu	Ser 80
Ser	Leu	Val	Arg	Leu 85	Phe										

<210> 646
 <211> 96
 <212> PRT
 <213> homo sapiens

<400> 646

Lys 1	Ala	Pro	Asn	Pro 5	Ser	Val	Leu	His	Thr 10	Val	Arg	Met	Gln	Leu 15	Ile
Ala	Asp	Arg	Cys 20	Cys	Glu	Leu	Tyr	Ile 25	Cys	Lys	Arg	Cys	Phe 30	Thr	Thr
Ser	Ala	Gly 35	Phe	Ile	Thr	Ala	Ser 40	Trp	Ser	Arg	Val	Ala 45	Ile	Leu	Pro
Ala	Ile 50	Pro	Ala	Lys	Gln	Thr 55	Pro	Glu	Asn	Tyr 60	Pro	Leu	Arg	Ser	Gly
Val 65	Leu	Arg	Lys	Phe	Leu 70	Glu	Pro	Lys	Ile	Arg 75	Arg	Asn	Pro	Gly	Leu 80
Ser	Phe	Leu	Arg	Ser 85	Lys	Met	Tyr	Tyr	Gln 90	Leu	Arg	Pro	Gly	Glu 95	His

<210> 647
 <211> 92
 <212> PRT
 <213> homo sapiens

<400> 647

Ser 1	Ser	Ala	Cys	Arg 5	Cys	Thr	Thr	Arg	Ser 10	Thr	Gly	Gln	Gln	Ser 15	Ala
Ala	Ser	Gly	Arg 20	Cys	Gly	Gly	Pro	Arg 25	Gly	Trp	Gly	Pro	Ser 30	Thr	Gly
Ala	Thr	Pro 35	Arg	Gln	Leu	Thr	Met 40	Asn	Ile	Pro	Phe	Gln 45	Ser	Ile	His
Phe 50	Ile	Thr	Tyr	Glu	Phe	Leu 55	Gln	Glu	Gln	Val	Asn 60	Pro	His	Arg	Thr

Tyr 65	Asn	Pro	Gln	Ser	His 70	Ile	Ile	Ser	Gly	Gly 75	Leu	Ala	Gly	Ala	Leu 80
Ala	Ala	Ala	Ala	Arg 85	Gly	Pro	Leu	Asp	Val 90	Leu	Arg				

<210> 648

<211> 280

<212> PRT

<213> homo sapiens

<400> 648

Ala 1	Val	Gly	Ser	Ala 5	Ala	Leu	Phe	Lys	Asp 10	Gly	Gly	Gly	Gly	Thr 15	Ser
Ala	Ala	Glu	Ala 20	Gly	Ala	Ala	Gly	Gln 25	Arg	Leu	Arg	Ser	Val 30	Asn	Cys
Leu	Ala	Tyr 35	Asp	Glu	Ala	Ile	Met 40	Ala	Gln	Gln	Asp	Arg 45	Ile	Gln	Gln
Glu	Ile 50	Ala	Val	Gln	Asn	Pro 55	Leu	Val	Ser	Glu	Arg 60	Leu	Glu	Leu	Ser
Val 65	Leu	Tyr	Lys	Glu	Tyr 70	Ala	Glu	Asp	Asp	Asn 75	Ile	Tyr	Gln	Gln	Lys 80
Ile	Lys	Asp	Leu	His 85	Lys	Lys	Tyr	Ser	Tyr 90	Ile	Arg	Lys	Thr	Arg 95	Pro
Asp	Gly	Asn	Cys 100	Phe	Tyr	Arg	Ala	Phe 105	Gly	Phe	Ser	His	Leu 110	Glu	Ala
Leu	Leu	Asp 115	Asp	Ser	Lys	Glu	Leu 120	Gln	Arg	Phe	Lys	Ala 125	Val	Ser	Ala
Lys	Ser 130	Lys	Glu	Asp	Leu	Val 135	Ser	Gln	Gly	Phe	Thr 140	Glu	Phe	Thr	Ile
Glu 145	Asp	Phe	His	Asn	Thr 150	Phe	Met	Asp	Leu	Ile 155	Glu	Gln	Val	Glu	Lys 160
Gln	Thr	Ser	Val	Ala 165	Asp	Leu	Leu	Ala	Ser 170	Phe	Asn	Asp	Gln	Ser 175	Thr
Ser	Asp	Tyr	Leu 180	Val	Val	Tyr	Leu	Arg 185	Leu	Leu	Thr	Ser	Gly 190	Tyr	Leu
Gln	Arg	Glu 195	Ser	Lys	Phe	Phe	Glu 200	His	Phe	Ile	Glu	Gly 205	Gly	Arg	Thr
Val	Lys 210	Glu	Phe	Cys	Gln	Gln 215	Glu	Val	Glu	Pro	Met 220	Cys	Lys	Glu	Ser
Asp 225	His	Ile	His	Ile	Ile 230	Ala	Leu	Ala	Gln	Ala 235	Leu	Ser	Val	Ser	Ile 240
Gln	Val	Glu	Tyr	Met 245	Asp	Arg	Gly	Glu	Gly 250	Gly	Thr	Thr	Asn	Pro 255	His
Ile	Phe	Pro	Glu 260	Gly	Ser	Glu	Pro	Lys 265	Val	Tyr	Leu	Leu	Tyr 270	Arg	Pro

Gly His Tyr Asp Ile Leu Tyr Lys
275 280

<210> 649
<211> 244
<212> PRT
<213> homo sapiens

<400> 649

Asp 1	His	Leu	Gln	Pro 5	Gln	Lys	Asn	Leu	Cys 10	Thr	Cys	Leu	Ala	Pro 15	Glu
Arg	Gly	Gly	Gln 20	Gln	Gly	Ser	Ser	Gly 25	Leu	Glu	Pro	Ala	Leu 30	Phe	Val
Glu	Asp	Ile 35	Val	Val	Ser	Arg	Pro 40	Val	Glu	Lys	Val	Asp 45	Leu	Gly	Leu
Gly	Ala 50	Leu	Arg	Glu	Asp	Val 55	Arg	Ile	Gly	Gly	Ala 60	Ala	Leu	Ala	Ala
Val 65	His	Val	Leu	His	Leu 70	Asp	Gly	His	Ala	Glu 75	Gly	Leu	Gly	Gln	Arg 80
Asn	Asp	Val	Asp	Val 85	Val	Ala	Leu	Leu	Ala 90	His	Gly	Leu	His	Leu 95	Leu
Leu	Ala	Glu	Leu 100	Leu	Asp	Ser	Pro	Ser 105	Thr	Leu	Asp	Glu	Val 110	Leu	Glu
Glu	Leu	Ala 115	Leu	Ala	Leu	Gln	Val 120	Ala	Arg	Gly	Glu	Gln 125	Pro	Gln	Val
Asp	His 130	Lys	Val	Val	Gly	Gly 135	Ala	Leu	Val	Ile	Glu 140	Gly	Gly	Gln	Gln
Val 145	Gly	Asp	Arg	Gly	Leu 150	Leu	Leu	His	Leu	Leu 155	Asn	Gln	Val	His	Glu 160
Arg	Val	Val	Glu	Ile 165	Leu	Asn	Cys	Glu	Phe 170	Ser	Glu	Ala	Leu	Gly 175	His
Gln	Val	Phe	Leu 180	Ala	Leu	Gly	Arg	His 185	Ser	Leu	Glu	Pro	Leu 190	Gln	Leu
Leu	Ala	Val 195	Ile	Gln	Gln	Cys	Leu 200	Gln	Val	Gly	Glu	Ser 205	Glu	Ser	Pro
Ile	Glu 210	Thr	Val	Ala	Val	Arg 215	Pro	Gly	Leu	Ala	Asp 220	Val	Arg	Val	Leu
Phe 225	Val	Glu	Val	Leu	Asp 230	Leu	Leu	Leu	Ile	Asp 235	Val	Val	Ile	Phe	Ser 240
Ile	Leu	Leu	Val												

<210> 650
<211> 424
<212> PRT
<213> homo sapiens

<400> 650

Leu 1	Thr	Thr	Thr	Cys 5	Val	Ser	Ser	Ser	Ala 10	Pro	Ser	Lys	Thr	Ser 15	Leu
Ile	Met	Asn	Pro 20	His	Ala	Ser	Thr	Asn 25	Gly	Gln	Leu	Ser	Val 30	His	Thr
Pro	Lys	Arg 35	Glu	Ser	Leu	Ser	His 40	Glu	Glu	His	Pro	His 45	Ser	His	Pro
Leu	Tyr 50	Gly	His	Gly	Val	Cys 55	Lys	Trp	Pro	Gly	Cys 60	Glu	Ala	Val	Cys
Glu 65	Asp	Phe	Gln	Ser	Phe 70	Leu	Lys	His	Leu	Asn 75	Ser	Glu	His	Ala	Leu 80
Asp	Asp	Arg	Ser	Thr 85	Ala	Gln	Cys	Arg	Val 90	Gln	Met	Gln	Val	Val 95	Gln
Gln	Leu	Glu	Leu 100	Gln	Leu	Ala	Lys	Asp 105	Lys	Glu	Arg	Leu	Gln 110	Ala	Met
Met	Thr	His 115	Leu	His	Val	Lys	Ser 120	Thr	Glu	Pro	Lys	Ala 125	Ala	Pro	Gln
Pro	Leu 130	Asn	Leu	Val	Ser	Ser 135	Val	Thr	Leu	Ser	Lys 140	Ser	Ala	Ser	Glu
Ala 145	Ser	Pro	Gln	Ser	Leu 150	Pro	His	Thr	Pro	Thr 155	Thr	Pro	Thr	Ala	Pro 160
Leu	Thr	Pro	Val	Thr 165	Gln	Gly	Pro	Ser	Val 170	Ile	Thr	Thr	Thr	Ser 175	Met
His	Thr	Val	Gly 180	Pro	Ile	Arg	Arg	Arg 185	Tyr	Ser	Asp	Lys	Tyr 190	Asn	Val
Pro	Ile	Ser 195	Ser	Ala	Asp	Ile	Ala 200	Gln	Asn	Gln	Glu	Phe 205	Tyr	Lys	Asn
Ala	Glu 210	Val	Arg	Pro	Pro	Phe 215	Thr	Tyr	Ala	Ser	Leu 220	Ile	Arg	Gln	Ala
Ile 225	Leu	Glu	Ser	Pro	Glu 230	Lys	Gln	Leu	Thr	Leu 235	Asn	Glu	Ile	Tyr	Asn 240
Trp	Phe	Thr	Arg	Met 245	Phe	Ala	Tyr	Phe	Arg 250	Arg	Asn	Ala	Ala	Thr 255	Trp
Lys	Asn	Ala	Val 260	Arg	His	Asn	Leu	Ser 265	Leu	His	Lys	Cys	Phe 270	Val	Arg
Val	Glu	Asn 275	Val	Lys	Gly	Ala	Val 280	Trp	Thr	Val	Asp	Glu 285	Val	Glu	Phe
Gln	Lys 290	Arg	Arg	Pro	Gln	Lys 295	Ile	Ser	Gly	Asn	Pro 300	Ser	Leu	Ile	Lys
Asn 305	Met	Gln	Ser	Ser	His 310	Ala	Tyr	Cys	Thr	Pro 315	Leu	Asn	Ala	Ala	Leu 320
Gln	Ala	Ser	Met	Ala	Glu	Asn	Ser	Ile	Pro	Leu	Tyr	Thr	Thr	Ala	Ser

				325					330					335			
Met	Gly	Asn	Pro	Thr	Leu	Gly	Asn	Leu	Ala	Ser	Ala	Ile	Arg	Glu	Glu		
			340					345					350				
Leu	Asn	Gly	Ala	Met	Glu	His	Thr	Asn	Ser	Asn	Glu	Ser	Asp	Ser	Ser		
		355					360					365					
Pro	Gly	Arg	Ser	Pro	Met	Gln	Ala	Val	His	Pro	Val	His	Val	Lys	Glu		
	370					375					380						
Glu	Pro	Leu	Asp	Pro	Glu	Glu	Ala	Glu	Gly	Pro	Leu	Ser	Leu	Val	Thr		
385					390					395					400		
Thr	Ala	Asn	His	Ser	Pro	Asp	Phe	Asp	His	Asp	Arg	Asp	Tyr	Glu	Asp		
				405					410					415			
Glu	Pro	Val	Asn	Glu	Asp	Met	Glu										
			420														

<210> 651
 <211> 117
 <212> PRT
 <213> homo sapiens

<400> 651

Ser	Thr	Asn	Ala	Gly	Cys	Thr	Ala	Val	Arg	Ala	Thr	Ala	Cys	Lys	Arg		
1				5					10					15			
Gln	Arg	Ala	Pro	Ala	Ser	His	Asp	Asp	Pro	Pro	Ala	Cys	Glu	Val	Tyr		
			20					25					30				
Arg	Thr	Gln	Ser	Arg	Pro	Ser	Ala	Leu	Glu	Ser	Gly	Ile	Lys	Cys	His		
		35					40					45					
Ser	Leu	Gln	Val	Arg	Ile	Gly	Gly	Phe	Ser	Thr	Glu	Leu	Thr	Ser	Tyr		
	50					55					60						
Ser	Asn	Asp	Pro	Asn	Arg	Pro	Pro	Asp	Ser	Arg	His	Pro	Arg	Pro	Leu		
65					70					75					80		
Cys	His	His	Asn	His	Gln	His	Ala	His	Gly	Gly	Thr	His	Pro	Gln	Ala		
				85					90					95			
Val	Leu	Arg	Gln	Ile	Gln	Arg	Ala	His	Phe	Val	Ser	Arg	Tyr	Cys	Ala		
			100					105					110				
Glu	Pro	Arg	Ile	Leu													
			115														

<210> 652
 <211> 426
 <212> PRT
 <213> homo sapiens

<400> 652

Pro	Glu	Ala	Gly	Leu	Phe	Ser	Cys	Ser	Glu	Gln	Ser	Asp	Phe	Pro	Glu		
1				5					10					15			
His	Ile	Phe	Ile	Met	Ile	His	Thr	Asn	Leu	Lys	Lys	Lys	Phe	Ser	Cys		
			20					25					30				

Cys	Val	Leu 35	Val	Phe	Leu	Leu	Phe 40	Ala	Val	Ile	Cys	Val 45	Trp	Lys	Glu
Lys	Lys 50	Lys	Gly	Ser	Tyr	Tyr 55	Asp	Ser	Phe	Lys	Leu 60	Gln	Thr	Lys	Glu
Phe 65	Gln	Val	Leu	Lys	Ser 70	Leu	Gly	Lys	Leu	Ala 75	Met	Gly	Ser	Asp	Ser 80
Gln	Ser	Val	Ser	Ser 85	Ser	Ser	Thr	Gln	Asp 90	Pro	His	Arg	Gly	Arg 95	Gln
Thr	Leu	Gly	Ser 100	Leu	Arg	Gly	Leu	Ala 105	Lys	Ala	Lys	Pro	Glu 110	Ala	Ser
Phe	Gln	Val 115	Trp	Asn	Lys	Asp	Ser 120	Ser	Ser	Lys	Asn	Leu 125	Ile	Pro	Arg
Leu	Gln 130	Lys	Ile	Trp	Lys	Asn 135	Tyr	Leu	Ser	Met	Asn 140	Lys	Tyr	Lys	Val
Ser 145	Tyr	Lys	Gly	Pro	Gly 150	Pro	Gly	Ile	Lys	Phe 155	Ser	Ala	Glu	Ala	Leu 160
Arg	Cys	His	Leu	Arg 165	Asp	His	Val	Asn	Val 170	Ser	Met	Val	Glu	Val 175	Thr
Asp	Phe	Pro	Phe 180	Asn	Thr	Ser	Glu	Trp 185	Glu	Gly	Tyr	Leu	Pro 190	Lys	Glu
Ser	Ile	Arg 195	Thr	Lys	Ala	Gly	Pro 200	Trp	Gly	Arg	Cys	Ala 205	Val	Val	Ser
Ser	Ala 210	Gly	Ser	Leu	Lys	Ser 215	Ser	Gln	Leu	Gly	Arg 220	Glu	Ile	Asp	Asp
His 225	Asp	Ala	Val	Leu	Arg 230	Phe	Asn	Gly	Ala	Pro 235	Thr	Ala	Asn	Phe	Gln 240
Gln	Asp	Val	Gly	Thr 245	Lys	Thr	Thr	Ile	Arg 250	Leu	Met	Asn	Ser	Gln 255	Leu
Val	Thr	Thr	Glu 260	Lys	Arg	Phe	Leu	Lys 265	Asp	Ser	Leu	Tyr	Asn 270	Glu	Gly
Ile	Leu	Ile 275	Val	Trp	Asp	Pro	Ser 280	Val	Tyr	His	Ser	Asp 285	Ile	Pro	Lys
Trp	Tyr 290	Gln	Asn	Pro	Asp	Tyr 295	Asn	Phe	Phe	Asn	Asn 300	Tyr	Lys	Thr	Tyr
Arg 305	Lys	Leu	His	Pro	Asn 310	Gln	Pro	Phe	Tyr	Ile 315	Leu	Lys	Pro	Gln	Met 320
Pro	Trp	Glu	Leu	Trp 325	Asp	Ile	Leu	Gln	Glu 330	Ile	Ser	Pro	Glu	Glu 335	Ile
Gln	Pro	Asn	Pro 340	Pro	Ser	Ser	Gly	Met 345	Leu	Gly	Ile	Ile	Ile 350	Met	Met
Thr	Leu	Cys 355	Asp	Gln	Val	Asp	Ile 360	Tyr	Glu	Ser	Leu	Pro 365	Ser	Lys	Arg

Lys	Thr	Asp	Val	Cys	Tyr	Tyr	Tyr	Gln	Lys	Phe	Phe	Asp	Ser	Ala	Cys
	370					375					380				
Thr	Met	Gly	Ala	Tyr	His	Pro	Leu	Leu	Tyr	Glu	Lys	Asn	Leu	Val	Lys
385					390					395					400
His	Leu	Asn	Gln	Gly	Thr	Asp	Glu	Asp	Ile	Tyr	Leu	Leu	Gly	Lys	Ala
				405					410					415	
Thr	Leu	Pro	Gly	Phe	Arg	Thr	Ile	His	Cys						
			420					425							

<210> 653

<211> 139

<212> PRT

<213> homo sapiens

<400> 653

Arg	Cys	Val	Gln	Gly	Ser	His	Phe	Val	Leu	Ser	Arg	Lys	Thr	Ser	Leu
1				5					10					15	
Leu	Leu	Ala	Asn	Pro	Pro	Gly	Ala	Ala	Gly	Pro	Ser	Gly	Pro	Gln	Glu
			20					25					30		
Leu	Ala	Leu	Leu	Ser	Met	Gly	Gly	Lys	Val	Tyr	Trp	Val	Cys	Arg	Pro
		35					40					45			
Arg	Pro	Ile	Phe	Leu	Arg	Met	Ile	Lys	Thr	His	Leu	Cys	Trp	Phe	Met
	50					55					60				
Val	Thr	Cys	Ala	Ala	Gly	Phe	Gly	Asp	Ala	Glu	Val	Cys	Arg	Ser	Ile
65					70					75					80
Ser	Gly	Gly	Leu	Asp	Ala	Val	Leu	Pro	Phe	Ser	Leu	Trp	Cys	Trp	Leu
				85					90					95	
Cys	Gly	Leu	Cys	Gly	Thr	Phe	Cys	Pro	Leu	Ala	Arg	Cys	Thr	Leu	Gly
			100					105					110		
Arg	Gly	Gly	Cys	Gly	Cys	Ser	Ala	Arg	Ser	Val	Ala	Ala	Ala	Arg	Ser
		115					120					125			
Ala	Pro	Thr	Pro	Val	Gly	Ile	Gly	Ser	Leu	Cys					
	130					135									

<210> 654

<211> 243

<212> PRT

<213> homo sapiens

<400> 654

Trp	Arg	Gln	Leu	Ala	Arg	Gly	Trp	Gly	Ala	Leu	Ser	Arg	Ala	Ser	Cys
1				5					10					15	
Pro	Ala	Leu	Pro	Arg	Leu	Ala	Asn	Asn	Thr	Val	Arg	Met	Ala	Lys	Gly
			20					25					30		
Asp	Pro	Lys	Lys	Pro	Lys	Gly	Lys	Met	Ser	Ala	Tyr	Ala	Phe	Phe	Val
		35					40					45			

Gln	Thr	Cys	Arg	Glu	Glu	His	Lys	Lys	Lys	Asn	Pro	Glu	Val	Pro	Val
	50					55					60				
Asn	Phe	Ala	Glu	Phe	Ser	Lys	Lys	Cys	Ser	Glu	Arg	Trp	Lys	Thr	Met
65					70					75					80
Ser	Gly	Lys	Glu	Lys	Ser	Lys	Phe	Asp	Glu	Met	Ala	Lys	Ala	Asp	Lys
				85					90					95	
Val	Arg	Tyr	Asp	Arg	Glu	Met	Lys	Asp	Tyr	Gly	Pro	Ala	Lys	Gly	Gly
			100					105						110	
Lys	Lys	Lys	Lys	Asp	Pro	Asn	Ala	Pro	Lys	Arg	Pro	Pro	Ser	Gly	Phe
		115					120					125			
Phe	Leu	Phe	Cys	Ser	Glu	Phe	Arg	Pro	Lys	Ile	Lys	Ser	Thr	Asn	Pro
	130					135					140				
Gly	Ile	Ser	Ile	Gly	Asp	Val	Ala	Lys	Lys	Leu	Gly	Glu	Met	Trp	Asn
145					150					155					160
Asn	Leu	Asn	Asp	Ser	Glu	Lys	Gln	Pro	Tyr	Ile	Thr	Lys	Thr	Ala	Lys
				165					170					175	
Leu	Lys	Glu	Lys	Tyr	Glu	Lys	Asp	Val	Ala	Asp	Tyr	Lys	Ser	Lys	Gly
			180					185					190		
Lys	Phe	Asp	Gly	Ala	Lys	Gly	Pro	Ala	Lys	Val	Ala	Arg	Lys	Lys	Val
		195					200					205			
Glu	Glu	Glu	Asp	Glu	Glu	Asp	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly
	210					215						220			
Gly	Thr	Tyr	Ser	Arg	Val	Gly	Trp	Trp	Ser	Ser	Pro	Lys	Glu	Gly	Glu
225					230					235					240
Arg	Arg	Asn													

<210> 655

<211> 110

<212> PRT

<213> homo sapiens

<400> 655

Thr	Glu	Gln	Glu	Glu	Ser	Arg	Arg	Trp	Pro	Phe	Gly	Ser	Ile	Arg	Ile
1				5					10					15	
Leu	Leu	Leu	Leu	Ala	Ser	Leu	Ser	Trp	Ser	Ile	Ile	Leu	His	Phe	Pro
			20					25					30		
Ile	Ile	Ala	His	Phe	Ile	Cys	Leu	Cys	His	Phe	Ile	Lys	Phe	Arg	Phe
		35					40					45			
Leu	Phe	Pro	Gly	His	Arg	Leu	Pro	Pro	Leu	Arg	Ala	Leu	Leu	Gly	Lys
	50					55					60				
Phe	Arg	Lys	Ile	Asp	Arg	Asp	Leu	Trp	Val	Phe	Leu	Leu	Met	Phe	Phe
65					70					75					80
Ser	Ala	Cys	Leu	His	Lys	Glu	Gly	Ile	Ser	Gly	His	Leu	Ala	Leu	Trp
				85					90					95	

Phe Leu Gly Val Thr Phe Ser His Pro Asp Cys Ile Val Arg
100 105 110

<210> 656

<211> 356

<212> PRT

<213> homo sapiens

<400> 656

Val 1	Gly	Cys	Ser	His 5	Ala	Ala	Gln	Leu	His 10	Ser	Ala	Pro	Glu	Leu 15	Gln
Thr	Thr	Arg	Gln 20	Glu	Leu	Ser	His	Ala 25	Leu	Tyr	Gln	His	Asp 30	Ala	Ala
Cys	Arg	Val 35	Ile	Ala	Arg	Leu	Thr 40	Lys	Glu	Val	Thr	Ala 45	Ala	Arg	Glu
Ala	Leu 50	Ala	Thr	Leu	Lys	Pro 55	Gln	Ala	Gly	Leu	Ile 60	Val	Pro	Gln	Ala
Val 65	Pro	Ser	Ser	Gln	Pro 70	Ser	Val	Val	Gly	Ala 75	Gly	Glu	Pro	Met	Asp 80
Leu	Gly	Glu	Leu	Val 85	Gly	Met	Thr	Pro	Glu 90	Ile	Ile	Gln	Lys	Leu 95	Gln
Asp	Lys	Ala	Thr 100	Val	Leu	Thr	Thr	Glu 105	Arg	Lys	Lys	Arg	Gly 110	Lys	Thr
Val	Pro	Glu 115	Glu	Leu	Val	Lys	Pro 120	Glu	Glu	Leu	Ser	Lys 125	Tyr	Arg	Gln
Val	Ala 130	Ser	His	Val	Gly	Leu 135	His	Ser	Ala	Ser	Ile 140	Pro	Gly	Ile	Leu
Ala 145	Leu	Asp	Leu	Cys	Pro 150	Ser	Asp	Thr	Asn	Lys 155	Ile	Leu	Thr	Gly	Gly 160
Ala	Asp	Lys	Asn	Val 165	Val	Val	Phe	Asp	Lys 170	Ser	Ser	Glu	Gln	Ile 175	Leu
Ala	Thr	Leu	Lys 180	Gly	His	Thr	Lys	Lys 185	Val	Thr	Ser	Val	Val 190	Phe	His
Pro	Ser	Gln 195	Asp	Leu	Val	Phe	Ser 200	Ala	Ser	Pro	Asp	Ala 205	Thr	Ile	Arg
Ile	Trp 210	Ser	Val	Pro	Asn	Ala 215	Ser	Cys	Val	Gln	Val	Val	Arg	Ala	His
Glu 225	Ser	Ala	Val	Thr	Gly 230	Leu	Ser	Leu	His	Ala 235	Thr	Gly	Asp	Tyr	Leu 240
Leu	Ser	Ser	Ser	Asp 245	Asp	Gln	Tyr	Trp	Ala 250	Phe	Ser	Asp	Ile	Gln 255	Thr
Gly	Arg	Val	Leu 260	Thr	Lys	Val	Thr	Asp 265	Glu	Thr	Ser	Gly	Cys 270	Ser	Leu
Thr	Cys	Ala 275	Gln	Phe	His	Pro	Asp 280	Gly	Leu	Ile	Phe	Gly 285	Thr	Gly	Thr

Met	Asp	Ser	Gln	Ile	Lys	Ile	Trp	Asp	Leu	Lys	Glu	Arg	Thr	Asn	Val
	290					295					300				
Ala	Asn	Phe	Pro	Gly	His	Ser	Gly	Pro	Ile	Thr	Ser	Ile	Ala	Phe	Ser
305					310					315					320
Glu	Asn	Gly	Tyr	Tyr	Leu	Ala	Thr	Ala	Ala	Asp	Asp	Ser	Ser	Val	Lys
				325					330					335	
Leu	Trp	Asp	Leu	Arg	Lys	Leu	Arg	Thr	Leu	Arg	Leu	Cys	Ser	Trp	Ile
			340					345					350		
Thr	Thr	Leu	Arg												
		355													

<210> 657

<211> 240

<212> PRT

<213> homo sapiens

<400> 657

Leu	Ala	Gln	Ile	Pro	Glu	Leu	Asp	Arg	Gly	Val	Ile	Ser	Arg	Cys	Ser
1				5					10					15	
Gln	Val	Val	Thr	Ile	Leu	Arg	Glu	Gly	Asp	Ala	Ser	Asp	Gly	Ala	Arg
			20					25					30		
Val	Ala	Arg	Glu	Val	Gly	His	Ile	Ser	Thr	Phe	Leu	Gln	Val	Pro	Asp
		35					40					45			
Leu	Asp	Leu	Arg	Val	His	Gly	Ser	Cys	Ser	Lys	Asp	Glu	Ser	Val	Arg
	50					55					60				
Val	Glu	Leu	Cys	Thr	Gly	Glu	Arg	Ala	Ala	Gly	Gly	Leu	Ile	Cys	His
	65				70					75				80	
Leu	Gly	Glu	His	Thr	Pro	Cys	Leu	Asp	Val	Arg	Glu	Ser	Pro	Val	Leu
				85					90					95	
Ile	Ile	Gly	Gly	Ala	Gln	Glu	Ile	Val	Ala	Ser	Gly	Met	Lys	Ala	Glu
			100					105					110		
Ala	Cys	His	Ser	Thr	Leu	Met	Gly	Pro	Asn	His	Leu	Tyr	Thr	Arg	Gly
		115					120					125			
Ile	Gly	Asp	Arg	Pro	Asn	Pro	Asp	Ser	Gly	Ile	Gly	Gly	Ser	Arg	Lys
	130					135					140				
His	Gln	Val	Leu	Gly	Arg	Val	Lys	His	His	Ala	Gly	Asp	Leu	Leu	Gly
	145				150					155					160
Met	Ala	Phe	Glu	Gly	Ser	Gln	Asp	Leu	Phe	Arg	Thr	Phe	Val	Lys	His
				165					170					175	
Asn	Asp	Ile	Phe	Ile	Arg	Pro	Thr	Ser	Glu	Asp	Leu	Val	Gly	Val	Gly
			180					185					190		
Arg	Ala	Glu	Val	Gln	Gly	Gln	Asp	Pro	Arg	Asn	Ala	Gly	Thr	Val	Gln
		195					200					205			
Pro	His	Val	Gly	Cys	His	Leu	Pro	Val	Phe	Ala	Glu	Leu	Phe	Trp	Leu

210						215						220					
His	Gln	Leu	Leu	Arg	His	Ser	Leu	Pro	Ser	Leu	Leu	Ala	Leu	Arg	Gly		
225					230					235					240		

<210> 658
 <211> 162
 <212> PRT
 <213> homo sapiens

<400> 658

Glu	His	Asn	Ser	Lys	Ser	Ser	Phe	Ile	Asn	Ile	Lys	Arg	Ala	Tyr	Leu		
1				5					10					15			
Ala	Lys	Asp	Thr	Gln	Ile	Lys	Glu	Ser	Leu	Trp	Leu	Arg	Thr	Gln	Gly		
			20					25					30				
Arg	Glu	Val	Pro	Gly	Leu	Cys	Pro	Cys	Trp	Ala	Arg	Arg	Arg	Leu	Gly		
		35					40					45					
Thr	Lys	Trp	Glu	Lys	Cys	Trp	Glu	Gly	Leu	Ser	Gly	Arg	Gly	His	Lys		
	50					55					60						
Ser	Ser	Gly	Gly	Gln	His	Cys	Arg	Gln	Val	Met	Gly	Gly	Thr	His	Gly		
65					70					75					80		
Asp	Leu	Ala	Ala	Asn	Ser	Cys	Cys	Gly	Gly	Val	Ser	Leu	Val	Leu	Pro		
				85					90				95				
Pro	Gly	Gly	Pro	Leu	Leu	Gly	Ser	Trp	Arg	Gly	Pro	Thr	Lys	Gly	His		
			100					105					110				
Arg	Thr	Gly	Ser	Pro	Gly	Trp	Leu	Val	Gln	Leu	Gly	Met	Lys	Ala	Arg		
		115					120					125					
Glu	Lys	Arg	Val	Leu	Cys	Ser	Gly	Arg	Ile	Gly	Pro	Asp	Ala	Glu	Ala		
	130					135					140						
Glu	Ala	Leu	Pro	Val	Thr	Cys	Gly	Arg	Ser	Ala	Leu	Ser	Leu	Pro	Gly		
145					150					155					160		
Thr	Leu																

<210> 659
 <211> 148
 <212> PRT
 <213> homo sapiens

<400> 659

Arg	Leu	Trp	Thr	Ala	Phe	His	Gly	Leu	Arg	Ala	Gly	Asp	Glu	Ala	Thr		
1				5					10					15			
Arg	Arg	Pro	Gly	Leu	Pro	Glu	His	Leu	His	Gly	Pro	Ala	Val	Ser	His		
			20					25					30				
Arg	Gly	Asp	Gly	Gln	Arg	Asp	Pro	Ala	Tyr	Leu	Cys	Trp	Gln	Gln	Glu		
		35					40					45					
Arg	His	Gly	Ala	Pro	Glu	Glu	Arg	Tyr	His	Pro	Cys	Pro	Gly	Pro	Ser		
	50					55					60						

Gln 65	Arg	Val	Pro	Gly	Arg 70	Asp	Arg	Ala	Glu	Arg 75	Pro	His	Val	Thr	Gly 80
Ser	Ala	Ser	Ala	Ser 85	Ala	Ser	Gly	Pro	Ile 90	Arg	Pro	Leu	Gln	Ser 95	Thr
Arg	Phe	Ser	Leu 100	Ala	Phe	Ile	Pro	Ser 105	Cys	Thr	Asn	His	Pro 110	Gly	Leu
Pro	Val	Leu 115	Cys	Pro	Leu	Val	Gly 120	Pro	Leu	Gln	Glu	Pro 125	Arg	Ser	Gly
Pro	Pro 130	Gly	Gly	Ser	Thr	Lys 135	Asp	Thr	Pro	Pro	Gln 140	Gln	Glu	Leu	Ala
Ala 145	Arg	Ser	Pro												

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